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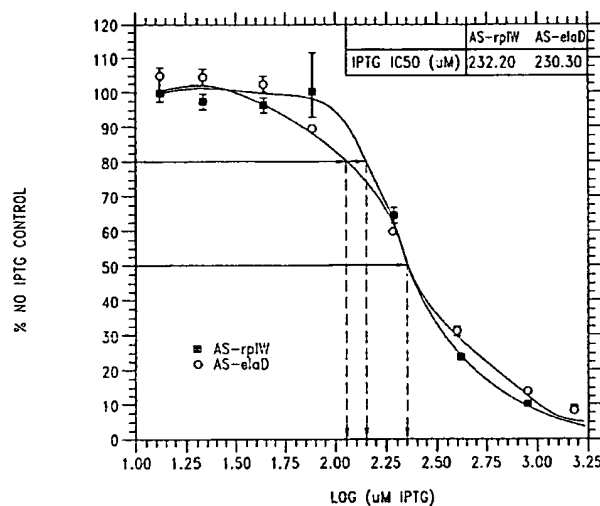
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(54) Title: **IDENTIFICATION OF ESSENTIAL GENES IN MICROORGANISMS**

(57) Abstract: The sequences of antisense nucleic acids which inhibit the proliferation of prokaryotes are disclosed. Cell-based assays which employ the antisense nucleic acids to identify and develop antibiotics are also disclosed. The antisense nucleic acids can also be used to identify proteins required for proliferation, express these proteins or portions thereof, obtain antibodies capable of specifically binding to the expressed proteins, and to use those expressed proteins as a screen to isolate candidate molecules for rational drug discovery programs. The nucleic acids can also be used to screen for homologous nucleic acids that are required for proliferation in cells other than *Staphylococcus aureus*, *Salmonella typhimurium*, *Klebsiella pneumoniae*, and *Pseudomonas aeruginosa*. The nucleic acids of the present invention can also be used in various assay systems to screen for proliferation required genes in other organisms.



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IDENTIFICATION OF ESSENTIAL GENES IN MICROORGANISMSSequence Listing

The present application is being filed along with quadruplicate copies of a CD-ROM marked "Copy 1 - SEQUENCE LISTING PART," "Copy 2 - SEQUENCE LISTING PART,"
5 "Copy 3 - SEQUENCE LISTING PART," and "CRF" containing a Sequence Listing in electronic format. The quadruplicate copies of the CD-ROM each contain a file entitled 034VPC_final.ST25.txt, created on March 15, 2002, which is 181,323,311 bytes in size.

Background of the Invention

Since the discovery of penicillin, the use of antibiotics to treat the ravages of bacterial
10 infections has saved millions of lives. With the advent of these "miracle drugs," for a time it was popularly believed that humanity might, once and for all, be saved from the scourge of bacterial infections. In fact, during the 1980s and early 1990s, many large pharmaceutical companies cut back or eliminated antibiotics research and development. They believed that infectious disease caused by bacteria finally had been conquered and that markets for new drugs were limited.
15 Unfortunately, this belief was overly optimistic.

The tide is beginning to turn in favor of the bacteria as reports of drug resistant bacteria become more frequent. The United States Centers for Disease Control announced that one of the most powerful known antibiotics, vancomycin, was unable to treat an infection of the common *Staphylococcus aureus* (staph). This organism is commonly found in our environment and is
20 responsible for many nosocomial infections. The import of this announcement becomes clear when one considers that vancomycin was used for years to treat infections caused by *Staphylococcus* species as well as other stubborn strains of bacteria. In short, bacteria are becoming resistant to our most powerful antibiotics. If this trend continues, it is conceivable that we will return to a time when what are presently considered minor bacterial infections are fatal diseases.

Over-prescription and improper prescription habits by some physicians have caused an
25 indiscriminate increase in the availability of antibiotics to the public. The patients are also partly responsible, since they will often improperly use the drug, thereby generating yet another population of bacteria that is resistant, in whole or in part, to traditional antibiotics.

The bacterial pathogens that have haunted humanity remain, in spite of the development of
30 modern scientific practices to deal with the diseases that they cause. Drug resistant bacteria are now an increasing threat to the health of humanity. A new generation of antibiotics is needed to once again deal with the pending health threat that bacteria present.

Discovery of New Antibiotics

As more and more bacterial strains become resistant to the panel of available antibiotics,
35 new antibiotics are required to treat infections. In the past, practitioners of pharmacology would have to rely upon traditional methods of drug discovery to generate novel, safe and efficacious compounds for the treatment of disease. Traditional drug discovery methods involve blindly testing potential drug candidate-molecules, often selected at random, in the hope that one might prove to be

an effective treatment for some disease. The process is painstaking and laborious, with no guarantee of success. Today, the average cost to discover and develop a new drug exceeds US \$500 million, and the average time from laboratory to patient is 15 years. Improving this process, even incrementally, would represent a huge advance in the generation of novel antimicrobial agents.

5 Newly emerging practices in drug discovery utilize a number of biochemical techniques to provide for directed approaches to creating new drugs, rather than discovering them at random. For example, gene sequences and proteins encoded thereby that are required for the proliferation of a cell or microorganism make excellent targets since exposure of bacteria to compounds active against these targets would result in the inactivation of the cell or microorganism. Once a target is
10 identified, biochemical analysis of that target can be used to discover or to design molecules that interact with and alter the functions of the target. Use of physical and computational techniques to analyze structural and biochemical properties of targets in order to derive compounds that interact with such targets is called rational drug design and offers great potential. Thus, emerging drug discovery practices use molecular modeling techniques, combinatorial chemistry approaches, and
15 other means to produce and screen and/or design large numbers of candidate compounds.

Nevertheless, while this approach to drug discovery is clearly the way of the future, problems remain. For example, the initial step of identifying molecular targets for investigation can be an extremely time consuming task. It may also be difficult to design molecules that interact with the target by using computer modeling techniques. Furthermore, in cases where the function of the
20 target is not known or is poorly understood, it may be difficult to design assays to detect molecules that interact with and alter the functions of the target. To improve the rate of novel drug discovery and development, methods of identifying important molecular targets in pathogenic cells or microorganisms and methods for identifying molecules that interact with and alter the functions of such molecular targets are urgently required.

25 *Escherichia coli* represents an excellent model system to understand bacterial biochemistry and physiology. The estimated 4288 genes scattered along the 4.6×10^6 base pairs of the *Escherichia coli* (*E. coli*) chromosome offer tremendous promise for the understanding of bacterial biochemical processes. In turn, this knowledge will assist in the development of new tools for the diagnosis and treatment of bacteria-caused human disease. The entire *E. coli* genome has been
30 sequenced, and this body of information holds a tremendous potential for application to the discovery and development of new antibiotic compounds. Yet, in spite of this accomplishment, the general functions or roles of many of these genes are still unknown. For example, the total number of proliferation-required genes contained within the *E. coli* genome is unknown, but has been variously estimated at around 200 to 700 (Armstrong, K.A. and Fan, D.P. Essential Genes in the
35 *metB-malB* Region of *Escherichia coli* K12, 1975, J. Bacteriol. 126: 48-55).

Staphylococcus aureus is a Gram positive microorganism which is the causative agent of many infectious diseases. Local infection by *Staphylococcus aureus* can cause abscesses on skin and cellulitis in subcutaneous tissues and can lead to toxin-related diseases such as toxic shock and

scalded skin syndromes. *Staphylococcus aureus* can cause serious systemic infections such as osteomyelitis, endocarditis, pneumonia, and septicemia. *Staphylococcus aureus* is also a common cause of food poisoning, often arising from contact between prepared food and infected food industry workers. Antibiotic resistant strains of *Staphylococcus aureus* have recently been
5 identified, including those that are now resistant to all available antibiotics, thereby severely limiting the options of care available to physicians.

Pseudomonas aeruginosa is an important Gram negative opportunistic pathogen. It is the most common Gram negative found in nosocomial infections. *P. aeruginosa* is responsible for 16% of nosocomial pneumonia cases, 12% of hospital-acquired urinary tract infections, 8% of surgical
10 wound infections, and 10% of bloodstream infections. Immunocompromised patients, such as neutropenic cancer and bone marrow transplant patients, are particularly susceptible to opportunistic infections. In this group of patients, *P. aeruginosa* is responsible for pneumonia and septicemia with attributable deaths reaching 30%. *P. aeruginosa* is also one of the most common and lethal pathogens responsible for ventilator-associated pneumonia in intubated patients, with directly
15 attributable death rates reaching 38%. Although *P. aeruginosa* outbreaks in burn patients are rare, it is associated with 60% death rates. In the AIDS population, *P. aeruginosa* is associated with 50% of deaths. Cystic fibrosis patients are characteristically susceptible to chronic infection by *P. aeruginosa*, which is responsible for high rates of illness and death. Current antibiotics work poorly for CF infections (Van Delden & Igelwsky. 1998. Emerging Infectious Diseases 4:551-560;
20 references therein).

The gram negative enteric bacterial genus, *Salmonella*, encompasses at least 2 species. One of these, *S. enterica*, is divided into multiple subspecies and thousands of serotypes or serovars (Brenner, et al. 2000 J. Clin. Microbiol. 38:2465-2467). The *S. enterica* human pathogens include serovars Typhi, Paratyphi, Typhimurium, Choleraesuis, and many others deemed so closely related
25 that they are variants of a widespread species. Worldwide, disease in humans caused by *Salmonella* is a very serious problem. In many developing countries, *S. enterica* ser. Typhi still causes often-fatal typhoid fever. This problem has been reduced or eliminated in wealthy industrial states. However, enteritis induced by *Salmonella* is widespread and is the second most common disease caused by contaminated food in the United States (Edwards, BH 1999 "Salmonella and Shigella
30 species" Clin. Lab Med. 19(3):469-487). Though usually self-limiting in healthy individuals, others such as children, seniors, and those with compromising illnesses can be at much greater risk of serious illness and death.

Some *S. enterica* serovars (e.g. Typhimurium) cause a localized infection in the gastrointestinal tract. Other serovars (i.e. Typhi and Paratyphi) cause a much more serious systemic
35 infection. In animal models, these roles can be reversed which has allowed the use of the relatively safe *S. enterica* ser. Typhimurium as a surrogate in mice for the typhoid fever agent, *S. enterica* ser. Typhi. In mice, *S. enterica* ser Typhimurium causes a systemic infection similar in outcome to typhoid fever. Years of study of the *Salmonella* have led to the identification of many determinants

of virulence in animals and humans. *Salmonella* is interesting in its ability to localize to and invade the intestinal epithelium, induce morphologic changes in target cells via injection of certain cell-remodeling proteins, and to reside intracellularly in membrane-bound vesicles (Wallis, TS and Galyov, EE 2000 "Molecular basis of *Salmonella*-induced enteritis." Molec. Microb. 36:997-1005; Falkow, S "The evolution of pathogenicity in *Escherichia*, *Shigella*, and *Salmonella*," Chap. 149 in Neidhardt, et al. eds pp 2723-2729; Gulig, PA "Pathogenesis of Systemic Disease," Chap. 152 in Neidhardt, et al. ppp 2774-2787). The immediate infection often results in a severe watery diarrhea but *Salmonella* also can establish and maintain a subclinical carrier state in some individuals. Spread is via food contaminated with sewage.

10 The gene products implicated in *Salmonella* pathogenesis include type three secretion systems (TTSS), proteins affecting cytoplasmic structure of the target cells, many proteins carrying out functions necessary for survival and proliferation of *Salmonella* in the host, as well as "traditional" factors such as endotoxin and secreted exotoxins. Additionally, there must be factors mediating species-specific illnesses. Despite this most of the genomes of *S. enterica* ser. Typhi (see
15 http://www.sanger.ac.uk/Projects/S_typhi/ for the genome database) and *S. enterica* ser. Typhimurium (see <http://genome.wustl.edu/gsc/bacterial/salmonella.shtml> for the genome database) are highly conserved and are mutually useful for gene identification in multiple serovars. The *Salmonella* are a complex group of enteric bacteria causing disease similar to but distinct from other gram negative enterics such as *E. coli* and have been a focus of biomedical research for the
20 last century.

Enterococcus faecalis, a Gram positive bacterium, is by far the most common member of the enterococci to cause infections in humans. *Enterococcus faecium* generally accounts for less than 20% of clinical isolates. Enterococci infections are mostly hospital-acquired though they are also associated with some community-acquired infections. Of nosocomial infections enterococci
25 account for 12% of bacteremia, 15% of surgical wound infections, 14% of urinary tract infections, and 5 to 15% of endocarditis cases (Huycke, M. M., D. F., Sahm and M. S. Gilmore. 1998. Emerging Infectious Diseases 4:239-249). Additionally enterococci are frequently associated with intraabdominal and pelvic infections. Enterococci infections are often hard to treat because they are resistant to a vast array of antimicrobial drugs, including aminoglycosides, penicillin, ampicillin
30 and vancomycin. The development of multiple-drug resistant (MDR) enterococci has made this bacteria a major concern for treating nosocomial infections.

Current drug discovery methods involve screening large number of prospective therapeutic compounds to identify those that are effective therapeutic agents or that can be optimized to provide an effective therapeutic agents. For example, the compounds to be evaluated for therapeutic
35 activity may be members of a library of compounds generated by combinatorial chemistry or members of a library of natural products.

Unfortunately, current methods are laborious and time consuming and may yield compounds which have already been identified or which act on gene products which are already

targeted by an existing therapeutic agent. In addition, a large number of compounds have been identified which have antimicrobial activity but which cannot be administered to individuals suffering from infection due to the fact that their targets are unknown.

The above reasons underscore the urgency of developing new antibiotics that are effective against *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, and *Salmonella typhimurium*. Accordingly, there is an urgent need for more novel methods to identify and characterize bacterial genomic sequences that encode gene products involved in proliferation, and are thereby potential new targets for antibiotic development. Likewise, there is a need for rapid screening techniques which yield novel compounds or compounds which act on novel targets as well as a need for methods which permit the identification of the target on which a compound with antimicrobial activity acts.

Prior to the present invention, the discovery of *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, and *Salmonella typhimurium* genes required for proliferation of the microorganism was a painstaking and slow process. Rapid screening techniques for identifying novel targets on which novel compounds act were undeveloped. While the detection and identification of new cellular drug targets within a *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, and *Salmonella typhimurium* cell is key for novel antibiotic development and effective treatment, the current methods of drug target discovery available prior to this invention have required painstaking processes requiring years of effort.

Summary of the Invention

Some aspects of the present invention are described in the numbered paragraphs below.

1. A purified or isolated nucleic acid sequence comprising a nucleotide sequence consisting essentially of one of SEQ ID NOs: 1-6213, wherein expression of said nucleic acid inhibits proliferation of a cell.
2. The nucleic acid sequence of Paragraph 1, wherein said nucleotide sequence is complementary to at least a portion of a coding sequence of a gene whose expression is required for proliferation of a cell.
3. The nucleic acid of Paragraph 1, wherein said nucleic acid sequence is complementary to at least a portion of a nucleotide sequence of an RNA required for proliferation of a cell.
4. The nucleic acid of Paragraph 3, wherein said RNA is an RNA comprising a sequence of nucleotides encoding more than one gene product.
5. A purified or isolated nucleic acid comprising a fragment of one of SEQ ID NOs: 1-6213, said fragment selected from the group consisting of fragments comprising at least 10, at least 20, at least 25, at least 30, at least 50 and more than 50 consecutive nucleotides of one of SEQ ID NOs: 1-6213.

6. The fragment of Paragraph 5, wherein said fragment is included in a nucleic acid obtained from an organism selected from the group consisting of *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* and any species falling within the genera of any of the above species.

7. The fragment of Paragraph 5, wherein said fragment is included in a nucleic acid obtained from an organism other than *Escherichia coli*.

8. A vector comprising a promoter operably linked to the nucleic acid of any one of Paragraphs 1-7.

9. The vector of Paragraph 8, wherein said promoter is active in a microorganism selected from the group consisting of *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*,

Mycobacterium leprae, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*,
 5 *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*,
 10 *Yersinia pestis* and any species falling within the genera of any of the above species.

10. A host cell containing the vector of Paragraph 8 or Paragraph 9.

11. A purified or isolated antisense nucleic acid comprising a nucleotide sequence complementary to at least a portion of an intragenic sequence, intergenic sequence, sequences spanning at least a portion of two or more genes, 5' noncoding region, or 3' noncoding region
 15 within an operon comprising a proliferation-required gene whose activity or expression is inhibited by an antisense nucleic acid comprising the nucleotide sequence of one of SEQ ID NOs.: 1-6213.

12. The purified or isolated antisense nucleic acid of Paragraph 11, wherein said antisense nucleic acid is complementary to a nucleic acid from an organism selected from the group consisting of *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*,
 20 *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*,
 25 *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*,
 30 *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*,
 35 *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma*

urealyticum, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* and any species falling within the genera of any of the above species.

13. The purified or isolated antisense nucleic acid of Paragraph 11, wherein said nucleotide sequence is complementary to a nucleotide sequence of a nucleic acid from an organism other than *E. coli*.

14. The purified or isolated antisense nucleic acid of Paragraph 11, wherein said proliferation-required gene comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397.

15. A purified or isolated nucleic acid comprising a nucleotide sequence having at least 70% identity to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 1-6213, fragments comprising at least 25 consecutive nucleotides of SEQ ID NOS.: 1-6213, the nucleotide sequences complementary to SEQ ID NOS.: 1-6213 and the sequences complementary to fragments comprising at least 25 consecutive nucleotides of SEQ ID NOS.: 1-6213 as determined using BLASTN version 2.0 with the default parameters.

16. The purified or isolated nucleic acid of Paragraph 15, wherein said nucleic acid is obtained from an organism selected from the group consisting of *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* and any species falling within the genera of any of the above species.

17. The nucleic acid of Paragraph 15, wherein said nucleic acid is obtained from an organism other than *E. coli*.

18. A vector comprising a promoter operably linked to a nucleic acid encoding a polypeptide whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence of any one of SEQ ID NOs.: 1-6213.

19. The vector of Paragraph 18, wherein said nucleic acid encoding said polypeptide is
 5 obtained from an organism selected from the group consisting of *Acinetobacter baumannii*,
Anaplasma marginale, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella*
pertussis, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia*
mallei, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis*
glabrata), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*,
 10 *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia*
pneumoniae, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*,
Clostridium difficile, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*,
Cryptococcus neoformans, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*,
Escherichia coli, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella*
 15 *pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*,
Mycobacterium avium, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*,
Mycoplasma genitalium, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*,
Nocardia asteroides, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*,
Proteus mirabilis, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas*
 20 *syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*,
Salmonella typhi, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*,
Shigella sonnei, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*,
Streptococcus pneumoniae, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*,
Ureaplasma urealyticum, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia*
 25 *enterocolitica*, *Yersinia pestis* and any species falling within the genera of any of the above species.

20. The vector of Paragraph 18, wherein said nucleotide sequence encoding said polypeptide is obtained from an organism other than *E. coli*.

21. A host cell containing the vector of Paragraph 18.

22. The vector of Paragraph 18, wherein said polypeptide comprises a polypeptide
 30 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 42398-
 78581.

23. The vector of Paragraph 18, wherein said promoter is operably linked to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397.

24. A purified or isolated polypeptide comprising a polypeptide whose expression is
 35 inhibited by an antisense nucleic acid comprising a nucleotide sequence of any one of SEQ ID
 NOs.: 1-6213, or a fragment selected from the group consisting of fragments comprising at least 5,

at least 10, at least 20, at least 30, at least 40, at least 50, at least 60 or more than 60 consecutive amino acids of one of the said polypeptides.

25. The polypeptide of Paragraph 24, wherein said polypeptide comprises an amino acid sequence of any one of SEQ ID NOs.: 42398-78581 or a fragment comprising at least 5, at least 10, at least 20, at least 30, at least 40, at least 50, at least 60 or more than 60 consecutive amino acids of a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42398-78581.

26. The polypeptide of Paragraph 24, wherein said polypeptide is obtained from an organism selected from the group consisting of *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* and any species falling within the genera of any of the above species.

27. The polypeptide of Paragraph 24, wherein said polypeptide is obtained from an organism other than *E. coli*.

28. A purified or isolated polypeptide comprising a polypeptide having at least 25% amino acid identity to a polypeptide whose expression is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, or at least 25% amino acid identity to a fragment comprising at least 10, at least 20, at least 30, at least 40, at least 50, at least 60 or more than 60 consecutive amino acids of a polypeptide whose expression is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 as determined using FASTA version 3.0t78 with the default parameters.

29. The polypeptide of Paragraph 28, wherein said polypeptide has at least 25% identity to a polypeptide comprising one of SEQ ID NOs: 42398-78581 or at least 25% identity to a fragment comprising at least 5, at least 10, at least 20, at least 30, at least 40, at least 50, at least 60 or more than 60 consecutive amino acids of a polypeptide comprising one of SEQ ID NOs.: 42398-78581 as determined using FASTA version 3.0t78 with the default parameters.

30. The polypeptide of Paragraph 28, wherein said polypeptide is obtained from an organism selected from the group consisting of *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* and any species falling within the genera of any of the above species.

31. The polypeptide of Paragraph 28, wherein said polypeptide is obtained from an organism other than *E. coli*.

32. An antibody capable of specifically binding the polypeptide of one of Paragraphs 28-31.

33. A method of producing a polypeptide, comprising introducing a vector comprising a promoter operably linked to a nucleic acid comprising a nucleotide sequence encoding a polypeptide whose expression is inhibited by an antisense nucleic acid comprising one of SEQ ID NOs.: 1-6213 into a cell.

34. The method of Paragraph 33, further comprising the step of isolating said polypeptide.

35. The method of Paragraph 33, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42398-78581.

36. The method of Paragraph 33, wherein said nucleic acid encoding said polypeptide is obtained from an organism selected from the group consisting of *Acinetobacter baumannii*,
 5 *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*,
 10 *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*,
 15 *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*,
 20 *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* and any species falling within the genera of any of the above species.

25 37. The method of Paragraph 33, wherein said nucleic acid encoding said polypeptide is obtained from an organism other than *E. coli*.

38. The method of Paragraph 33, wherein said promoter is operably linked to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397.

30 39. A method of inhibiting proliferation of a cell in an individual comprising inhibiting the activity or reducing the amount of a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 or inhibiting the activity or reducing the amount of a nucleic acid encoding said gene product.

35 40. The method of Paragraph 39, wherein said method comprises inhibiting said activity or reducing said amount of a gene product in an organism selected from the group consisting of *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*,

Burkholderia fungorum, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*,
 5 *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*,
 10 *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*,
 15 *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* and any species falling within the genera of any of the above species.

20 41. The method of Paragraph 39, wherein said method comprises inhibiting said activity or reducing said amount of a gene product in an organism other than *E. coli*.

42. The method of Paragraph 39, wherein said gene product is present in an organism other than *E. coli*.

25 43. The method of Paragraph 39, wherein said gene product comprises a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs.: 42398-78581.

44. A method for identifying a compound which influences the activity of a gene product required for proliferation, said gene product comprising a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, said method comprising:

30 contacting said gene product with a candidate compound; and
 determining whether said compound influences the activity of said gene product.

45. The method of Paragraph 44, wherein said gene product is from an organism selected from the group consisting of *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*,
 35 *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*,

Clostridium acetobutylicum, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*,
 5 *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*,
 10 *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*,
 15 *Yersinia pestis* and any species falling within the genera of any of the above species.

46. The method of Paragraph 44, wherein said gene product is from an organism other than *E. coli*.

47. The method of Paragraph 44, wherein said gene product is a polypeptide and said activity is an enzymatic activity.

20 48. The method of Paragraph 44, wherein said gene product is a polypeptide and said activity is a carbon compound catabolism activity.

49. The method of Paragraph 44, wherein said gene product is a polypeptide and said activity is a biosynthetic activity.

25 50. The method of Paragraph 44, wherein said gene product is a polypeptide and said activity is a transporter activity.

51. The method of Paragraph 44, wherein said gene product is a polypeptide and said activity is a transcriptional activity.

52. The method of Paragraph 44, wherein said gene product is a polypeptide and said activity is a DNA replication activity.

30 53. The method of Paragraph 44, wherein said gene product is a polypeptide and said activity is a cell division activity.

54. The method of Paragraph 44, wherein said gene product is an RNA.

35 55. The method of Paragraph 44, wherein said gene product is a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42398-78581.

56. A compound identified using the method of Paragraph 44.

57. A method for identifying a compound or nucleic acid having the ability to reduce the activity or level of a gene product required for proliferation, said gene product comprising a

gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, said method comprising:

- (a) contacting a target gene or RNA encoding said gene product with a candidate compound or nucleic acid; and
- (b) measuring an activity of said target.

58. The method of Paragraph 57, wherein said target gene or RNA is from an organism selected from the group consisting of *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* and any species falling within the genera of any of the above species.

59. The method of Paragraph 57, wherein said target gene or RNA is from an organism other than *E. coli*.

60. The method of Paragraph 57, wherein said gene product is from an organism other than *E. coli*.

61. The method of Paragraph 57, wherein said target is a messenger RNA molecule and said activity is translation of said messenger RNA.

62. The method of Paragraph 57, wherein said target is a messenger RNA molecule and said activity is transcription of a gene encoding said messenger RNA.

63. The method of Paragraph 57, wherein said target is a gene and said activity is transcription of said gene.

64. The method of Paragraph 57, wherein said target is a nontranslated RNA and said activity is processing or folding of said nontranslated RNA or assembly of said nontranslated RNA into a protein/RNA complex.

65. The method of Paragraph 57, wherein said target is a messenger RNA molecule encoding a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOS.: 42398-78581.

66. The method of Paragraph 57, wherein said target comprises a nucleic acid selected from the group consisting of SEQ ID NOS.: 6214-42397.

67. A compound or nucleic acid identified using the method of Paragraph 57.

68. A method for identifying a compound which reduces the activity or level of a gene product required for proliferation of a cell, wherein the activity or expression of said gene product is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 1-6213, said method comprising the steps of:

(a) providing a sublethal level of an antisense nucleic acid comprising a nucleotide sequence complementary to a nucleic acid comprising a nucleotide sequence encoding said gene product in a cell to reduce the activity or amount of said gene product in said cell, thereby producing a sensitized cell;

(b) contacting said sensitized cell with a compound; and

(c) determining the degree to which said compound inhibits proliferation of said sensitized cell relative to a cell which does not contain said antisense nucleic acid.

69. The method of Paragraph 68, wherein said determining step comprises determining whether said compound inhibits the growth of said sensitized cell to a greater extent than said compound inhibits the growth of a nonsensitized cell.

70. The method of Paragraph 68, wherein said cell is a Gram positive bacterium.

71. The method of Paragraph 68, wherein said Gram positive bacterium is selected from the group consisting of *Staphylococcus* species, *Streptococcus* species, *Enterococcus* species, *Mycobacterium* species, *Clostridium* species, and *Bacillus* species.

72. The method of Paragraph 68, wherein said bacterium is *Staphylococcus aureus*.

73. The method of Paragraph 72, wherein said *Staphylococcus* species is coagulase negative.

74. The method of Paragraph 72, wherein said bacterium is selected from the group consisting of *Staphylococcus aureus* RN450 and *Staphylococcus aureus* RN4220.

75. The method of Paragraph 68, wherein said cell is an organism selected from the group consisting of *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*),

Candida dubliniensis, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*,
5 *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*,
10 *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*,
15 *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* and any species falling within the genera of any of the above species.

76. The method of Paragraph 68, wherein said cell is not an *E. coli* cell.

77. The method of Paragraph 68, wherein said gene product is from an organism other than *E. coli*.

20 78. The method of Paragraph 68, wherein said antisense nucleic acid is transcribed from an inducible promoter.

79. The method of Paragraph 68, further comprising the step of contacting said cell with a concentration of inducer which induces transcription of said antisense nucleic acid to a sublethal level.

25 80. The method of Paragraph 68, wherein growth inhibition is measured by monitoring optical density of a culture growth solution.

81. The method of Paragraph 68, wherein said gene product is a polypeptide.

82. The method of Paragraph 81, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42398-78581.

30 83. The method of Paragraph 68, wherein said gene product is an RNA.

84. The method of Paragraph 68, wherein nucleic acid encoding said gene product comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397.

85. A compound identified using the method of Paragraph 68.

86. A method for inhibiting cellular proliferation comprising introducing an effective
35 amount of a compound with activity against a gene whose activity or expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 or a compound with activity against the product of said gene into a population of cells expressing said gene.

87. The method of Paragraph 86, wherein said compound is an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, or a proliferation-inhibiting portion thereof.

88. The method of Paragraph 86, wherein said proliferation inhibiting portion of one of
5 SEQ ID NOs.: 1-6213 is a fragment comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 51 consecutive nucleotides of one of SEQ ID NOs.: 1-6213.

89. The method of Paragraph 86, wherein said population is a population of Gram positive bacteria.

90. The method of Paragraph 89, wherein said population of Gram positive bacteria is
10 selected from the group consisting of a population of *Staphylococcus* species, *Streptococcus* species, *Enterococcus* species, *Mycobacterium* species, *Clostridium* species, and *Bacillus* species.

91. The method of Paragraph 86, wherein said population is a population of *Staphylococcus aureus*.

92. The method of Paragraph 91, wherein said population is a population of a
15 bacterium selected from the group consisting of *Staphylococcus aureus* RN450 and *Staphylococcus aureus* RN4220.

93. The method of Paragraph 86, wherein said population is a population of a bacterium selected from the group consisting of *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*,
25 *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*,
30 *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*,
35 *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* and any species falling within the genera of any of the above species.

94. The method of Paragraph 86, wherein said population is a population of an organism other than *E. coli*.

95. The method of Paragraph 86, wherein said product of said gene is from an organism other than *E. coli*.

5 96. The method of Paragraph 86, wherein said gene encodes a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42398-78581.

97. The method of Paragraph 86, wherein said gene comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397.

10 98. A composition comprising an effective concentration of an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, or a proliferation-inhibiting portion thereof in a pharmaceutically acceptable carrier.

99. The composition of Paragraph 98, wherein said proliferation-inhibiting portion of one of SEQ ID NOs.: 1-6213 comprises at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive nucleotides of one of SEQ ID NOs.: 1-6213.

15 100. A method for inhibiting the activity or expression of a gene in an operon required for proliferation wherein the activity or expression of at least one gene in said operon is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-6213, said method comprising contacting a cell in a cell population with an antisense nucleic acid complementary to at least a portion of said operon.

20 101. The method of Paragraph 100, wherein said antisense nucleic acid comprises a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 or a proliferation-inhibiting portion thereof.

102. The method of Paragraph 100, wherein said cell is selected from the group consisting of *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*,

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- Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* and any species falling within the genera of any of the above species.
103. The method of Paragraph 100, wherein said cell is not an *E. coli* cell.
104. The method of Paragraph 100, wherein said gene is from an organism other than *E. coli*.
105. The method of Paragraph 100, wherein said cell is contacted with said antisense nucleic acid by introducing a plasmid which expresses said antisense nucleic acid into said cell population.
106. The method of Paragraph 100, wherein said cell is contacted with said antisense nucleic acid by introducing a phage which encodes said antisense nucleic acid into said cell population.
107. The method of Paragraph 100, wherein said cell is contacted with said antisense nucleic acid by expressing said antisense nucleic acid from the chromosome of cells in said cell population.
108. The method of Paragraph 100, wherein said cell is contacted with said antisense nucleic acid by introducing a promoter adjacent to a chromosomal copy of said antisense nucleic acid such that said promoter directs the transcription of said antisense nucleic acid.
109. The method of Paragraph 100, wherein said cell is contacted with said antisense nucleic acid by introducing a retron which expresses said antisense nucleic acid into said cell population.
110. The method of Paragraph 100, wherein said cell is contacted with said antisense nucleic acid by introducing a ribozyme into said cell-population, wherein a binding portion of said ribozyme comprises said antisense nucleic acid.
111. The method of Paragraph 100, wherein said cell is contacted with said antisense nucleic acid by introducing a liposome comprising said antisense nucleic acid into said cell.
112. The method of Paragraph 100, wherein said cell is contacted with said antisense nucleic acid by electroporation of said antisense nucleic acid into said cell.
113. The method of Paragraph 100, wherein said antisense nucleic acid is a fragment comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive nucleotides of one of SEQ ID NOs.: 1-6213.
114. The method of Paragraph 100 wherein said antisense nucleic acid is a synthetic oligonucleotide.
115. The method of Paragraph 100, wherein said gene comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397.

116. A method for identifying a gene which is required for proliferation of a cell comprising:

- (a) contacting a cell with an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, wherein said cell is a cell other than the organism from which said nucleic acid was obtained;
- (b) determining whether said nucleic acid inhibits proliferation of said cell; and
- (c) identifying the gene in said cell which encodes the mRNA which is complementary to said antisense nucleic acid or a portion thereof.

117. The method of Paragraph 116, wherein said cell is selected from the group consisting of *Staphylococcus* species, *Streptococcus* species, *Enterococcus* species, *Mycobacterium* species, *Clostridium* species, and *Bacillus* species.

118. The method of Paragraph 116 wherein said cell is selected from the group consisting of *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* and any species falling within the genera of any of the above species.

119. The method of Paragraph 116, wherein said cell is not *E. coli*.

120. The method of Paragraph 116, further comprising operably linking said antisense nucleic acid to a promoter which is functional in said cell, said promoter being included in a vector, and introducing said vector into said cell.

121. A method for identifying a compound having the ability to inhibit proliferation of a cell comprising:

- 5 (a) identifying a homolog of a gene or gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs. 1-6213 in a test cell, wherein said test cell is not the cell from which said nucleic acid was obtained;
- (b) identifying an inhibitory nucleic acid sequence which inhibits the activity of said homolog in said test cell;
- 10 (c) contacting said test cell with a sublethal level of said inhibitory nucleic acid, thus sensitizing said cell;
- (d) contacting the sensitized cell of step (c) with a compound; and
- (e) determining the degree to which said compound inhibits proliferation of said sensitized cell relative to a cell which does not contain said inhibitory nucleic acid.

122. The method of Paragraph 121, wherein said determining step comprises
15 determining whether said compound inhibits proliferation of said sensitized test cell to a greater extent than said compound inhibits proliferation of a nonsensitized test cell.

123. The method of Paragraph 121, wherein step (a) comprises identifying a nucleic acid homologous to a gene or gene product whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs. 1-6213 or a nucleic acid encoding a homologous
20 polypeptide to a polypeptide whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs. 1-6213 by using an algorithm selected from the group consisting of BLASTN version 2.0 with the default parameters and FASTA version 3.0t78 algorithm with the default parameters to identify said homologous nucleic acid or said nucleic acid encoding a homologous polypeptide in a database.

25 124. The method of Paragraph 121 wherein said step (a) comprises identifying a homologous nucleic acid or a nucleic acid comprising a sequence of nucleotides encoding a homologous polypeptide by identifying nucleic acids which hybridize to said nucleic acid selected from the group consisting of SEQ ID NOs. 1-6213 or the complement of said nucleic acid selected from the group consisting of SEQ ID NOs. 1-6213.

30 125. The method of Paragraph 121 wherein step (a) comprises expressing a nucleic acid selected from the group consisting of SEQ ID NOs. 1-6213 in said test cell.

126. The method of Paragraph 121, wherein step (a) comprises identifying a homologous nucleic acid or a nucleic acid encoding a homologous polypeptide in a test cell selected from the group consisting of *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus*
35 *fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida*

pseudotropicalis), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*,
 5 *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*,
 10 *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*,
 15 *Yersinia pestis* and any species falling within the genera of any of the above species.

127. The method of Paragraph 121, wherein step (a) comprises identifying a homologous nucleic acid or a nucleic acid encoding a homologous polypeptide in a test cell other than *E. coli*.

20 128. The method of Paragraph 121, wherein said inhibitory nucleic acid is an antisense nucleic acid.

129. The method of Paragraph 121, wherein said inhibitory nucleic acid comprises an antisense nucleic acid to a portion of said homolog.

25 130. The method of Paragraph 121, wherein said inhibitory nucleic acid comprises an antisense nucleic acid to a portion of the operon encoding said homolog.

131. The method of Paragraph 121, wherein the step of contacting the cell with a sublethal level of said inhibitory nucleic acid comprises directly contacting the surface of said cell with said inhibitory nucleic acid.

30 132. The method of Paragraph 121, wherein the step of contacting the cell with a sublethal level of said inhibitory nucleic acid comprises transcribing an antisense nucleic acid complementary to at least a portion of the RNA transcribed from said homolog in said cell.

133. The method of Paragraph 121, wherein said gene product comprises a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOS.: 42398-78581.

35 134. The method of Paragraph 121, wherein said gene comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397.

135. A compound identified using the method of Paragraph 121.

136. A method of identifying a compound having the ability to inhibit proliferation comprising:

- (a) contacting a test cell with a sublethal level of a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs. 1-6213 or a portion thereof which inhibits the proliferation of the cell from which said nucleic acid was obtained, thus sensitizing said test cell;
- (b) contacting the sensitized test cell of step (a) with a compound; and
- (c) determining the degree to which said compound inhibits proliferation of said sensitized test cell relative to a cell which does not contain said nucleic acid.

137. The method of Paragraph 136, wherein said determining step comprises determining whether said compound inhibits proliferation of said sensitized test cell to a greater extent than said compound inhibits proliferation of a nonsensitized test cell.

138. A compound identified using the method of Paragraph 136.

139. The method of Paragraph 136, wherein said test cell is selected from the group consisting of *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* and any species falling within the genera of any of the above species.

140. The method of Paragraph 136, wherein the test cell is not *E. coli*.

141. A method for identifying a compound having activity against a biological pathway required for proliferation comprising:

(a) sensitizing a cell by providing a sublethal level of an antisense nucleic acid complementary to a nucleic acid encoding a gene product required for proliferation, wherein the activity or expression of said gene product is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID
 5 NOs.: 1-6213, in said cell to reduce the activity or amount of said gene product;

(b) contacting the sensitized cell with a compound; and

(c) determining the degree to which said compound inhibits the growth of said sensitized cell relative to a cell which does not contain said antisense nucleic acid.

142. The method of Paragraph 141, wherein said determining step comprises
 10 determining whether said compound inhibits the growth of said sensitized cell to a greater extent than said compound inhibits the growth of a nonsensitized cell.

143. The method of Paragraph 141, wherein said cell is selected from the group consisting of bacterial cells, fungal cells, plant cells, and animal cells.

144. The method of Paragraph 141, wherein said cell is a Gram positive bacterium.

15 145. The method of Paragraph 144, wherein said Gram positive bacterium is selected from the group consisting of *Staphylococcus* species, *Streptococcus* species, *Enterococcus* species, *Mycobacterium* species, *Clostridium* species, and *Bacillus* species.

146. The method of Paragraph 145, wherein said Gram positive bacterium is *Staphylococcus aureus*.

20 147. The method of Paragraph 146, wherein said Gram positive bacterium is selected from the group consisting of *Staphylococcus aureus* RN450 and *Staphylococcus aureus* RN4220.

148. The method of Paragraph 141, wherein said cell is selected from the group consisting of *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*,
 25 *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*,
 30 *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*,
 35 *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella*

typhimurium, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*,

5 *Yersinia pestis* and any species falling within the genera of any of the above species.

149. The method of Paragraph 141, wherein said cell is not an *E. coli* cell.

150. The method of Paragraph 141, wherein said gene product is from an organism other than *E. coli*.

151. The method of Paragraph 141, wherein said antisense nucleic acid is transcribed
10 from an inducible promoter.

152. The method of Paragraph 141, further comprising contacting the cell with an agent which induces transcription of said antisense nucleic acid from said inducible promoter, wherein said antisense nucleic acid is transcribed at a sublethal level.

153. The method of Paragraph 141, wherein inhibition of proliferation is measured by
15 monitoring the optical density of a liquid culture.

154. The method of Paragraph 141, wherein said gene product comprises a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOS.: 42398-78581.

155. The method of Paragraph 141, wherein said nucleic acid encoding said gene
20 product comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397.

156. A compound identified using the method of Paragraph 141.

157. A method for identifying a compound having the ability to inhibit cellular proliferation comprising:

25 (a) contacting a cell with an agent which reduces the activity or level of a gene product required for proliferation of said cell, wherein said gene product is a gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 1-6213;

(b) contacting said cell with a compound; and

30 (c) determining whether said compound reduces proliferation of said contacted cell by acting on said gene product.

158. The method of Paragraph 157, wherein said determining step comprises determining whether said compound reduces proliferation of said contacted cell to a greater extent than said compound reduces proliferation of cells which have not been contacted with said agent.

35 159. The method of Paragraph 157, wherein said cell is selected from the group consisting of *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida*

glabrata (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*,
5 *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma*
10 *pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*,
15 *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* and any species falling within the genera of any of the above species.

160. The method of Paragraph 157, wherein said cell is not an *E. coli* cell.

20 161. The method of Paragraph 157, wherein said gene product is from an organism other than *E. coli*.

162. The method of Paragraph 157, wherein said agent which reduces the activity or level of a gene product required for proliferation of said cell comprises an antisense nucleic acid to a gene or operon required for proliferation.

25 163. The method of Paragraph 157, wherein said agent which reduces the activity or level of a gene product required for proliferation of said cell comprises a compound known to inhibit growth or proliferation of a cell.

164. The method of Paragraph 157, wherein said cell contains a mutation which reduces the activity or level of said gene product required for proliferation of said cell.

30 165. The method of Paragraph 157, wherein said mutation is a temperature sensitive mutation.

166. The method of Paragraph 157, wherein said gene product comprises a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42398-78581.

35 167. A compound identified using the method of Paragraph 157.

168. A method for identifying the biological pathway in which a proliferation-required gene or its gene product lies, wherein said gene or gene product comprises a gene or gene product

whose activity or expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-6213, said method comprising:

(a) providing a sublethal level of an antisense nucleic acid which inhibits the activity of said proliferation-required gene or gene product in a test cell;

5 (b) contacting said test cell with a compound known to inhibit growth or proliferation of a cell, wherein the biological pathway on which said compound acts is known; and

(c) determining the degree to which said proliferation of said test cell is inhibited relative to a cell which was not contacted with said compound.

10 169. The method of Paragraph 168, wherein said determining step comprises determining whether said test cell has a substantially greater sensitivity to said compound than a cell which does not express said sublethal level of said antisense nucleic acid.

170. The method of Paragraph 168, wherein said gene product comprises a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42398-
15 78581.

171. The method of Paragraph 168, wherein said test cell is selected from the group consisting of *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*,
25 *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*,
30 *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* and any species falling within the genera of any of the above species.

172. The method of Paragraph 168, wherein said test cell is not an *E. coli* cell.

173. The method of Paragraph 168, wherein said gene product is from an organism other than *E. coli*.

174. A method for determining the biological pathway on which a test compound acts comprising:

5 (a) providing a sublethal level of an antisense nucleic acid complementary to a proliferation-required nucleic acid in a first cell, wherein the activity or expression of said proliferation-required nucleic acid is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs.: 1-6213 and wherein the biological pathway in which said proliferation-required nucleic acid or a protein encoded
10 by said proliferation-required nucleic acid lies is known,

(b) contacting said first cell with said test compound; and

(c) determining the degree to which said test compound inhibits proliferation of said first cell relative to a cell which does not contain said antisense nucleic acid.

175. The method of Paragraph 174, wherein said determining step comprises
15 determining whether said first cell has a substantially greater sensitivity to said test compound than a cell which does not express said sublethal level of said antisense nucleic acid.

176. The method of Paragraph 174, further comprising:

(d) providing a sublethal level of a second antisense nucleic acid complementary to
20 a second proliferation-required nucleic acid in a second cell, wherein said second proliferation-required nucleic acid is in a different biological pathway than said proliferation-required nucleic acid in step (a); and

(e) determining whether said second cell does not have a substantially greater
25 sensitivity to said test compound than a cell which does not express said sublethal level of said second antisense nucleic acid, wherein said test compound is specific for the biological pathway against which the antisense nucleic acid of step (a) acts if said first cell has a substantially greater sensitivity to said test compound than said second cell.

177. The method of Paragraph 174, wherein said first cell is selected from the group consisting of *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*,
30 *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*,
35 *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*,

Mycobacterium leprae, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*,
5 *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*,
10 *Yersinia pestis* and any species falling within the genera of any of the above species.

178. The method of Paragraph 174, wherein said first cell is not an *E. coli* cell.

179. The method of Paragraph 174, wherein said proliferation-required nucleic acid is from an organism other than *E. coli*.

180. A purified or isolated nucleic acid comprising a sequence selected from the group
15 consisting of SEQ ID NOs.: 1-6213.

181. A compound which interacts with a gene or gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence of one of SEQ ID NOs.: 1-6213 to inhibit proliferation.

182. The compound of Paragraph 181, wherein said gene product is a polypeptide
20 comprising one of SEQ ID NOs.: 42398-78581.

183. The compound of Paragraph 181, wherein said gene comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397.

184. A compound which interacts with a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence of one of SEQ ID NOs.: 1-6213 to
25 inhibit proliferation.

185. A method for manufacturing an antibiotic comprising the steps of:
screening one or more candidate compounds to identify a compound that reduces the activity or level of a gene product required for proliferation, said gene product comprising a gene product whose activity or expression is inhibited by an antisense nucleic acid comprising a
30 nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213; and
manufacturing the compound so identified.

186. The method of Paragraph 185, wherein said screening step comprises performing any one of the methods of Paragraphs 44, 68, 121, 136, 141, and 157.

187. The method of Paragraph 185, wherein said gene product is a polypeptide
35 comprising one of SEQ ID NOs.: 42398-78581.

188. A method for inhibiting proliferation of a cell in a subject comprising administering an effective amount of a compound that reduces the activity or level of a gene product required for proliferation of said cell, said gene product comprising a gene product whose activity or expression

is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 to said subject.

189. The method of Paragraph 188 wherein said subject is selected from the group consisting of vertebrates, mammals, avians, and human beings.

5 190. The method of Paragraph 188, wherein said gene product comprises a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42398-78581.

191. The method of Paragraph 188, wherein said cell is selected from the group consisting of *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*,
 10 *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*,
 15 *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*,
 20 *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* and any species falling within the genera of any of the above species.

30 192. The method of Paragraph 188, wherein said cell is not *E. coli*.

193. The method of Paragraph 188, wherein said gene product is from an organism other than *E. coli*.

194. A purified or isolated nucleic acid consisting essentially of the coding sequence of one of SEQ ID NOs: 6214-42397.

35 195. A fragment of the nucleic acid of Paragraph 8, said fragment comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive nucleotides of one of SEQ ID NOs: 6214-42397.

196. A purified or isolated nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397, fragments comprising at least 25 consecutive nucleotides of SEQ ID NOs.: 6214-42397, the nucleotide sequences complementary to SEQ ID NOs.: 6214-42397, and the
 5 nucleotide sequences complementary to fragments comprising at least 25 consecutive nucleotides of SEQ ID NOs.: 6214-42397 as determined using BLASTN version 2.0 with the default parameters.

197. The nucleic acid of Paragraph 196, wherein said nucleic acid is from an organism selected from the group consisting of *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*,
 10 *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*,
 15 *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*,
 20 *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*,
 25 *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* and any species falling within the genera of any of the above species.

30 198. The nucleic acid of Paragraph 196, wherein said nucleic acid is from an organism other than *E. coli*.

199. A method of inhibiting proliferation of a cell comprising inhibiting the activity or reducing the amount of a gene product in said cell or inhibiting the activity or reducing the amount of a nucleic acid encoding said gene product in said cell, wherein said gene product is selected from
 35 the group consisting of a gene product having having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at

least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-6213.

200. The method of Paragraph 199, wherein said method comprises inhibiting said activity or reducing said amount of said gene product or inhibiting the activity or reducing the amount of a nucleic acid encoding said gene product in an organism selected from the group consisting of *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* and any species falling within the genera of any of the above species.

201. The method of Paragraph 199, wherein said method comprises inhibiting said activity or reducing said amount of said gene product or inhibiting the activity or reducing the amount of a nucleic acid encoding said gene product in an organism other than *E. coli*.

202. The method of Paragraph 199, wherein said gene product is from an organism other than *E. coli*.

203. The method of Paragraph 199, wherein said gene product comprises a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOS.: 42398-78581 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOS: 42398-78581.

204. The method of Paragraph 199, wherein said gene product is encoded by a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate conditions.

205. A method for identifying a compound which influences the activity of a gene product required for proliferation comprising:

contacting a candidate compound with a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 1-6213, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOS.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOS.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented

by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 1-6213; and

determining whether said candidate compound influences the activity of said gene product.

- 5 206. The method of Paragraph 205, wherein said gene product is from an organism selected from the group consisting of *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*,
10 *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*,
15 *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* and any species falling within the genera of any of the above species.

207. The method of Paragraph 205, wherein said gene product is from an organism other than *E. coli*.

208. The method of Paragraph 205, wherein said gene product is a polypeptide selected
30 from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 42398-78581 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 42398-78581.

209. The method of Paragraph 205, wherein said gene product is encoded by a nucleic
35 acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID

NOS.: 6214-42397 under stringent conditions, and a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate conditions.

210. A compound identified using the method of Paragraph 205.

211. A method for identifying a compound or nucleic acid having the ability to reduce
5 the activity or level of a gene product required for proliferation comprising:

(a) providing a target that is a gene or RNA, wherein said target comprises a nucleic acid that encodes a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is
10 inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleic acid identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group
15 consisting of SEQ ID NOS.: 1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOS.: 1-6213, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOS.: 1-6213 under stringent conditions, a gene product
20 encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOS.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID
25 NOS.: 1-6213;

(b) contacting said target with a candidate compound or nucleic acid; and

(c) measuring an activity of said target.

212. The method of Paragraph 211, wherein said target gene or RNA is from an organism selected from the group consisting of *Acinetobacter baumannii*, *Anaplasma marginale*,
30 *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*,
35 *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*,

Listeria monocytogenes, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*,
5 *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma*
10 *urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* and any species falling within the genera of any of the above species.

213. The method of Paragraph 211, wherein said target gene or RNA is from an organism other than *E. coli*.

214. The method of Paragraph 211, wherein said gene product is from an organism other
15 than *E. coli*.

215. The method of Paragraph 211, wherein said target is a messenger RNA molecule and said activity is translation of said messenger RNA.

216. The method of Paragraph 211, wherein said compound is a nucleic acid and said activity is translation of said gene product.

20 217. The method of Paragraph 211, wherein said target is a gene and said activity is transcription of said gene.

218. The method of Paragraph 211, wherein said target is a nontranslated RNA and said activity is processing or folding of said nontranslated RNA or assembly of said nontranslated RNA into a protein/RNA complex.

25 219. The method of Paragraph 211, wherein said target gene is a messenger RNA molecule encoding a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOS.: 42398-78581 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOS.: 42398-78581.

30 220. The method of Paragraph 11, wherein said target gene comprises a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.:
35 6214-42397 under stringent conditions, and a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate conditions.

221. A compound or nucleic acid identified using the method of Paragraph 211.

222. A method for identifying a compound which reduces the activity or level of a gene product required for proliferation of a cell comprising:

- 5 (a) providing a sublethal level of an antisense nucleic acid complementary to a nucleic acid encoding said gene product in a cell to reduce the activity or amount of said gene product in said cell, thereby producing a sensitized cell, wherein said gene product is selected from the group consisting of a gene product having having at least 70% nucleic acid identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as
10 determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited
15 by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-6213, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid comprising a
20 nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 1-6213;
- 25 (b) contacting said sensitized cell with a compound; and
- (c) determining the degree to which said compound inhibits the growth of said sensitized cell relative to a cell which does not contain said antisense nucleic acid.

223. The method of Paragraph 222, wherein said determining step comprises determining whether said compound inhibits the growth of said sensitized cell to a greater extent
30 than said compound inhibits the growth of a nonsensitized cell.

224. The method of Paragraph 222, wherein said sensitized cell is a Gram positive bacterium.

225. The method of Paragraph 224, wherein said Gram positive bacterium is selected from the group consisting of *Staphylococcus* species, *Streptococcus* species, *Enterococcus* species,
35 *Mycobacterium* species, *Clostridium* species, and *Bacillus* species.

226. The method of Paragraph 225, wherein said bacterium is *Staphylococcus aureus*.

227. The method of Paragraph 224, wherein said *Staphylococcus* species is coagulase negative.

228. The method of Paragraph 226, wherein said bacterium is selected from the group consisting of *Staphylococcus aureus* RN450 and *Staphylococcus aureus* RN4220.

229. The method of Paragraph 222, wherein said sensitized cell is an organism selected from the group consisting of *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* and any species falling within the genera of any of the above species.

230. The method of Paragraph 222, wherein said cell is an organism other than *E. coli*.

231. The method of Paragraph 222, wherein said gene product is from an organism other than *E. coli*.

232. The method of Paragraph 222, wherein said antisense nucleic acid is transcribed from an inducible promoter.

233. The method of Paragraph 222, further comprising the step of contacting said cell with a concentration of inducer which induces transcription of said antisense nucleic acid to a sublethal level.

234. The method of Paragraph 222, wherein growth inhibition is measured by monitoring optical density of a culture medium.

235. The method of Paragraph 222, wherein said gene product is a polypeptide.

236. The method of Paragraph 235, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of

SEQ ID NOs.: 42398-78581 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 42398-78581.

237. The method of Paragraph 222, wherein said gene product is an RNA.

238. The method of Paragraph 222, wherein said nucleic acid encoding said gene
5 product comprises a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleic acid identity as determined using BLASTN version 2.0 with the default parameters to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid which hybridizes to a sequence selected from the group consisting of
10 SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate conditions.

239. A compound identified using the method of Paragraph 222.

240. A method for inhibiting cellular proliferation comprising introducing a compound
15 with activity against a gene product or a compound with activity against a gene encoding said gene product into a population of cells expressing said gene product, wherein said gene product is selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product
20 whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited
25 by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of
30 SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of
SEQ ID NOs: 1-6213.

241. The method of Paragraph 240, wherein said compound is an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, or a
35 proliferation-inhibiting portion thereof.

242. The method of Paragraph 240, wherein said proliferation inhibiting portion of one of SEQ ID NOs.: 1-6213 is a fragment comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 51 consecutive nucleotides of one of SEQ ID NOs.: 1-6213.

243. The method of Paragraph 240, wherein said population is a population of Gram positive bacteria.

244. The method of Paragraph 243, wherein said population of Gram positive bacteria is selected from the group consisting of a population of *Staphylococcus* species, *Streptococcus* species, *Enterococcus* species, *Mycobacterium* species, *Clostridium* species, and *Bacillus* species.

245. The method of Paragraph 243, wherein said population is a population of *Staphylococcus aureus*.

246. The method of Paragraph 245, wherein said population is a population of a bacterium selected from the group consisting of *Staphylococcus aureus* RN450 and *Staphylococcus aureus* RN4220.

247. The method of Paragraph 240, wherein said population is a population of a bacterium selected from the group consisting of *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* and any species falling within the genera of any of the above species.

248. The method of Paragraph 240, wherein said population is a population of an organism other than *E. coli*.

249. The method of Paragraph 240, wherein said product of said gene is from an organism other than *E. coli*.

250. The method of Paragraph 240, wherein said gene product is selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using

FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 42398-78581 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs.: 42398-78581.

251. The method of Paragraph 240, wherein said gene comprises a nucleic acid selected
5 from the group consisting of a nucleic acid comprising a nucleic acid having at least 70%
nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters
to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a
nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected
from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic
10 acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the
group consisting of SEQ ID NOS.: 6214-42397 under moderate condtions.

252. A preparation comprising an effective concentration of an antisense nucleic acid in
a pharmaceutically acceptable carrier wherein said antisense nucleic acid is selected from the group
consisting of a nucleic acid comprising a sequence having at least 70% nucleotide sequence identity
15 as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence
selected from the group consisting of SEQ ID NOs.: 1-6213 or a proliferation-inhibiting portion
thereof, a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected
from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, and a nucleic acid
comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group
20 consisting of SEQ ID NOs.: 1-6213 under moderate conditions.

253. The preparation of Paragraph 252, wherein said proliferation-inhibiting portion of
one of SEQ ID NOs.: 1-6213 comprises at least 10, at least 20, at least 25, at least 30, at least 50 or
more than 50 consecutive nucleotides of one of SEQ ID NOs.: 1-6213.

254. A method for inhibiting the activity or expression of a gene in an operon which
25 encodes a gene product required for proliferation comprising contacting a cell in a cell population
with an antisense nucleic acid comprising at least a proliferation-inhibiting portion of said operon in
an antisense orientation, wherein said gene product is selected from the group consisting of a gene
product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0
with the default parameters to a gene product whose expression is inhibited by an antisense nucleic
30 acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213,
a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as
determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a
gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide
sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product having at least
35 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to
a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide
sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a
nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the

group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213.

255. The method of Paragraph 254, wherein said antisense nucleic acid comprises a nucleotide sequence having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a proliferation inhibiting portion thereof, a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, and a nucleic acid which comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions.

256. The method of Paragraph 254, wherein said cell is selected from the group consisting of *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* and any species falling within the genera of any of the above species.

257. The method of Paragraph 254, wherein said cell is not an *E. coli* cell.

258. The method of Paragraph 254, wherein said gene is from an organism other than *E. coli*.

259. The method of Paragraph 254, wherein said cell is contacted with said antisense nucleic acid by introducing a plasmid which transcribes said antisense nucleic acid into said cell population.

260. The method of Paragraph 254, wherein said cell is contacted with said antisense nucleic acid by introducing a phage which transcribes said antisense nucleic acid into said cell population.

261. The method of Paragraph 254, wherein said cell is contacted with said antisense nucleic acid by transcribing said antisense nucleic acid from the chromosome of cells in said cell population.

262. The method of Paragraph 254, wherein said cell is contacted with said antisense nucleic acid by introducing a promoter adjacent to a chromosomal copy of said antisense nucleic acid such that said promoter directs the synthesis of said antisense nucleic acid.

263. The method of Paragraph 254, wherein said cell is contacted with said antisense nucleic acid by introducing a retron which expresses said antisense nucleic acid into said cell population.

264. The method of Paragraph 254, wherein said cell is contacted with said antisense nucleic acid by introducing a ribozyme into said cell-population, wherein a binding portion of said ribozyme is complementary to said antisense oligonucleotide.

265. The method of Paragraph 254, wherein said cell is contacted with said antisense nucleic acid by introducing a liposome comprising said antisense oligonucleotide into said cell.

266. The method of Paragraph 254, wherein said cell is contacted with said antisense nucleic acid by electroporation of said antisense nucleic acid into said cell.

267. The method of Paragraph 254, wherein said antisense nucleic acid has at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence comprising at least 10, at least 20, at least 25, at least 30, at least 50 or more than 50 consecutive nucleotides of one of SEQ ID NOS.: 1-6213.

268. The method of Paragraph 254 wherein said antisense nucleic acid is a synthetic oligonucleotide.

269. The method of Paragraph 254, wherein said gene comprises a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate conditions.

270. A method for identifying a gene which is required for proliferation of a cell comprising:

- (a) contacting a cell with an antisense nucleic acid selected from the group consisting of a nucleic acid at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 or a proliferation-inhibiting portion thereof, a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, wherein said cell is a cell other than the organism from which said nucleic acid was obtained;
- (b) determining whether said nucleic acid inhibits proliferation of said cell; and
- (c) identifying the gene in said cell which encodes the mRNA which is complementary to said antisense nucleic acid or a portion thereof.

271. The method of Paragraph 270, wherein said cell is selected from the group consisting of *Staphylococcus* species, *Streptococcus* species, *Enterococcus* species, *Mycobacterium* species, *Clostridium* species, and *Bacillus* species.

272. The method of Paragraph 270 wherein said cell is selected from the group consisting of *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* and any species falling within the genera of any of the above species.

273. The method of Paragraph 270, wherein said cell is not *E. coli*.

274. The method of Paragraph 270, further comprising operably linking said antisense nucleic acid to a promoter which is functional in said cell, said promoter being included in a vector, and introducing said vector into said cell.

275. A method for identifying a compound having the ability to inhibit proliferation of a
5 cell comprising:

(a) identifying a homolog of a gene or gene product whose activity or level is inhibited by an antisense nucleic acid in a test cell, wherein said test cell is not the microorganism from which the antisense nucleic acid was obtained, wherein said antisense nucleic acid is selected from the group consisting of a nucleic acid having at least 70%
10 nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOs. 1-6213, a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected
15 from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions;

(b) identifying an inhibitory nucleic acid sequence which inhibits the activity of said homolog in said test cell;

(c) contacting said test cell with a sublethal level of said inhibitory nucleic acid, thus sensitizing said cell;

20 (d) contacting the sensitized cell of step (c) with a compound; and

(e) determining the degree to which said compound inhibits proliferation of said sensitized cell relative to a cell which does not express said inhibitory nucleic acid.

276. The method of Paragraph 275, wherein said determining step comprises determining whether said compound inhibits proliferation of said sensitized test cell to a greater
25 extent than said compound inhibits proliferation of a nonsensitized test cell.

277. The method of Paragraph 275, wherein step (a) comprises identifying a homologous nucleic acid to a gene or gene product whose activity or level is inhibited by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID
30 NOs. 1-6213 or a nucleic acid encoding a homologous polypeptide to a polypeptide whose activity or level is inhibited by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOs. 1-6213 by using an algorithm selected from the group consisting of BLASTN version 2.0 with the default parameters and FASTA version 3.0t78
35 algorithm with the default parameters to identify said homologous nucleic acid or said nucleic acid encoding a homologous polypeptide in a database.

278. The method of Paragraph 275 wherein said step (a) comprises identifying a homologous nucleic acid or a nucleic acid encoding a homologous polypeptide by identifying

nucleic acids comprising nucleotide sequences which hybridize to said nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOs. 1-6213 or the complement of the nucleotide sequence of said nucleic acid selected from the group consisting of SEQ ID NOs. 1-6213.

279. The method of Paragraph 275 wherein step (a) comprises expressing a nucleic acid having at least 70% nucleic acid identity as determined using BLASTN version 2.0 with the default parameters to a sequence selected from the group consisting of SEQ ID NOs. 1-6213 in said test cell.

280. The method of Paragraph 275, wherein step (a) comprises identifying a homologous nucleic acid or a nucleic acid encoding a homologous polypeptide in an test cell selected from the group consisting of *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* and any species falling within the genera of any of the above species.

281. The method of Paragraph 275, wherein step (a) comprises identifying a homologous nucleic acid or a nucleic acid encoding a homologous polypeptide in a test cell other than *E. coli*.

282. The method of Paragraph 275, wherein said inhibitory nucleic acid is an antisense nucleic acid.

283. The method of Paragraph 275, wherein said inhibitory nucleic acid comprises an antisense nucleic acid to a portion of said homolog.

284. The method of Paragraph 275, wherein said inhibitory nucleic acid comprises an antisense nucleic acid to a portion of the operon encoding said homolog.

5 285. The method of Paragraph 275, wherein the step of contacting the cell with a sublethal level of said inhibitory nucleic acid comprises directly contacting said cell with said inhibitory nucleic acid.

286. The method of Paragraph 275, wherein the step of contacting the cell with a sublethal level of said inhibitory nucleic acid comprises expressing an antisense nucleic acid to said
10 homolog in said cell.

287. The method of Paragraph 275, wherein said gene product comprises a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOS.: 42398-78581.

288. The method of Paragraph 275, wherein said gene comprises a nucleic acid selected
15 from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid
20 comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate conditions.

289. A compound identified using the method of Paragraph 275.

290. A method of identifying a compound having the ability to inhibit proliferation comprising:

25 (a) sensitizing a test cell by contacting said test cell with a sublethal level of an antisense nucleic acid, wherein said antisense nucleic acid is selected from the group consisting of a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS. 1-6213 or a portion thereof which inhibits the
30 proliferation of the cell from which said nucleic acid was obtained, a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOS.: 1-6213 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOS.: 1-6213 under moderate conditions;

35 (b) contacting the sensitized test cell of step (a) with a compound; and

(c) determining the degree to which said compound inhibits proliferation of said sensitized test cell relative to a cell which does not contain said antisense nucleic acid.

291. The method of Paragraph 290, wherein said determining step comprises determining whether said compound inhibits proliferation of said sensitized test cell to a greater extent than said compound inhibits proliferation of a nonsensitized test cell.

292. A compound identified using the method of Paragraph 290.

5 293. The method of Paragraph 290, wherein said test cell is selected from the group consisting of *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*,
10 *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*,
15 *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* and any species falling within the genera of any of the above species.

294. The method of Paragraph 290, wherein the test cell is not *E. coli*.

295. A method for identifying a compound having activity against a biological pathway required for proliferation comprising:

30 (a) sensitizing a cell by providing a sublethal level of an antisense nucleic acid complementary to a nucleic acid encoding a gene product required for proliferation, wherein said gene product is selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.:
35 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid

comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 1-6213;

(b) contacting the sensitized cell with a compound; and

(c) determining the extent to which said compound inhibits the growth of said sensitized cell relative to a cell which does not contain said antisense nucleic acid.

296. The method of Paragraph 295, wherein said determining step comprises determining whether said compound inhibits the growth of said sensitized cell to a greater extent than said compound inhibits the growth of a nonsensitized cell.

297. The method of Paragraph 295, wherein said cell is selected from the group consisting of bacterial cells, fungal cells, plant cells, and animal cells.

298. The method of Paragraph 295, wherein said cell is a Gram positive bacterium.

299. The method of Paragraph 298, wherein said Gram positive bacterium is selected from the group consisting of *Staphylococcus* species, *Streptococcus* species, *Enterococcus* species, *Mycobacterium* species, *Clostridium* species, and *Bacillus* species.

300. The method of Paragraph 299, wherein said Gram positive bacterium is *Staphylococcus aureus*.

301. The method of Paragraph 298, wherein said Gram positive bacterium is selected from the group consisting of *Staphylococcus aureus* RN450 and *Staphylococcus aureus* RN4220.

302. The method of Paragraph 295, wherein said cell is selected from the group consisting of *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria*

monocytogenes, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*,
 5 *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*,
 10 *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* and any species falling within the genera of any of the above species.

303. The method of Paragraph 295, wherein said cell is not an *E. coli* cell.

304. The method of Paragraph 295, wherein said gene product is from an organism other than *E. coli*.

15 305. The method of Paragraph 295, wherein said antisense nucleic acid is transcribed from an inducible promoter.

306. The method of Paragraph 305, further comprising contacting the cell with an agent which induces expression of said antisense nucleic acid from said inducible promoter, wherein said antisense nucleic acid is expressed at a sublethal level.

20 307. The method of Paragraph 295, wherein inhibition of proliferation is measured by monitoring the optical density of a liquid culture.

308. The method of Paragraph 295, wherein said gene product comprises a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a sequence selected from the group consisting of SEQ ID NOS.: 42398-78581.

25 309. The method of Paragraph 295, wherein said nucleic acid encoding said gene product comprises a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid comprising a nucleotide sequence which hybridizes to
 30 a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate conditions.

310. A compound identified using the method of Paragraph 295.

35 311. A method for identifying a compound having the ability to inhibit cellular proliferation comprising:

(a) contacting a cell with an agent which reduces the activity or level of a gene product required for proliferation of said cell, wherein said gene product is selected from

the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product
 5 encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the
 10 default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid comprising a
 15 nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213;

(b) contacting said cell with a compound; and
 20 (c) determining the degree to which said compound reduces proliferation of said contacted cell relative to a cell which was not contacted with said agent.

312. The method of Paragraph 311, wherein said determining step comprises determining whether said compound reduces proliferation of said contacted cell to a greater extent than said compound reduces proliferation of cells which have not been contacted with said agent.

25 313. The method of Paragraph 311, wherein said cell is selected from the group consisting of *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*,
 30 *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella*

haemolytica, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*,
 5 *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* and any species falling within the genera of any of the above species.

314. The method of Paragraph 311, wherein said cell is not an *E. coli* cell.

10 315. The method of Paragraph 311, wherein said gene product is from an organism other than *E. coli*.

316. The method of Paragraph 311, wherein said agent which reduces the activity or level of a gene product required for proliferation of said cell comprises an antisense nucleic acid to a gene or operon required for proliferation.

15 317. The method of Paragraph 311, wherein said agent which reduces the activity or level of a gene product required for proliferation of said cell comprises a compound known to inhibit growth or proliferation of a cell.

318. The method of Paragraph 311, wherein said cell contains a mutation which reduces the activity or level of said gene product required for proliferation of said cell.

20 319. The method of Paragraph 311, wherein said mutation is a temperature sensitive mutation.

320. The method of Paragraph 311, wherein said gene product comprises a gene product comprises a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to an amino acid sequence selected from the group
 25 consisting of SEQ ID NOs.: 42398-78581.

321. A compound identified using the method of Paragraph 311.

322. A method for identifying the biological pathway in which a proliferation-required gene product or a gene encoding a proliferation-required gene product lies comprising:

(a) providing a sublethal level of an antisense nucleic acid which inhibits the
 30 activity or reduces the level of said gene encoding a proliferation-required gene product or said said proliferation-required gene product in a test cell, wherein said proliferation-required gene product is selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic
 35 acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid

comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 1-6213;

(b) contacting said test cell with a compound known to inhibit growth or proliferation of a cell, wherein the biological pathway on which said compound acts is known; and

(c) determining the degree to which said compound inhibits proliferation of said test cell relative to a cell which does not contain said antisense nucleic acid.

323. The method of Paragraph 322, wherein said determining step comprises determining whether said test cell has a substantially greater sensitivity to said compound than a cell which does not express said sublethal level of said antisense nucleic acid.

324. The method of Paragraph 322, wherein said gene product comprises a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42398-78581.

325. The method of Paragraph 322, wherein said test cell is selected from the group consisting of *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*,

Pseudomonas aeruginosa, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* and any species falling within the genera of any of the above species.

326. The method of Paragraph 322, wherein said test cell is not an *E. coli* cell.

327. The method of Paragraph 322, wherein said gene product is from an organism other than *E. coli*.

328. A method for determining the biological pathway on which a test compound acts comprising:

(a) providing a sublethal level of an antisense nucleic acid complementary to a proliferation-required nucleic acid in a cell, thereby producing a sensitized cell, wherein said antisense nucleic acid is selected from the group consisting of a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-6213 or a proliferation-inhibiting portion thereof, a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions and wherein the biological pathway in which said proliferation-required nucleic acid or a protein encoded by said proliferation-required polypeptide lies is known,

(b) contacting said cell with said test compound; and

(c) determining the degree to which said compound inhibits proliferation of said sensitized cell relative to a cell which does not contain said antisense nucleic acid.

329. The method of Paragraph 328, wherein said determining step comprises determining whether said sensitized cell has a substantially greater sensitivity to said test compound than a cell which does not express said sublethal level of said antisense nucleic acid.

330. The method of Paragraph 328, further comprising:

(d) providing a sublethal level of a second antisense nucleic acid complementary to a second proliferation-required nucleic acid in a second cell, wherein said second proliferation-required nucleic acid is in a different biological pathway than said proliferation-required nucleic acid in step (a); and

(e) determining whether said second cell does not have a substantially greater sensitivity to said test compound than a cell which does not express said sublethal level of said second antisense nucleic acid, wherein said test compound is specific for the biological

pathway against which the antisense nucleic acid of step (a) acts if said sensitized cell has substantially greater sensitivity to said test compound than said second cell.

331. The method of Paragraph 328, wherein said sensitized cell is selected from the group consisting of *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*,
 5 *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium*
 10 *acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*,
 15 *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella*
 20 *typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* and any species falling within the genera of any of the above species.

25 332. The method of Paragraph 328, wherein said sensitized cell is not an *E. coli* cell.

333. The method of Paragraph 328, wherein said proliferation-required nucleic acid is from an organism other than *E. coli*.

334. A compound which inhibits proliferation by interacting with a gene encoding a gene product required for proliferation or with a gene product required for proliferation, wherein
 30 said gene product is selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using
 35 BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product

whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213.

335. The compound of Paragraph 334, wherein said gene product comprises a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a sequence selected from the group consisting of SEQ ID NOs.: 42398-78581.

336. The compound of Paragraph 334, wherein said gene comprises a nucleic acid selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate condtions.

337. A method for manufacturing an antibiotic comprising the steps of:
screening one or more candidate compounds to identify a compound that reduces the activity or level of a gene product required for proliferation wherein said gene product is selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the

gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 1-6213 ; and

manufacturing the compound so identified.

338. The method of Paragraph 337, wherein said screening step comprises performing
5 any one of the methods of Paragraphs 205, 211, 222, 275, 290, 295, 311.

339. The method of Paragraph 337, wherein said gene product comprises a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42398-78581.

10 340. A method for inhibiting proliferation of a cell in a subject comprising administering an effective amount of a compound that reduces the activity or level of a gene product required for proliferation of said cell, wherein said gene product is selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic
15 acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product having at least
20 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a
25 nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 1-6213.

341. The method of Paragraph 340 wherein said subject is selected from the group
30 consisting of vertebrates, mammals, avians, and human beings.

342. The method of Paragraph 340, wherein said gene product comprises a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42398-78581.

35 343. The method of Paragraph 340, wherein said cell is selected from the group consisting of *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida*

glabrata (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*,
 5 *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*,
 10 *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*,
 15 *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* and any species falling within the genera of any of the above species.

344. The method of Paragraph 340, wherein said cell is not *E. coli*.

20 345. The method of Paragraph 340, wherein said gene product is from an organism other than *E. coli*.

346. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

25 obtaining a culture comprising a plurality of strains wherein each strain in said culture overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 is overexpressed;

30 contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

35 identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture.

347. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain in said culture overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397 is overexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture.

348. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain in said culture overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42938-78581 is overexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture.

349. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain in said culture overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide

sequence selected from the group consisting of SEQ ID NOs: 1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-6213 is overexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture.

350. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain in said culture overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate conditions is overexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture.

351. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

5 obtaining a culture comprising a plurality of strains wherein each strain in said culture overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product comprises a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 42938-78581 and a polypeptide whose activity may be
10 complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 42938-78581 is overexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which
15 said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture.

20 352. The method of Paragraph 346, 347, 348, 349, 350 or 351, wherein said culture includes at least one strain which does not overexpresses a gene product which is essential for proliferation of said organism.

353. The method of Paragraph 346, 347, 348, 349, 350 or 351, wherein said strains which overexpress said gene products comprise a nucleic acid encoding said gene product which is
25 essential for proliferation of said organism operably linked to a regulatable promoter.

354. The method of Paragraph 346, 347, 348, 349, 350 or 351, wherein said strains which overexpress said gene products a nucleic acid encoding said gene product which is essential for proliferation of said organism operably linked to a constitutive promoter.

355. The method of Paragraph 346, 347, 348, 349, 350 or 351, wherein said
30 identification step comprises determining the nucleotide sequence of a nucleic acid encoding said gene product in said cell which proliferated more rapidly in said culture.

356. The method of Paragraph 346, 347, 348, 349, 350 or 351, wherein said identification step comprises performing an amplification reaction to identify the nucleic acid encoding said gene product in said cell which proliferated more rapidly in said cell culture.

35 357. The method of Paragraph 356, wherein the products of said amplification reaction are labeled with a detectable dye.

358. The method of Paragraph 346, 347, 348, 349, 350 or 351, wherein said identification step comprises performing a hybridization procedure.

359. The method of Paragraph 346, 347, 348, 349, 350 or 351, wherein said identification step comprises contacting a nucleic acid array with a nucleic acid encoding said gene product in said cell which proliferated more rapidly in said cell culture.

360. The method of Paragraph 346, 347, 348, 349, 350 or 351, wherein said organism is
5 selected from the group consisting of bacteria, fungi, and protozoa.

361. The method of Paragraph 346, 347, 348, 349, 350 or 351, wherein said culture is a culture of an organism selected from the group consisting of *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*,
10 *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*,
15 *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*,
25 *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* and any species falling within the genera of any of the above species.

362. The method of Paragraph 346, 347, 348, 349, 350 or 351, wherein said compound is obtained from a library of natural compounds.

30 363. The method of Paragraph 346, 347, 348, 349, 350 or 351, wherein said compound is obtained from a library of synthetic compounds.

364. The method of Paragraph 346, 347, 348, 349, 350 or 351, wherein said compound is present in a crude or partially purified state.

35 365. The method of Paragraph 346, 347, 348, 349, 350 or 351, further comprising determining whether said gene product in said strain which proliferated more rapidly in said culture has a counterpart in at least one other organism.

366. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining an array of strains on a solid growth medium wherein each strain overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 is overexpressed;

contacting said array of strains with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly on said solid medium.

367. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining an array of strains on a solid growth medium wherein each strain overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397 is overexpressed;

contacting said array of strains with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly on said solid medium.

368. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining an array of strains on a solid growth medium wherein each strain overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42938-78581 is overexpressed;

contacting said array of strains with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly on said solid medium.

369. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

5 obtaining an array of strains on a solid growth medium wherein each strain overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression
10 is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the
15 group consisting of SEQ ID NOs.: 1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide
20 sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide
25 sequence selected from the group consisting of SEQ ID NOs.: 1-6213 is overexpressed;

contacting said array of strains with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not
30 overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly on said solid medium.

370. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

35 obtaining an array of strains on a solid growth medium wherein each strain overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid

comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of
5 SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate conditions is overexpressed;

contacting said array of strains with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene
10 product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly on said solid medium.

15 371. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining an array of strains on a solid growth medium wherein each strain overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product comprises a polypeptide
20 selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOS.: 42938-78581 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOS: 42938-78581 is overexpressed;

25 contacting said array of strains with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

30 identifying the gene product which is overexpressed in a strain which proliferated more rapidly on said solid medium.

372. The method of Paragraph 366, 367, 368, 369, 370 or 371, wherein at least one strain in said array does not overexpresses a gene product which is essential for proliferation of said organism.

35 373. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a plurality of cultures, wherein each culture comprises a plurality of strains wherein each strain overexpresses a different gene product which is essential for

proliferation of said organism, wherein said culture comprises a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 is overexpressed;

contacting each of said cultures with a different concentration of said compound;

5 and

identifying the gene product which is overexpressed in a strain whose proliferation is inhibited by said compound.

374. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

10 obtaining a plurality of cultures, wherein each culture comprises a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397 is overexpressed;

15 contacting each of said cultures with a different concentration of said compound; and

identifying the gene product which is overexpressed in a strain whose proliferation is inhibited by said compound.

375. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

20 obtaining a plurality of cultures, wherein each culture comprises a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42938-78581 is overexpressed;

25 contacting each of said cultures with a different concentration of said compound; and

identifying the gene product which is overexpressed in a strain whose proliferation is inhibited by said compound.

30 376. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

35 obtaining a plurality of cultures, wherein each culture comprises a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene

product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS: 1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 1-6213, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS: 1-6213 is overexpressed;

contacting each of said cultures with a different concentration of said compound;
and

identifying the gene product which is overexpressed in a strain whose proliferation is inhibited by said compound.

377. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a plurality of cultures, wherein each culture comprises a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate conditions is overexpressed;

contacting each of said cultures with a different concentration of said compound;
and

identifying the gene product which is overexpressed in a strain whose proliferation is inhibited by said compound.

378. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

5 obtaining a plurality of cultures, wherein each culture comprises a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product comprises a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 42938-78581 and a polypeptide whose activity may be complemented by a polypeptide selected from the group
10 consisting of SEQ ID NOs: 42938-78581 is overexpressed;
contacting each of said cultures with a different concentration of said compound;
and
identifying the gene product which is overexpressed in a strain whose proliferation is inhibited by said compound.

15 379. The method of Paragraph 373, 374, 375, 376, 377 or 378, wherein at least one strain in said plurality of cultures does not overexpress a gene product which is essential for proliferation of said organism.

380. A method of profiling a compound's activity comprising:
performing the method of Paragraph 346 on a first culture using a first compound;
20 performing the method of Paragraph 346 on a second culture using a second compound; and
comparing the strains identified in said first culture to the strains identified in said second culture.

381. A method of profiling a compound's activity comprising:
25 performing the method of Paragraph 347 on a first culture using a first compound;
performing the method of Paragraph 347 on a second culture using a second compound; and
comparing the strains identified in said first culture to the strains identified in said second culture.

30 382. A method of profiling a compound's activity comprising:
performing the method of Paragraph 348 on a first culture using a first compound;
performing the method of Paragraph 348 on a second culture using a second compound; and
comparing the strains identified in said first culture to the strains identified in said
35 second culture.

383. A method of profiling a compound's activity comprising:
performing the method of Paragraph 349 on a first culture using a first compound;

performing the method of Paragraph 349 on a second culture using a second compound; and

comparing the strains identified in said first culture to the strains identified in said second culture.

5 384. A method of profiling a compound's activity comprising:
performing the method of Paragraph 350 on a first culture using a first compound;
performing the method of Paragraph 350 on a second culture using a second compound; and

10 comparing the strains identified in said first culture to the strains identified in said second culture.

385. A method of profiling a compound's activity comprising:
performing the method of Paragraph 351 on a first culture using a first compound;
performing the method of Paragraph 351 on a second culture using a second compound; and

15 comparing the strains identified in said first culture to the strains identified in said second culture.

386. A method of profiling a first compound's activity comprising:
growing an array of strains on a first solid medium comprising said first compound and on a second solid medium comprising a second compound, wherein each strain in said array overexpresses a different gene product which is essential for proliferation of an organism, wherein said culture comprises a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 is overexpressed, and wherein said first compound and said second compound inhibit the proliferation of said organism; and

20 25 comparing the pattern of strains which grow on said first solid medium with the pattern of strains which grow on said second solid medium.

387. A method of profiling a first compound's activity comprising:
growing an array of strains on a first solid medium comprising said first compound and on a second solid medium comprising a second compound, wherein each strain in said array overexpresses a different gene product which is essential for proliferation of an organism, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397 is overexpressed, and wherein said first compound and said second compound inhibit the proliferation of said organism; and

30 35 comparing the pattern of strains which grow on said first solid medium with the pattern of strains which grow on said second solid medium.

388. A method of profiling a first compound's activity comprising:

growing an array of strains on a first solid medium comprising said first compound and on a second solid medium comprising a second compound, wherein each strain in said array overexpresses a different gene product which is essential for proliferation of an organism, wherein said culture comprises a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42938-78581 is overexpressed, and wherein said first compound and said second compound inhibit the proliferation of said organism; and

comparing the pattern of strains which grow on said first solid medium with the pattern of strains which grow on said second solid medium.

389. A method of profiling a first compound's activity comprising:

growing an array of strains on a first solid medium comprising said first compound and on a second solid medium comprising a second compound, wherein each strain in said array overexpresses a different gene product which is essential for proliferation of an organism, wherein said culture comprises a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 is overexpressed, and wherein said first compound and said second compound inhibit the proliferation of said organism; and

comparing the pattern of strains which grow on said first solid medium with the pattern of strains which grow on said second solid medium.

390. A method of profiling a first compound's activity comprising:

growing an array of strains on a first solid medium comprising said first compound and on a second solid medium comprising a second compound, wherein each strain in said array overexpresses a different gene product which is essential for proliferation of an organism, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate conditions is overexpressed, and wherein said first compound and said second compound inhibit the proliferation of said organism; and

comparing the pattern of strains which grow on said first solid medium with the pattern of strains which grow on said second solid medium.

391. A method of profiling a first compound's activity comprising:

growing an array of strains on a first solid medium comprising said first compound and on a second solid medium comprising a second compound, wherein each strain in said array overexpresses a different gene product which is essential for proliferation of an organism, wherein said culture comprises a strain in which a gene product comprises a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOS.: 42938-78581 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOS.: 42938-78581 is overexpressed, and wherein said first compound and said second compound inhibit the proliferation of said organism; and

comparing the pattern of strains which grow on said first solid medium with the pattern of strains which grow on said second solid medium.

392. The method of any one of Paragraphs 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390 or 391, wherein said first compound is present in a crude or partially purified state.

393. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 1-6213 is underexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress said gene product on which said compound acts; and

identifying the gene product which is underexpressed in a strain which proliferated more slowly in said culture.

394. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397 is underexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress said gene product on which said compound acts; and

identifying the gene product which is underexpressed in a strain which proliferated more slowly in said culture.

395. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42938-78581 is underexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress said gene product on which said compound acts; and

identifying the gene product which is underexpressed in a strain which proliferated more slowly in said culture.

396. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 is underexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress said gene product on which said compound acts; and

identifying the gene product which is underexpressed in a strain which proliferated more slowly in said culture.

397. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid

comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate conditions is underexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress said gene product on which said compound acts; and

identifying the gene product which is underexpressed in a strain which proliferated more slowly in said culture.

398. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product comprises a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOS.: 42938-78581 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOS.: 42938-78581 is underexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress said gene product on which said compound acts; and

identifying the gene product which is underexpressed in a strain which proliferated more slowly in said culture.

399. The method of Paragraph 393, 394, 395, 396, 397 or 398, wherein at least one strain in said culture does not underexpresses a gene product which is essential for proliferation of said organism.

400. The method of Paragraph 393, 394, 395, 396, 397 or 398, wherein said strains which underexpresses said gene products comprise a nucleic acid complementary to at least a portion of a gene encoding said gene product which is essential for proliferation of said organism operably linked to a regulatable promoter.

401. The method of Paragraph 393, 394, 395, 396, 397 or 398, wherein said strains which underexpress said gene products express an antisense nucleic acid complementary to at least

a portion of a gene encoding said gene product which is essential for proliferation of said organism, wherein expression of said antisense nucleic acid reduces expression of said gene product in said strain.

402. The method of Paragraph 393, 394, 395, 396, 397 or 398, wherein said
5 identification step comprises determining the nucleotide sequence of a nucleic acid encoding said gene product in said strain which proliferated more slowly.

403. The method of Paragraph 393, 394, 395, 396, 397 or 398, wherein said identification step comprises performing an amplification reaction to identify the nucleic acid encoding said gene product in said cell which proliferated more slowly.

10 404. The method of Paragraph 393, 394, 395, 396, 397 or 398, wherein the products of said amplification reaction are labeled with a detectable dye.

405. The method of Paragraph 404, wherein said identification step comprises performing a hybridization procedure.

15 406. The method of Paragraph 393, 394, 395, 396, 397 or 398, wherein said identification step comprises contacting a nucleic acid array with a nucleic acid encoding said gene product in said cell which proliferated more slowly.

407. The method of Paragraph 393, 394, 395, 396, 397 or 398, wherein said organism is selected from the group consisting of bacteria, fungi, protozoa.

20 408. The method of Paragraph 393, 394, 395, 396, 397 or 398, wherein said culture is a culture of an organism selected from the group consisting of *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr*
25 (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*,
30 *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*,
35 *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*,

Ureaplasma urealyticum, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* and any species falling within the genera of any of the above species.

409. The method of Paragraph 393, 394, 395, 396, 397 or 398, wherein said compound is obtained from a library of natural compounds.

5 410. The method of Paragraph 393, 394, 395, 396, 397 or 398, wherein said compound is obtained from a library of synthetic compounds.

411. The method of Paragraph 393, 394, 395, 396, 397 or 398, wherein said compound is present in a crude or partially purified state.

412. The method of Paragraph 393, 394, 395, 396, 397 or 398, further comprising
10 determining whether said gene product in said strain which proliferated more slowly in said culture has a counterpart in at least one other organism.

413. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a plurality of cultures, each culture comprising a plurality of strains
15 wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 is underexpressed;

contacting each of said cultures with a different concentration of said compound;
20 and

identifying the gene product which is underexpressed in a strain whose rate of proliferation is reduced by said compound.

414. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

25 obtaining a plurality of cultures, each culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397 is underexpressed;

30 contacting each of said cultures with a different concentration of said compound; and

identifying the gene product which is underexpressed in a strain whose rate of proliferation is reduced by said compound.

415. A method for identifying the gene product on which a compound which inhibits
35 proliferation of an organism acts comprising:

obtaining a plurality of cultures, each culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene

product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42938-78581 is underexpressed;

contacting each of said cultures with a different concentration of said compound;
and

5 identifying the gene product which is underexpressed in a strain whose rate of proliferation is reduced by said compound.

416. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a plurality of cultures, each culture comprising a plurality of strains
10 wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a
15 nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-
20 6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group
25 consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group
30 consisting of SEQ ID NOs.: 1-6213 is underexpressed;

contacting each of said cultures with a different concentration of said compound;
and

identifying the gene product which is underexpressed in a strain whose rate of proliferation is reduced by said compound.

35 417. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a plurality of cultures, each culture comprising a plurality of strains
wherein each strain underexpresses a different gene product which is essential for

proliferation of said organism, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a
5 nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate
10 conditions is underexpressed;

contacting each of said cultures with a different concentration of said compound;
and

identifying the gene product which is underexpressed in a strain whose rate of proliferation is reduced by said compound.

15 418. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a plurality of cultures, each culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene
20 product comprises a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOS.: 42938-78581 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOS: 42938-78581 is underexpressed;

25 contacting each of said cultures with a different concentration of said compound;
and

identifying the gene product which is underexpressed in a strain whose rate of proliferation is reduced by said compound.

30 419. A method of profiling a compound's activity comprising:

performing the method of Paragraph 393 on a first culture using a first compound;
performing the method of Paragraph 393 on a second culture using a second
compound; and

comparing the strains identified in said first culture to the strains identified in said second culture.

35 420. A method of profiling a compound's activity comprising:

performing the method of Paragraph 394 on a first culture using a first compound;
performing the method of Paragraph 394 on a second culture using a second
compound; and

comparing the strains identified in said first culture to the strains identified in said second culture.

421. A method of profiling a compound's activity comprising:

performing the method of Paragraph 395 on a first culture using a first compound;

5 performing the method of Paragraph 395 on a second culture using a second compound; and

comparing the strains identified in said first culture to the strains identified in said second culture.

422. A method of profiling a compound's activity comprising

10 performing the method of Paragraph 396 on a first culture using a first compound;

performing the method of Paragraph 396 on a second culture using a second compound; and

comparing the strains identified in said first culture to the strains identified in said second culture.

15 423. A method of profiling a compound's activity comprising

performing the method of Paragraph 397 on a first culture using a first compound;

performing the method of Paragraph 397 on a second culture using a second compound; and

20 comparing the strains identified in said first culture to the strains identified in said second culture.

424. A method of profiling a compound's activity comprising

performing the method of Paragraph 398 on a first culture using a first compound;

performing the method of Paragraph 398 on a second culture using a second compound; and

25 comparing the strains identified in said first culture to the strains identified in said second culture.

425. A method of profiling a first compound's activity comprising:

growing an array of strains on a first solid medium comprising said first compound and on a second solid medium comprising a second compound, wherein said array comprises a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of an organism, wherein said culture comprises a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 is underexpressed, and wherein said first compound and said second compound inhibit the proliferation of said organism; and

35 comparing the pattern of strains which grow on said first solid medium with the pattern of strains which grow on said second solid medium.

426. A method of profiling a first compound's activity comprising:

growing an array of strains on a first solid medium comprising said first compound and on a second solid medium comprising a second compound, wherein said array comprises a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of an organism, wherein said culture comprises a strain
5 in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397 is underexpressed, and wherein said first compound and said second compound inhibit the proliferation of said organism; and

comparing the pattern of strains which grow on said first solid medium with the
10 pattern of strains which grow on said second solid medium.

427. A method of profiling a first compound's activity comprising:

growing an array of strains on a first solid medium comprising said first compound and on a second solid medium comprising a second compound, wherein said array comprises a plurality of strains wherein each strain underexpresses a different gene product
15 which is essential for proliferation of an organism, wherein said culture comprises a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42938-78581 is underexpressed, and wherein said first compound and said second compound inhibit the proliferation of said organism; and

comparing the pattern of strains which grow on said first solid medium with the
20 pattern of strains which grow on said second solid medium.

428. A method of profiling a first compound's activity comprising:

growing an array of strains on a first solid medium comprising said first compound and on a second solid medium comprising a second compound, wherein said array comprises a plurality of strains wherein each strain underexpresses a different gene product
25 which is essential for proliferation of an organism, wherein said culture comprises a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.:
30 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-6213, a gene product having at least 25% amino acid identity as determined using FASTA
35 version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group

consisting of SEQ ID NOS.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 1-6213 is underexpressed, and wherein said first compound and said second compound inhibit the proliferation of said organism; and

comparing the pattern of strains which grow on said first solid medium with the pattern of strains which grow on said second solid medium.

429. A method of profiling a first compound's activity comprising:

growing an array of strains on a first solid medium comprising said first compound and on a second solid medium comprising a second compound, wherein said array comprises a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of an organism, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate conditions is underexpressed, and wherein said first compound and said second compound inhibit the proliferation of said organism; and

comparing the pattern of strains which grow on said first solid medium with the pattern of strains which grow on said second solid medium.

430. A method of profiling a first compound's activity comprising:

growing an array of strains on a first solid medium comprising said first compound and on a second solid medium comprising a second compound, wherein said array comprises a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of an organism, wherein said culture comprises a strain in which a gene product comprises a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOS.: 42938-78581 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOS.: 42938-78581 is underexpressed, and wherein said first compound and said second compound inhibit the proliferation of said organism; and

comparing the pattern of strains which grow on said first solid medium with the pattern of strains which grow on said second solid medium.

431. The method of any one of Paragraphs 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429 or 430, wherein said first compound is present in a crude or partially purified state.

5 432. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a plurality of cultures comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product whose activity or
10 level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 is underexpressed;

contacting each of said plurality of cultures with a varying concentration of a regulatory agent which regulates the level of expression of said gene products which are essential for proliferation of said organism; and

15 identifying the gene product which is underexpressed in a strain whose rate of proliferation is reduced by said compound.

433. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a plurality of cultures comprising a plurality of strains wherein each
20 strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397 is underexpressed;

contacting each of said plurality of cultures with a varying concentration of a
25 regulatory agent which regulates the level of expression of said gene products which are essential for proliferation of said organism; and

identifying the gene product which is underexpressed in a strain whose rate of proliferation is reduced by said compound.

30 434. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a plurality of cultures comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42938-78581 is
35 underexpressed;

contacting each of said plurality of cultures with a varying concentration of a regulatory agent which regulates the level of expression of said gene products which are essential for proliferation of said organism; and

identifying the gene product which is underexpressed in a strain whose rate of proliferation is reduced by said compound.

435. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

5 obtaining a plurality of cultures comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product
10 whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide
15 sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.:
20 1-6213 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 is underexpressed;

contacting each of said plurality of cultures with a varying concentration of a regulatory agent which regulates the level of expression of said gene products which are essential for proliferation of said organism; and

30 identifying the gene product which is underexpressed in a strain whose rate of proliferation is reduced by said compound.

436. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

35 obtaining a plurality of cultures comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as

determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate conditions is underexpressed;

contacting each of said plurality of cultures with a varying concentration of a regulatory agent which regulates the level of expression of said gene products which are essential for proliferation of said organism; and

identifying the gene product which is underexpressed in a strain whose rate of proliferation is reduced by said compound.

437. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a plurality of cultures comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product comprises a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOS.: 42938-78581 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOS.: 42938-78581 is underexpressed;

contacting each of said plurality of cultures with a varying concentration of a regulatory agent which regulates the level of expression of said gene products which are essential for proliferation of said organism; and

identifying the gene product which is underexpressed in a strain whose rate of proliferation is reduced by said compound.

438. A culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 1-6213 is overexpressed.

439. A culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 is overexpressed.

440. A culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture

comprises a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42938-78581 is overexpressed.

441. A culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture
5 comprises a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as
10 determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide
15 sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose
20 activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 is overexpressed.

442. A culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture
25 comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected
30 from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate conditions is overexpressed.

443. A culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture
35 comprises a strain in which a gene product comprises a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 42938-78581

and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 42938-78581 is overexpressed.

444. The culture of Paragraph 438, 439, 440, 441, 442 or 443, wherein said strains which overexpress said gene products comprise a nucleic acid encoding said gene product which is essential for proliferation of said organism operably linked to a regulatable promoter.

445. The culture of Paragraph 438, 439, 440, 441, 442 or 443, wherein said strains which overexpress said gene products comprise a nucleic acid encoding said gene product which is essential for proliferation of said organism operably linked to a constitutive promoter.

446. The culture of Paragraph 438, 439, 440, 441, 442 or 443, wherein said culture is a culture of an organism selected from the group consisting of *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* and any species falling within the genera of any of the above species.

447. A culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 is underexpressed.

448. A culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture

comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397 is underexpressed.

449. A culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture
5 comprises a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42938-78581 is underexpressed.

450. A culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product selected from the group consisting of a gene product
10 having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a
15 gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a
20 nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid
25 comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 is underexpressed.

451. A culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide
30 sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic
35 acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate conditions is underexpressed.

452. A culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture

comprises a strain in which a gene product comprises a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 42938-78581 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 42938-78581 is underexpressed.

453. The culture of Paragraph 447, 448, 449, 450, 451 or 452, wherein said strains which underexpress said gene products comprise a nucleic acid encoding said gene product which is essential for proliferation of said organism operably linked to a regulatable promoter.

454. The culture of Paragraph 447, 448, 449, 450, 451 or 452, wherein said strains which underexpress said gene products comprise a nucleic acid encoding said gene product which is essential for proliferation of said organism operably linked to a constitutive promoter.

455. The culture of Paragraph 447, 448, 449, 450, 451 or 452, wherein said culture is a culture of an organism selected from the group consisting of *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefir* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* and any species falling within the genera of any of the above species.

456. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the overexpressed genes has been altered so

as to include a nucleotide sequence which can be used to generate a unique product corresponding to each of the overexpressed genes, wherein said culture comprises a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 is overexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

457. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the overexpressed genes has been altered so as to include a nucleotide sequence which can be used to generate a unique product corresponding to each of the overexpressed genes, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397 is overexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

458. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the overexpressed genes has been altered so as to include a nucleotide sequence which can be used to generate a unique product corresponding to each of the overexpressed genes, wherein said culture comprises a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42938-78581 is overexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

459. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the overexpressed genes has been altered so as to include a nucleotide sequence which can be used to generate a unique product corresponding to each of the overexpressed genes, wherein said culture comprises a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 is overexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

460. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

5 obtaining a culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the overexpressed genes has been altered so as to include a nucleotide sequence which can be used to generate a unique product corresponding to each of the overexpressed genes, wherein said culture comprises a strain
10 in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid comprising a nucleotide sequence which hybridizes to a
15 sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate conditions is overexpressed;

20 contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

25 identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

461. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

30 obtaining a culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the overexpressed genes has been altered so as to include a nucleotide sequence which can be used to generate a unique product corresponding to each of the overexpressed genes, wherein said culture comprises a strain in which a gene product comprises a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version
35 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOS.: 42938-78581 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOS.: 42938-78581 is overexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

462. The method of Paragraph 456, 457, 458, 459, 460 or 461, wherein the nucleotide sequence of each of the genes encoding an overexpressed gene product has been altered by replacing the native promoters of said genes with promoters which facilitate overexpression of said gene products.

463. The method of Paragraph 456, 457, 458, 459, 460 or 461, wherein the nucleotide sequence of each of the genes encoding an overexpressed gene product has been altered by inserting a regulatory element into the native promoters of said genes with a promoter which facilitates overexpression of said gene products.

464. The method of Paragraph 463, wherein said regulatory element is selected from the group consisting of a regulatable promoter, an operator which is recognized by a repressor, a nucleotide sequence which is recognized by a transcriptional activator, a transcriptional terminator, a nucleotide sequence which introduces a bend in the DNA and an upstream activating sequence.

465. The method of Paragraph 456, 457, 458, 459, 460 or 461, wherein the step of identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene comprises performing an amplification reaction and detecting a unique amplification product corresponding to said gene.

466. The method of Paragraph 462, wherein the native promoter of each of the genes encoding a gene product essential for proliferation is replaced with the same promoter.

467. The method of Paragraph 462, wherein the native promoters of the genes encoding gene products essential for proliferation are replaced with a plurality of promoters selected to give a desired expression level for each gene product.

468. The method of Paragraph 462, wherein said promoters which replaced the native promoters in each strain comprise regulatable promoters.

469. The method of Paragraph 462, wherein said promoters which replaced the native promoters in each strain each strain comprise constitutive promoters.

470. The method of Paragraph 456, 457, 458, 459, 460 or 461, wherein said organism is selected from the group consisting of bacteria, fungi, and protozoa.

471. The method of Paragraph 456, 457, 458, 459, 460 or 461, wherein said culture is a culture of an organism selected from the group consisting of *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*,

Campylobacter jejuni, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium*
 5 *perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma*
 10 *genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*,
 15 *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* and any species falling within the genera of any of the above species.

472. A method for identifying the gene product on which a compound which inhibits
 20 proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the underexpressed genes has been altered so as to include a nucleotide sequence which can be used to generate a unique product
 25 corresponding to each of the underexpressed genes and wherein said culture comprises a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 is underexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit
 30 the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress the gene product on which said compound acts; and

identifying the gene product which is underexpressed in a strain which proliferated
 35 more rapidly in said culture by detecting the unique product corresponding to said gene.

473. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the underexpressed genes has been altered so as to include a nucleotide sequence which can be used to generate a unique product
5 corresponding to each of the underexpressed genes and wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397 is underexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said gene product on which
10 said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress the gene product on which said compound acts; and

identifying the gene product which is underexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

15 474. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the underexpressed genes has been altered
20 so as to include a nucleotide sequence which can be used to generate a unique product corresponding to each of the underexpressed genes, wherein said culture comprises a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42938-78581 is underexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit
25 the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress the gene product on which said compound acts; and

identifying the gene product which is underexpressed in a strain which proliferated
30 more rapidly in said culture by detecting the unique product corresponding to said gene.

475. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism
35 and wherein the nucleotide sequence of each of the underexpressed genes has been altered so as to include a nucleotide sequence which can be used to generate a unique product corresponding to each of the underexpressed genes, wherein said culture comprises a strain in which a gene product selected from the group consisting of a gene product having at

least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 1-6213, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 1-6213 is underexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress the gene product on which said compound acts; and

identifying the gene product which is underexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

476. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the underexpressed genes has been altered so as to include a nucleotide sequence which can be used to generate a unique product corresponding to each of the underexpressed genes, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent

conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate conditions is underexpressed;

5 contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress the gene product on which said compound acts; and

10 identifying the gene product which is underexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

477. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

15 obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the underexpressed genes has been altered so as to include a nucleotide sequence which can be used to generate a unique product corresponding to each of the underexpressed genes, wherein said culture comprises a strain in which a gene product comprises a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 20 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOS.: 42938-78581 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOS: 42938-78581 is underexpressed;

25 contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress the gene product on which said compound acts; and

30 identifying the gene product which is underexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

478. The method of Paragraph 472, 473, 474, 475, 476 or 477, wherein the nucleotide sequence of each of the genes encoding an underexpressed gene product has been altered by replacing the native promoters of said genes with promoters which facilitate underexpression of said gene products.

35 479. The method of Paragraph 472, 473, 474, 475, 476 or 477, wherein the nucleotide sequence of each of the genes encoding an underexpressed gene product has been altered by inserting a regulatory element into the native promoters of said genes with a promoter which facilitates underexpression of said gene products.

480. The method of Paragraph 479, wherein said regulatory element is selected from the group consisting of a regulatable promoter, an operator which is recognized by a repressor, a nucleotide sequence which is recognized by a transcriptional activator, a transcriptional terminator, a nucleotide sequence which introduces a bend in the DNA and an upstream activating sequence.

5 481. The method of Paragraph 472, 473, 474, 475, 476 or 477, wherein the step of identifying the gene product which is underexpressed in a strain which proliferated more slowly in said culture by detecting the unique product corresponding to said gene comprises performing an amplification reaction and detecting a unique amplification product corresponding to said gene.

482. The method of Paragraph 478, wherein the native promoter of each of the genes
10 encoding a gene product essential for proliferation is replaced with the same promoter.

483. The method of Paragraph 478, wherein the native promoters of the genes encoding gene products essential for proliferation are replaced with a plurality of promoters selected to give a desired expression level for each gene product.

484. The method of Paragraph 478, wherein said promoters which replaced the native
15 promoters in each strain comprise regulatable promoters.

485. The method of Paragraph 478, wherein said promoters which replaced the native promoters in each strain each strain comprise constitutive promoters.

486. The method of Paragraph 472, 473, 474, 475, 476 or 477, wherein said organism is selected from the group consisting of bacteria, fungi, and protozoa.

20 487. The method of Paragraph 472, 473, 474, 475, 476 or 477, wherein said culture is a culture of an organism selected from the group consisting of *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*),
25 *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*,
30 *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*,
35 *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*,

Streptococcus pneumoniae, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* and any species falling within the genera of any of the above species.

488. A method for determining the extent to which each of a plurality of strains are
5 present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or
collection of strains wherein said culture or collection of strains comprises a plurality of
strains wherein each strain overexpresses or underexpresses a different gene product which
is required for proliferation of said organism wherein said culture comprises a strain in
10 which a gene product whose activity or level is inhibited by a nucleic acid comprising a
nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 is
overexpressed or underexpressed;

performing an amplification reaction using a set of primer pairs which are
complementary to nucleotide sequences within or adjacent to the genes which encode said
15 gene products, wherein the members of said set of primer pairs are designed such that each
primer pair would yield an amplification product having a length distinguishable from the
lengths of the amplification products from the other primer pairs if a strain comprising the
nucleotide sequences complementary to said primer pair is present in said culture or
collection of strains; and

20 determining the lengths of the amplification products obtained in said amplification
reaction.

489. A method for determining the extent to which each of a plurality of strains are
present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or
25 collection of strains wherein said culture or collection of strains comprises a plurality of
strains wherein each strain overexpresses or underexpresses a different gene product which
is required for proliferation of said organism , wherein said culture comprises a strain in
which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected
from the group consisting of SEQ ID NOs.: 6214-42397 is overexpressed or
30 underexpressed;

performing an amplification reaction using a set of primer pairs which are
complementary to nucleotide sequences within or adjacent to the genes which encode said
gene products, wherein the members of said set of primer pairs are designed such that each
primer pair would yield an amplification product having a length distinguishable from the
35 lengths of the amplification products from the other primer pairs if a strain comprising the
nucleotide sequences complementary to said primer pair is present in said culture or
collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction.

490. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

5 obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism, wherein said culture comprises a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42938-78581 is overexpressed or underexpressed;

10 performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction.

20 491. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism, wherein said culture comprises a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group

consisting of SEQ ID NOS.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 1-6213 is overexpressed or underexpressed;

performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction.

492. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate conditions is overexpressed or underexpressed;

performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction.

493. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

5 obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism, wherein said culture comprises a strain in which a gene product comprising a polypeptide selected from the group consisting of a
10 polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 42938-78581 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 42938-78581 is overexpressed or underexpressed;

15 performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or
20 collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction.

494. The method of Paragraph 488, 489, 490, 491, 492 or 493, wherein one member of each primer pair for each of said genes is labeled with a detectable dye.

25 495. The method of Paragraph 488, 489, 490, 491, 492 or 493, wherein:

said nucleic acid sample is divided into N aliquots; and

said amplification reaction is performed on each aliquot using primer pairs complementary to nucleotide sequences within or adjacent to 1/N of the genes which encode said gene products, wherein one of the members of each primer pair in each aliquot
30 is labeled with a dye and wherein the dyes on the primers in each aliquot are distinguishable from one another.

496. The method of Paragraph 494, further comprising pooling the amplification products from each of the aliquots prior to determining the lengths of the amplification products.

35 497. The method of Paragraph 488, 489, 490, 491, 492 or 493, wherein the native promoters of said genes which encode said gene products have been replaced with a regulatable promoter and one of the primers in said primer pairs is complementary to a nucleotide sequence within said regulatable promoter.

498. The method of Paragraph 496, wherein the native promoters for each of said genes were replaced with the same regulatable promoter.

499. The method of Paragraph 496, wherein more than one regulatable promoter was used to replace the promoters of said genes such that some of said genes are under the control of a
5 different regulatable promoter.

500. A method for identifying the target of a compound which inhibits the proliferation of an organism comprising:

obtaining a first nucleic acid sample comprising nucleic acids from a first culture or collection of strains wherein said culture or collection of strains comprises a plurality of
10 strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism and wherein said culture or collection of strains has been contacted with said compound;

obtaining a second nucleic acid sample comprising nucleic acids from a second culture or collection of strains wherein said culture or collection of strains comprises the
15 same strains as said first culture or collection of strains wherein said second culture or collection of strains has not been contacted with said compound;

performing a first amplification reaction on said first nucleic acid sample using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs
20 are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains;

performing a second amplification reaction on said second nucleic acid sample
25 using the same set of primer pairs used in said first amplification reaction;

and comparing the amount of each amplification product in said first amplification reaction to the amount of that amplification product in said second amplification reaction, wherein an increased level of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding
30 to said amplification product is the target of said compound if said culture or strain overexpresses said gene products and a decreased level of of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products, wherein said first and second
35 cultures or collection of strains comprise a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 is overexpressed or underexpressed.

501. A method for identifying the target of a compound which inhibits the proliferation of an organism comprising:

obtaining a first nucleic acid sample comprising nucleic acids from a first culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism and wherein said culture or collection of strains has been contacted with said compound;

obtaining a second nucleic acid sample comprising nucleic acids from a second culture or collection of strains wherein said culture or collection of strains comprises the same strains as said first culture or collection of strains wherein said second culture or collection of strains has not been contacted with said compound;

performing a first amplification reaction on said first nucleic acid sample using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains;

performing a second amplification reaction on said second nucleic acid sample using the same set of primer pairs used in said first amplification reaction;

and comparing the amount of each amplification product in said first amplification reaction to the amount of that amplification product in said second amplification reaction, wherein an increased level of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products and a decreased level of of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products, wherein said first and second cultures or collection of strains comprise a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397 is overexpressed or underexpressed.

502. A method for identifying the target of a compound which inhibits the proliferation of an organism comprising:

obtaining a first nucleic acid sample comprising nucleic acids from a first culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which

is required for proliferation of said organism and wherein said culture or collection of strains has been contacted with said compound;

5 obtaining a second nucleic acid sample comprising nucleic acids from a second culture or collection of strains wherein said culture or collection of strains comprises the same strains as said first culture or collection of strains wherein said second culture or collection of strains has not been contacted with said compound;

performing a first amplification reaction on said first nucleic acid sample using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains;

15 performing a second amplification reaction on said second nucleic acid sample using the same set of primer pairs used in said first amplification reaction;

and comparing the amount of each amplification product in said first amplification reaction to the amount of that amplification product in said second amplification reaction, wherein an increased level of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products and a decreased level of of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products, wherein said first and second cultures or collection of strains comprise a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42938-78581 is overexpressed or underexpressed.

503. A method for identifying the target of a compound which inhibits the proliferation of an organism comprising:

30 obtaining a first nucleic acid sample comprising nucleic acids from a first culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism and wherein said culture or collection of strains has been contacted with said compound;

35 obtaining a second nucleic acid sample comprising nucleic acids from a second culture or collection of strains wherein said culture or collection of strains comprises the same strains as said first culture or collection of strains wherein said second culture or collection of strains has not been contacted with said compound;

performing a first amplification reaction on said first nucleic acid sample using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains;

performing a second amplification reaction on said second nucleic acid sample using the same set of primer pairs used in said first amplification reaction;

and comparing the amount of each amplification product in said first amplification reaction to the amount of that amplification product in said second amplification reaction, wherein an increased level of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products and a decreased level of of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products, wherein said first and second cultures or collection of strains comprise a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 is overexpressed or underexpressed.

504. A method for identifying the target of a compound which inhibits the proliferation of an organism comprising:

obtaining a first nucleic acid sample comprising nucleic acids from a first culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism and wherein said culture or collection of strains has been contacted with said compound;

obtaining a second nucleic acid sample comprising nucleic acids from a second culture or collection of strains wherein said culture or collection of strains comprises the same strains as said first culture or collection of strains wherein said second culture or collection of strains has not been contacted with said compound;

performing a first amplification reaction on said first nucleic acid sample using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains;

performing a second amplification reaction on said second nucleic acid sample using the same set of primer pairs used in said first amplification reaction;

and comparing the amount of each amplification product in said first amplification reaction to the amount of that amplification product in said second amplification reaction, wherein an increased level of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products and a decreased level of of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products, wherein said first and second cultures or collection of strains comprise a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from

the group consisting of SEQ ID NOS.: 6214-42397 under moderate conditions is overexpressed or underexpressed.

505. A method for identifying the target of a compound which inhibits the proliferation of an organism comprising:

5 obtaining a first nucleic acid sample comprising nucleic acids from a first culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism and wherein said culture or collection of strains has been contacted with said compound;

10 obtaining a second nucleic acid sample comprising nucleic acids from a second culture or collection of strains wherein said culture or collection of strains comprises the same strains as said first culture or collection of strains wherein said second culture or collection of strains has not been contacted with said compound;

15 performing a first amplification reaction on said first nucleic acid sample using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains;

20 performing a second amplification reaction on said second nucleic acid sample using the same set of primer pairs used in said first amplification reaction;

25 and comparing the amount of each amplification product in said first amplification reaction to the amount of that amplification product in said second amplification reaction, wherein an increased level of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products and a decreased level of of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that
30 the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products, wherein said first and second culture or collection of strains comprise a strain in which a gene product comprising a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the
35 group consisting of SEQ ID NOS.: 42938-78581 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOS: 42938-78581 is overexpressed or underexpressed.

506. The method of Paragraph 500, 501, 502, 503, 504 or 505, wherein one member of each primer pair for each of said genes is labeled with a detectable dye.

507. The method of Paragraph 500, 501, 502, 503, 504 or 505, wherein the native promoters of said genes which encode said gene products have been replaced with a regulatable promoter and one of the primers in said primer pairs is complementary to a nucleotide sequence within said regulatable promoter.

508. The method of Paragraph 500, 501, 502, 503, 504 or 505, wherein the native promoters for each of said genes were replaced with the same regulatable promoter.

509. The method of Paragraph 500, 501, 502, 503, 504 or 505, wherein more than one regulatable promoter was used to replace the promoters of said genes such that some of said genes are under the control of a different regulatable promoter.

510. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which transcribe an antisense nucleic acid complementary to a different gene product which is required for proliferation of said organism;

performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the nucleic acids which encode said antisense nucleic acids, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 is overexpressed or underexpressed.

511. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which transcribe an antisense nucleic acid complementary to a different gene product which is required for proliferation of said organism;

performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the nucleic acids which encode said antisense nucleic acids, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length

distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

5 determining the lengths of the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397 is overexpressed or underexpressed.

512. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

10 obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which transcribe an antisense nucleic acid complementary to a different gene product which is required for proliferation of said organism;

15 performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the nucleic acids which encode said antisense nucleic acids, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

20 determining the lengths of the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42938-78581 is overexpressed or underexpressed.

25 513. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

30 obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which transcribe an antisense nucleic acid complementary to a different gene product which is required for proliferation of said organism;

35 performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the nucleic acids which encode said antisense nucleic acids, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 is overexpressed or underexpressed.

514. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which transcribe an antisense nucleic acid complementary to a different gene product which is required for proliferation of said organism;

performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the nucleic acids which encode said antisense nucleic acids, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as

determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid
 5 comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate conditions is overexpressed or underexpressed.

515. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

10 obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which transcribe an antisense nucleic acid complementary to a different gene product which is required for proliferation of said organism;

15 performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the nucleic acids which encode said antisense nucleic acids, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present
 20 in said culture or collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene product comprising a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the
 25 group consisting of SEQ ID NOS.: 42938-78581 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOS: 42938-78581 is overexpressed or underexpressed.

516. The method of Paragraph 510, 511, 512, 513, 514 or 515, wherein one member of each primer pair for each of said genes is labeled with a detectable dye.

30 517. The method of Paragraph 510, 511, 512, 513, 514 or 515, wherein:

said nucleic acid sample is divided into N aliquots; and

said amplification reaction is performed on each aliquot using primer pairs complementary to nucleotide sequences within or adjacent to 1/N of the genes which encode said gene products, wherein one of the members of each primer pair in each aliquot
 35 is labeled with a dye and wherein the dyes on the primers in each aliquot are distinguishable from one another.

518. The method of Paragraph 517, further comprising pooling the amplification products from each of the aliquots prior to determining the lengths of the amplification products.

519. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which overexpress or underexpress a different gene product which is required for proliferation of said organism;

performing an amplification reaction using primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein said primer pairs are designed such that each primer pair would yield an amplification product which is distinguishable from the amplification products produced by the other primer pairs on the a basis selected from the group consisting of length, detectable label and both length and detectable label if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

identifying the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 is overexpressed or underexpressed.

520. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which overexpress or underexpress a different gene product which is required for proliferation of said organism;

performing an amplification reaction using primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein said primer pairs are designed such that each primer pair would yield an amplification product which is distinguishable from the amplification products produced by the other primer pairs on the a basis selected from the group consisting of length, detectable label and both length and detectable label if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

identifying the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397 is overexpressed or underexpressed.

521. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of

strains which overexpress or underexpress a different gene product which is required for proliferation of said organism;

performing an amplification reaction using primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein said primer pairs are designed such that each primer pair would yield an amplification product which is distinguishable from the amplification products produced by the other primer pairs on the a basis selected from the group consisting of length, detectable label and both length and detectable label if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

identifying the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42938-78581 is overexpressed or underexpressed.

522. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which overexpress or underexpress a different gene product which is required for proliferation of said organism;

performing an amplification reaction using primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein said primer pairs are designed such that each primer pair would yield an amplification product which is distinguishable from the amplification products produced by the other primer pairs on the a basis selected from the group consisting of length, detectable label and both length and detectable label if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

identifying the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide

sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 is overexpressed or underexpressed.

523. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which overexpress or underexpress a different gene product which is required for proliferation of said organism;

performing an amplification reaction using primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein said primer pairs are designed such that each primer pair would yield an amplification product which is distinguishable from the amplification products produced by the other primer pairs on the basis selected from the group consisting of length, detectable label and both length and detectable label if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

identifying the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate conditions is overexpressed or underexpressed.

524. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of

strains which overexpress or underexpress a different gene product which is required for proliferation of said organism;

performing an amplification reaction using primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein said primer pairs are designed such that each primer pair would yield an amplification product which is distinguishable from the amplification products produced by the other primer pairs on the basis selected from the group consisting of length, detectable label and both length and detectable label if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

identifying the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene product comprising a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 42938-78581 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 42938-78581 is overexpressed or underexpressed.

525. The method of Paragraph 519, 520, 521, 522, 523 or 524, wherein said primer pairs are divided into at least two sets, each primer pair comprises a primer which is labeled with a distinguishable dye, and the distinguishable dye used to label each set of primer pairs is distinguishable from the dye used to label the other sets of primer pairs.

526. The method of Paragraph 519, 520, 521, 522, 523 or 524, wherein:

said nucleic acid sample is divided into N aliquots; and

said amplification reaction is performed on each aliquot using primer pairs complementary to nucleotide sequences within or adjacent to 1/N of the genes which encode said gene products, wherein one of the members of each primer pair in each aliquot is labeled with a dye and wherein the dyes on the primers in each aliquot are distinguishable from one another.

527. The method of Paragraph 526, further comprising pooling the amplification products from each of the aliquots prior to determining the lengths of the amplification products.

528. The method of Paragraph 519, 520, 521, 522, 523 or 524, wherein the native promoters of said genes which encode said gene products have been replaced with a regulatable promoter and one of the primers in said primer pairs is complementary to a nucleotide sequence within said regulatable promoter.

529. The method of Paragraph 528, wherein the native promoters for each of said genes were replaced with the same regulatable promoter.

530. The method of Paragraph 528, wherein more than one regulatable promoter was used to replace the promoters of said genes such that some of said genes are under the control of a different regulatable promoter.

Definitions

By "biological pathway" is meant any discrete cell function or process that is carried out by a gene product or a subset of gene products. Biological pathways include anabolic, catabolic, enzymatic, biochemical and metabolic pathways as well as pathways involved in the production of cellular structures such as cell walls. Biological pathways that are usually required for proliferation of cells or microorganisms include, but are not limited to, cell division, DNA synthesis and replication, RNA synthesis (transcription), protein synthesis (translation), protein processing, protein transport, fatty acid biosynthesis, electron transport chains, cell wall synthesis, cell membrane production, synthesis and maintenance, and the like.

By "inhibit activity of a gene or gene product" is meant having the ability to interfere with the function of a gene or gene product in such a way as to decrease expression of the gene, in such a way as to reduce the level or activity of a product of the gene or in such a way as to inhibit the interaction of the gene or gene product with other biological molecules required for its activity. Agents which inhibit the activity of a gene include agents that inhibit transcription of the gene, agents that inhibit processing of the transcript of the gene, agents that reduce the stability of the transcript of the gene, and agents that inhibit translation of the mRNA transcribed from the gene. In microorganisms, agents which inhibit the activity of a gene can act to decrease expression of the operon in which the gene resides or alter the folding or processing of operon RNA so as to reduce the level or activity of the gene product. The gene product can be a non-translated RNA such as ribosomal RNA, a translated RNA (mRNA) or the protein product resulting from translation of the gene mRNA. Of particular utility to the present invention are antisense RNAs that have activities against the operons or genes to which they specifically hybridize.

By "activity against a gene product" is meant having the ability to inhibit the function or to reduce the level or activity of the gene product in a cell. This includes, but is not limited to, inhibiting the enzymatic activity of the gene product or the ability of the gene product to interact with other biological molecules required for its activity, including inhibiting the gene product's assembly into a multimeric structure.

By "activity against a protein" is meant having the ability to inhibit the function or to reduce the level or activity of the protein in a cell. This includes, but is not limited to, inhibiting the enzymatic activity of the protein or the ability of the protein to interact with other biological molecules required for its activity, including inhibiting the protein's assembly into a multimeric structure.

By "activity against a nucleic acid" is meant having the ability to inhibit the function or to reduce the level or activity of the nucleic acid in a cell. This includes, but is not limited to, inhibiting the ability of the nucleic acid interact with other biological molecules required for its activity, including inhibiting the nucleic acid's assembly into a multimeric structure.

By "activity against a gene" is meant having the ability to inhibit the function or expression of the gene in a cell. This includes, but is not limited to, inhibiting the ability of the gene to interact with other biological molecules required for its activity.

By "activity against an operon" is meant having the ability to inhibit the function or reduce the level of one or more products of the operon in a cell. This includes, but is not limited to, inhibiting the enzymatic activity of one or more products of the operon or the ability of one or more products of the operon to interact with other biological molecules required for its activity.

By "antibiotic" is meant an agent which inhibits the proliferation of a cell or microorganism.

By "*E. coli* or *Escherichia coli*" is meant *Escherichia coli* or any organism previously categorized as a species of *Shigella* including *Shigella boydii*, *Shigella flexneri*, *Shigella dysenteriae*, *Shigella sonnei*, *Shigella 2A*.

By "homologous coding nucleic acid" is meant a nucleic acid homologous to a nucleic acid encoding a gene product whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 or a portion thereof. In some embodiments, the homologous coding nucleic acid may have at least 97%, at least 95%, at least 90%, at least 85%, at least 80%, or at least 70% nucleotide sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42,397 and fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides thereof. In other embodiments the homologous coding nucleic acids may have at least 97%, at least 95%, at least 90%, at least 85%, at least 80%, or at least 70% nucleotide sequence identity to a nucleotide sequence selected from the group consisting of the nucleotide sequences complementary to one of SEQ ID NOs.: 1-6213 and fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides thereof. Identity may be measured using BLASTN version 2.0 with the default parameters or tBLASTX with the default parameters. (Altschul, S.F. et al. Gapped BLAST and PSI-BLAST: A New Generation of Protein Database Search Programs, *Nucleic Acid Res.* 25: 3389-3402 (1997). Alternatively a "homologous coding nucleic acid" could be identified by membership of the gene of interest to a functional orthologue cluster. All other members of that orthologue cluster would be considered homologues. Such a library of functional orthologue clusters can be found at <http://www.ncbi.nlm.nih.gov/COG>. A gene can be classified into a cluster of orthologous groups or COG by using the COGNITOR program available at the above web site, or by direct BLASTP comparison of the gene of interest to the members of the COGs and analysis of these results as described by Tatusov, R.L., Galperin, M.Y., Natale, D. A. and Koonin, E.V. (2000) The COG database: a tool for genome-scale analysis of protein functions and evolution. *Nucleic Acids Research* v. 28 n. 1, pp33-36.

Homologous coding nucleic acids and the homologous polypeptides which they encode may also be identified using a "reciprocal" best-hit analysis. To facilitate the identification of homologous coding nucleic acids and homologous polypeptides, paralogous genes within each of

51 organisms are identified and clustered prior to comparison to other organisms. Briefly, the polypeptide sequence of each polypeptide encoded by each open reading frame (ORF) in a given organism is compared to the polypeptide sequence encoded by every other ORF for that organism for each of the 51 pathogenic organisms (PathoSeq Sept 2001 release) using BLASTP 2.09
5 algorithm without filtering. Simultaneously, the polypeptide sequence encoded by each ORF of an organism is compared to the polypeptide sequences encoded by each of the ORFs in the remaining 51 organisms. Those polypeptides within a single organism that shared a higher degree of sequence identity to one another than to polypeptide sequences obtained from any other organisms are clustered as "paralog" sequences for "reciprocal" best-hit analysis.

10 For each reference organism, the 50 homologous coding nucleic acids (and the 50 homologous polypeptides which they encode) can be determined by identifying the ORFs in each of the 50 comparison organisms which encode a polypeptide sharing the highest degree of amino acid sequence identity to the polypeptide encoded by the ORF from the reference organism. The accuracy of the identification of the predicted homologous coding nucleic acids (and the
15 homologous polypeptides which they encode) is confirmed by a "reciprocal" BLAST analysis in which the polypeptide sequence of the predicted homologous polypeptide is compared against the polypeptides encoded by each of the ORFS in the reference organism using BLASTP 2.09 algorithm without filtering. Only those polypeptides that share the highest degree of amino acid sequence identity in each portion of the two-way comparison are retained for further analysis.

20 The term "homologous coding nucleic acid" also includes nucleic acids comprising nucleotide sequences which encode polypeptides having at least 99%, 95%, at least 90%, at least 85%, at least 80%, at least 70%, at least 60%, at least 50%, at least 40% or at least 25% amino acid identity or similarity to a polypeptide comprising the amino acid sequence of one of SEQ ID NOs: 42,398-78,581 or to a polypeptide whose expression is inhibited by a nucleic acid comprising a
25 nucleotide sequence of one of SEQ ID NOs: 1-6213 or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof as determined using the FASTA version 3.0t78 algorithm with the default parameters. Alternatively, protein identity or similarity may be identified using BLASTP with the default parameters, BLASTX with the default parameters, TBLASTN with the default parameters, or tBLASTX with the default parameters.
30 (Altschul, S.F. et al. Gapped BLAST and PSI-BLAST: A New Generation of Protein Database Search Programs, Nucleic Acid Res. 25: 3389-3402 (1997).

Additionally, homologous coding nucleic acids and the homologous polypeptides which they encode may be identified using a "reciprocal" best-hit analysis. To facilitate the identification of homologous coding nucleic acids and homologous polypeptides, paralogous genes within each of
35 51 organisms are identified and clustered prior to comparison to other organisms. Briefly, the polypeptide sequence of each polypeptide encoded by each open reading frame (ORF) in a given organism is compared to the polypeptide sequence encoded by every other ORF for that organism for each of the 51 pathogenic organisms (PathoSeq Sept 2001 release) using BLASTP 2.09

algorithm without filtering. Simultaneously, the polypeptide sequence encoded by each ORF of an organism is compared to the polypeptide sequences encoded by each of the ORFs in the remaining 51 organisms. Those polypeptides within a single organism that shared a higher degree of sequence identity to one another than to polypeptide sequences obtained from any other organisms are clustered as "paralog" sequences for "reciprocal" best-hit analysis.

For each reference organism, the 50 homologous coding nucleic acids (and the 50 homologous polypeptides which they encode) can be determined by identifying the ORFs in each of the 50 comparison organisms which encode a polypeptide sharing the highest degree of amino acid sequence identity to the polypeptide encoded by the ORF from the reference organism. The accuracy of the identification of the predicted homologous coding nucleic acids (and the homologous polypeptides which they encode) is confirmed by a "reciprocal" BLAST analysis in which the polypeptide sequence of the predicted homologous polypeptide is compared against the polypeptides encoded by each of the ORFS in the reference organism using BLASTP 2.09 algorithm without filtering. Only those polypeptides that share the highest degree of amino acid sequence identity in each portion of the two-way comparison are retained for further analysis.

The term "homologous coding nucleic acid" also includes coding nucleic acids which hybridize under stringent conditions to a nucleic acid selected from the group consisting of the nucleotide sequences complementary to one of SEQ ID NOS.: 6214-42,397 and coding nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of the sequences complementary to one of SEQ ID NOS.: 6214-42,397. As used herein, "stringent conditions" means hybridization to filter-bound nucleic acid in 6xSSC at about 45°C followed by one or more washes in 0.1xSSC/0.2% SDS at about 68°C. Other exemplary stringent conditions may refer, *e.g.*, to washing in 6xSSC/0.05% sodium pyrophosphate at 37°C, 48°C, 55°C, and 60°C as appropriate for the particular probe being used.

The term "homologous coding nucleic acid" also includes coding nucleic acids comprising nucleotide sequences which hybridize under moderate conditions to a nucleotide sequence selected from the group consisting of the sequences complementary to one of SEQ ID NOS.: 6214-42,397 and coding nucleic acids comprising nucleotide sequences which hybridize under moderate conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of the sequences complementary to one of SEQ ID NOS.: 6214-42,397. As used herein, "moderate conditions" means hybridization to filter-bound DNA in 6x sodium chloride/sodium citrate (SSC) at about 45°C followed by one or more washes in 0.2xSSC/0.1% SDS at about 42-65°C.

The term "homologous coding nucleic acids" also includes nucleic acids comprising nucleotide sequences which encode a gene product whose activity may be complemented by a gene encoding a gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 1-6213. In some embodiments, the

homologous coding nucleic acids may encode a gene product whose activity is complemented by the gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42,397. In other embodiments, the homologous coding nucleic acids may comprise a nucleotide sequence encode a gene product whose activity is
5 complemented by one of the polypeptides of SEQ ID NOs. 42,398-78,581.

The term "homologous antisense nucleic acid" includes nucleic acids comprising a nucleotide sequence having at least 97%, at least 95%, at least 90%, at least 85%, at least 80%, or at least 70% nucleotide sequence identity to a nucleotide sequence selected from the group consisting of one of the sequences of SEQ ID NOS. 1-6213 and fragments comprising at least 10, 15, 20, 25,
10 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides thereof. Homologous antisense nucleic acids may also comprising nucleotide sequences which have at least 97%, at least 95%, at least 90%, at least 85%, at least 80%, or at least 70% nucleotide sequence identity to a nucleotide sequence selected from the group consisting of the sequences complementary to one of sequences of SEQ ID NOS.: 6214-42,397 and fragments comprising at least 10, 15, 20, 25, 30, 35,
15 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides thereof. Nucleic acid identity may be determined as described above.

The term "homologous antisense nucleic acid" also includes antisense nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a nucleotide sequence complementary to one of SEQ ID NOs.: 1-6213 and antisense nucleic acids comprising
20 nucleotide sequences which hybridize under stringent conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of the sequence complementary to one of SEQ ID NOs. 1-6213. Homologous antisense nucleic acids also include antisense nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-
25 42,397 and antisense nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of one of SEQ ID NOS.: 6214-42,397.

The term "homologous antisense nucleic acid" also includes antisense nucleic acids comprising nucleotide sequences which hybridize under moderate conditions to a nucleotide
30 sequence complementary to one of SEQ ID NOs.: 1-6213 and antisense nucleic acids comprising nucleotide sequences which hybridize under moderate conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of the sequence complementary to one of SEQ ID NOs. 1-6213. Homologous antisense nucleic acids also include antisense nucleic acids comprising nucleotide sequences which hybridize under moderate
35 conditions to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42,397 and antisense nucleic acids which comprising nucleotide sequences hybridize under moderate conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of one of SEQ ID NOS.: 6214-42,397.

By "homologous polypeptide" is meant a polypeptide homologous to a polypeptide whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 or by a homologous antisense nucleic acid. The term "homologous polypeptide" includes polypeptides having at least 99%, 95%, at least 90%, at least 85%, at least 80%, at least 70%, at least 60%, at least 50%, at least 40% or at least 25% amino acid identity or similarity to a polypeptide whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 or by a homologous antisense nucleic acid, or polypeptides having at least 99%, 95%, at least 90%, at least 85%, at least 80%, at least 70%, at least 60%, at least 50%, at least 40% or at least 25% amino acid identity or similarity to a polypeptide to a fragment comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids of a polypeptide whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 or by a homologous antisense nucleic acid. Identity or similarity may be determined using the FASTA version 3.0t78 algorithm with the default parameters. Alternatively, protein identity or similarity may be identified using BLASTP with the default parameters, BLASTX with the default parameters, or TBLASTN with the default parameters. (Altschul, S.F. et al. Gapped BLAST and PSI-BLAST: A New Generation of Protein Database Search Programs, *Nucleic Acid Res.* 25: 3389-3402 (1997). Additionally, homologous coding nucleic acids and the homologous polypeptides which they encode may be identified using a "reciprocal" best-hit analysis. To facilitate the identification of homologous coding nucleic acids and homologous polypeptides, paralogous genes within each of 51 organisms are identified and clustered prior to comparison to other organisms. Briefly, the polypeptide sequence of each polypeptide encoded by each open reading frame (ORF) in a given organism is compared to the polypeptide sequence encoded by every other ORF for that organism for each of the 51 pathogenic organisms (PathoSeq Sept 2001 release) using BLASTP 2.09 algorithm without filtering. Simultaneously, the polypeptide sequence encoded by each ORF of an organism is compared to the polypeptide sequences encoded by each of the ORFs in the remaining 51 organisms. Those polypeptides within a single organism that shared a higher degree of sequence identity to one another than to polypeptide sequences obtained from any other organisms are clustered as "paralog" sequences for "reciprocal" best-hit analysis.

For each reference organism, the 50 homologous coding nucleic acids (and the 50 homologous polypeptides which they encode) can be determined by identifying the ORFs in each of the 50 comparison organisms which encode a polypeptide sharing the highest degree of amino acid sequence identity to the polypeptide encoded by the ORF from the reference organism. The accuracy of the identification of the predicted homologous coding nucleic acids (and the homologous polypeptides which they encode) is confirmed by a "reciprocal" BLAST analysis in which the polypeptide sequence of the predicted homologous polypeptide is compared against the polypeptides encoded by each of the ORFS in the reference organism using BLASTP 2.09

algorithm without filtering. Only those polypeptides that share the highest degree of amino acid sequence identity in each portion of the two-way comparison are retained for further analysis.

The term homologous polypeptide also includes polypeptides having at least 99%, 95%, at least 90%, at least 85%, at least 80%, at least 70%, at least 60%, at least 50%, at least 40% or at least 25% amino acid identity or similarity to a polypeptide selected from the group consisting of SEQ ID NOs: 42,398-78,581 and polypeptides having at least 99%, 95%, at least 90%, at least 85%, at least 80%, at least 70%, at least 60%, at least 50%, at least 40% or at least 25% amino acid identity or similarity to a fragment comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids of a polypeptide selected from the group consisting of SEQ ID NOs: 42,398-78,581.

The invention also includes polynucleotides, preferably DNA molecules, that hybridize to one of the nucleic acids of SEQ ID NOs.: 1-6213, SEQ ID NOs.: 6214-42,397 or the complements of any of the preceding nucleic acids. Such hybridization may be under stringent or moderate conditions as defined above or under other conditions which permit specific hybridization. The nucleic acid molecules of the invention that hybridize to these DNA sequences include oligodeoxynucleotides ("oligos") which hybridize to the target gene under highly stringent or stringent conditions. In general, for oligos between 14 and 70 nucleotides in length the melting temperature (T_m) is calculated using the formula:

$$T_m (^{\circ}\text{C}) = 81.5 + 16.6(\log[\text{monovalent cations (molar)}] + 0.41 (\% \text{ G+C}) - (500/N))$$

where N is the length of the probe. If the hybridization is carried out in a solution containing formamide, the melting temperature may be calculated using the equation:

$$T_m(^{\circ}\text{C}) = 81.5 + 16.6(\log[\text{monovalent cations (molar)}] + 0.41(\% \text{ G+C}) - (0.61) (\% \text{ formamide}) - (500/N))$$

where N is the length of the probe. In general, hybridization is carried out at about 20-25 degrees below T_m (for DNA-DNA hybrids) or about 10-15 degrees below T_m (for RNA-DNA hybrids).

Other hybridization conditions are apparent to those of skill in the art (see, for example, Ausubel, F.M. *et al.*, eds., 1989, *Current Protocols in Molecular Biology*, Vol. I, Green Publishing Associates, Inc. and John Wiley & Sons, Inc., New York, at pp. 6.3.1-6.3.6 and 2.10.3.

The term, *Salmonella*, is the generic name for a large group of gram negative enteric bacteria that are closely related to *Escherichia coli*. The diseases caused by *Salmonella* are often due to contamination of foodstuffs or the water supply and affect millions of people each year. Traditional methods of *Salmonella* taxonomy were based on assigning a separate species name to each serologically distinguishable strain (Kauffmann, F 1966 *The bacteriology of the Enterobacteriaceae*. Munksgaard, Copenhagen). Serology of *Salmonella* is based on surface antigens (O [somatic] and H [flagellar]). Over 2,400 serotypes or serovars of *Salmonella* are known (Popoff, et al. 2000 *Res. Microbiol.* 151:63-65). Therefore, each serotype was considered to

be a separate species and often given names, accordingly (e.g. *S. paratyphi*, *S. typhimurium*, *S. typhi*, *S. enteritidis*, etc.).

However, by the 1970s and 1980s it was recognized that this system was not only cumbersome, but also inaccurate. Then, many *Salmonella* species were lumped into a single species (all serotypes and subgenera I, II, and IV and all serotypes of *Arizona*) with a second subspecies, *S. bongorii* also recognized (Crosa, et al., 1973, J. Bacteriol. 115:307-315). Though species designations are based on the highly variable surface antigens, the *Salmonella* are very similar otherwise with a major exception being pathogenicity determinants.

There has been some debate on the correct name for the *Salmonella* species. Currently (Brenner, et al. 2000 J. Clin. Microbiol. 38:2465-2467), the accepted name is *Salmonella enterica*. *S. enterica* is divided into six subspecies (I, *S. enterica* subsp. *enterica*; II, *S. enterica*, subsp. *salamae*; IIIa, *S. enterica* subsp. *arizonae*; IIIb, *S. enterica* subsp. *diarizonae*; IV, *S. enterica* subsp. *houteanae*; and VI, *S. enterica* subsp. *indica*). Within subspecies I, serotypes are used to distinguish each of the serotypes or serovars (e.g. *S. enterica* serotype Enteritidis, *S. enterica* serotype Typhimurium, *S. enterica* serotype Typhi, and *S. enterica* serotype Choleraesuis, etc.). Current convention is to spell this out on first usage (*Salmonella enterica* ser. Typhimurium) and then use an abbreviated form (*Salmonella* Typhimurium or *S. Typhimurium*). Note, the genus and species names (*Salmonella enterica*) are italicized but not the serotype/serovar name (Typhimurium). Because the taxonomic committees have yet to officially approve of the actual species name, this latter system is what is employed by the CDC (Brenner, et al. 2000 J. Clin. Microbiol. 38:2465-2467). Due to the concerns of both taxonomic priority and medical importance, some of these serotypes might ultimately receive full species designations (*S. typhi* would be the most notable).

Therefore, as used herein "*Salmonella enterica* or *S. enterica*" includes serovars Typhi, Typhimurium, Paratyphi, Choleraesuis, etc." However, appeals of the "official" name are in process and the taxonomic designations may change (*S. choleraesuis* is the species name that could replace *S. enterica* based solely on priority).

By "identifying a compound" is meant to screen one or more compounds in a collection of compounds such as a combinatorial chemical library or other library of chemical compounds or to characterize a single compound by testing the compound in a given assay and determining whether it exhibits the desired activity.

By "inducer" is meant an agent or solution which, when placed in contact with a cell or microorganism, increases transcription, or inhibitor and/or promoter clearance/fidelity, from a desired promoter.

As used herein, "nucleic acid" means DNA, RNA, or modified nucleic acids. Thus, the terminology "the nucleic acid of SEQ ID NO: X" or "the nucleic acid comprising the nucleotide sequence" includes both the DNA sequence of SEQ ID NO: X and an RNA sequence in which the thymidines in the DNA sequence have been substituted with uridines in the RNA sequence and in which the deoxyribose backbone of the DNA sequence has been substituted with a ribose backbone

in the RNA sequence. Modified nucleic acids are nucleic acids having nucleotides or structures which do not occur in nature, such as nucleic acids in which the internucleotide phosphate residues with methylphosphonates, phosphorothioates, phosphoramidates, and phosphate esters. Nonphosphate internucleotide analogs such as siloxane bridges, carbonate bridges, thioester bridges, as well as many others known in the art may also be used in modified nucleic acids. Modified nucleic acids may also comprise, α -anomeric nucleotide units and modified nucleotides such as 1,2-dideoxy-d-ribofuranose, 1,2-dideoxy-1-phenylribofuranose, and N^4 , N^4 -ethano-5-methyl-cytosine are contemplated for use in the present invention. Modified nucleic acids may also be peptide nucleic acids in which the entire deoxyribose-phosphate backbone has been exchanged with a chemically completely different, but structurally homologous, polyamide (peptide) backbone containing 2-aminoethyl glycine units.

As used herein, "sub-lethal" means a concentration of an agent below the concentration required to inhibit all cell growth.

Brief Description of the Drawings

Figure 1A illustrates a method for replacing a promoter using a promoter replacement cassette comprising a 5' region homologous to the sequence which is 5' of the natural promoter in the chromosome, the promoter which is to replace the chromosomal promoter and a 3' region which is homologous to sequences 3' of the natural promoter in the chromosome.

Figure 1B illustrates a method for replacing a promoter using a promoter replacement cassette comprising a nucleic acid encoding an identifiable or selectable marker disposed between the 5' region which is homologous to the sequence 5' of the natural promoter and the promoter which is to replace the chromosomal promoter and a transcriptional terminator 3' of the gene encoding an identifiable or selectable marker.

Figures 2A and 2B illustrate one method for identifying amplification products which are underrepresented or overrepresented in a culture.

Figures 3A and 3B illustrate another method for identifying amplification products which are underrepresented or overrepresented in a culture.

Figure 4 illustrates the results of a hybridization analysis where the antisense nucleic acid expressed by a strain in the culture is not complementary to all or a portion of the gene encoding the target of the compound (i.e. a nonspecific strain).

Figure 5 illustrates the results of a hybridization analysis where the antisense nucleic acid expressed by a strain in the culture is complementary to all or a portion of the gene encoding the target of the compound, the hybridization intensity for that strain will be intimately correlated with the concentration of the compound (i.e. a specific strain).

Figure 6 illustrates an oligonucleotide comprising a lac operator flanked on each side by 40 nucleotides homologous to the promoter is the promoter which drives expression of the *yabB yabC ftsL ftsI murE* genes in an operon for use in inserting the lac operator into the promoter.

Figure 7 is an IPTG dose response curve in *E. coli* transformed with an IPTG-inducible plasmid containing either an antisense clone to the *E. coli* ribosomal protein *rplW* (AS-*rplW*) which is required for protein synthesis and essential for cell proliferation, or an antisense clone to the *elaD* (AS-*elaD*) gene which is not known to be involved in protein synthesis and which is also essential for proliferation.

Figure 8A is a tetracycline dose response curve in *E. coli* transformed with an IPTG-inducible plasmid containing antisense to *rplW* (AS-*rplW*) in the absence (0) or presence of IPTG at concentrations that result in 20% and 50% growth inhibition.

Figure 8B is a tetracycline dose response curve in *E. coli* transformed with an IPTG-inducible plasmid containing antisense to *elaD* (AS-*elaD*) in the absence (0) or presence of IPTG at concentrations that result in 20% and 50% growth inhibition.

Figure 9 is a graph showing the fold increase in tetracycline sensitivity of *E. coli* transfected with antisense clones to essential ribosomal proteins *L23* (AS-*rplW*) and *L7/L12* and *L10* (AS-*rplLrplJ*). Antisense clones to genes known to not be directly involved in protein synthesis, *atpB/E* (AS-*atpB/E*), *visC* (AS-*visC*), *elaD* (AS-*elaD*), *yohH* (AS-*yohH*), are much less sensitive to tetracycline.

Figure 10 illustrates the results of an assay in which *Staphylococcus aureus* cells transcribing an antisense nucleic acid complementary to the *gyrB* gene encoding the β subunit of gyrase were contacted with several antibiotics whose targets were known.

Figure 11 illustrates a microtitration plate which contains antibiotic and inducer at gradient concentrations in a matrix format in 10 times excess quantity.

Figure 12 illustrates the results of an experiment demonstrating that at appropriate concentrations of inducer, cells which overexpress the *defB* gene product were able to grow at elevated concentrations of the antibiotic actinonin.

Figure 13 illustrates the results of an experiment demonstrating that at appropriate concentrations of inducer cells which overexpress the *folA* gene product were able to grow at elevated concentrations of the antibiotic trimethoprim.

Figure 14 illustrates the results of an experiment demonstrating that overexpression of the *fabI* gene confers resistance to triclosan, which acts on the gene product of the *fabI* gene, but does not confer resistance to cerulenin, trimethoprim, or actinonin, each of which act on other gene products.

Figure 15 illustrates the results of an experiment demonstrating that overexpression of the *folA* gene confers resistance to trimethoprim, which acts on the gene product of the *folA* gene but does not confer resistance to triclosan, cerulenin, or actinonin, each of which act on other gene products.

Figure 16 illustrates the results of an experiment demonstrating that overexpression of the *defB* gene conferred resistance to actinonin, which acts on the gene product of the *defB* gene but

does not confer resistance to cerulenin, trimethoprim, or triclosan, each of which act on other gene products.

Figure 17 illustrates the results of an experiment demonstrating that overexpression of the *fabF* gene conferred resistance to cerulenin, which acts on the gene product of the *fabF* gene, β keto-acyl carrier protein synthase but does not confer resistance to triclosan, trimethoprim, or actinonin, each of which act on other gene products.

Figure 18 illustrates the results of experiments in which a mixture of nine strains was grown wells in a 96 well plate in medium containing various concentrations of inducer and a sufficient concentration of actinonin, cerulenin, triclosan or trimethoprim to inhibit the growth of strains which do not overexpress the targets of these antibiotics.

Detailed Description of Embodiments of the Invention

The present invention describes a group of prokaryotic genes and gene families required for cellular proliferation. Exemplary genes and gene families from *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Salmonella typhimurium*, *Acinetobacter baumannii*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Corynebacterium diphtheriae*, *Enterobacter cloacae*, *Enterococcus faecium*, *Haemophilus influenzae*, *Helicobacter pylori*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella multocida*, *Proteus mirabilis*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella paratyphi*, *Salmonella typhi*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus mutans*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholera* and *Yersinia pestis* are provided. A proliferation-required gene or gene family is one where, in the absence or substantial reduction of a gene transcript and/or gene product, growth or viability of the cell or microorganism is reduced or eliminated. Thus, as used herein, the terminology "proliferation-required" or "required for proliferation" encompasses instances where the absence or substantial reduction of a gene transcript and/or gene product completely eliminates cell growth as well as instances where the absence of a gene transcript and/or gene product merely reduces cell growth. These proliferation-required genes can be used as potential targets for the generation of new antimicrobial agents. To achieve that goal, the present invention also encompasses assays for analyzing proliferation-required genes and for identifying compounds which interact with the gene and/or gene products of the proliferation-required genes. In addition, the present invention contemplates the expression of genes and the purification of the proteins encoded by the nucleic acid sequences identified as required proliferation genes and reported herein. The purified proteins can be

used to generate reagents and screen small molecule libraries or other candidate compound libraries for compounds that can be further developed to yield novel antimicrobial compounds.

The present invention also describes methods for identification of nucleotide sequences homologous to these genes and polypeptides described herein, including nucleic acids comprising
 5 nucleotide sequences homologous to the nucleic acids of SEQ ID NOS.: 6214-42397 and polypeptides homologous to the polypeptides of SEQ ID NOs.: 42398-78581. For example, these sequences may be used to identify homologous coding nucleic acids, homologous antisense nucleic acids, or homologous polypeptides in microorganisms such as *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*,
 10 *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*,
 15 *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*,
 20 *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*,
 25 *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* or any species falling within the genera of any of the above species. In some embodiments, the homologous coding nucleic acids, homologous antisense nucleic acids, or
 30 homologous polypeptides are identified in an organism other than *E. coli*.

The homologous coding nucleic acids, homologous antisense nucleic acids, or homologous polypeptides, may then be used in each of the methods described herein, including methods of identifying compounds which inhibit the proliferation of the organism containing the homologous coding nucleic acid, homologous antisense nucleic acid or homologous polypeptide, methods of
 35 inhibiting the growth of the organism containing the homologous coding nucleic acid, homologous antisense nucleic acid or homologous polypeptide, methods of identifying compounds which influence the activity or level of a gene product required for proliferation of the organism containing the homologous coding nucleic acid, homologous antisense nucleic acid or homologous

polypeptide, methods for identifying compounds or nucleic acids having the ability to reduce the level or activity of a gene product required for proliferation of the organism containing the homologous coding nucleic acid, homologous antisense nucleic acid or homologous polypeptide, methods of inhibiting the activity or expression of a gene in an operon required for proliferation of the organism containing the homologous coding nucleic acid, homologous antisense nucleic acid or homologous polypeptide, methods for identifying a gene required for proliferation of the organism containing the homologous coding nucleic acid, homologous antisense nucleic acid or homologous polypeptide, methods for identifying the biological pathway in which a gene or gene product required for proliferation of the organism containing the homologous coding nucleic acid, homologous antisense nucleic acid or homologous polypeptide lies, methods for identifying compounds having activity against biological pathway required for proliferation of the organism containing the homologous coding nucleic acid, homologous antisense nucleic acid or homologous polypeptide, methods for determining the biological pathway on which a test compound acts in the organism containing the homologous coding nucleic acid, homologous antisense nucleic acid or homologous polypeptide, methods of replacing an endogenous promoter with a regulatable promoter which controls the expression of the homologous coding nucleic acid, homologous antisense nucleic acid or homologous polypeptide, methods of inserting an operator within or near an endogenous promoter to provide regulatable expression of the homologous coding nucleic acid, homologous antisense nucleic acid or homologous polypeptide, methods of identifying the target on which a compound acts in the organism containing the homologous coding nucleic acid, homologous antisense nucleic acid or homologous polypeptide, and methods of inhibiting the proliferation of the organism containing the homologous coding nucleic acid, homologous antisense nucleic acid or homologous polypeptide in a subject. In some embodiments of the present invention, the methods are performed using an organism, other than *E. coli* or a gene or gene product from an organism other than *E. coli*.

One embodiment of the present invention utilizes a novel method to identify proliferation-required sequences. Generally, a library of nucleic acid sequences from a given source are subcloned or otherwise inserted immediately downstream of an inducible promoter on an appropriate vector, such as a *Staphylococcus aureus*/*E. coli* or *Pseudomonas aeruginosa*/*E. coli* shuttle vector, or a vector which will replicate in both *Salmonella typhimurium* and *Klebsiella pneumoniae*, or other vector or shuttle vector capable of functioning in the intended organism, thus forming an expression library. It is generally preferred that expression is directed by a regulatable promoter sequence such that expression level can be adjusted by addition of variable concentrations of an inducer molecule or of an inhibitor molecule to the medium. For example, a number of regulatable promoters useful for regulating the expression of nucleic acid sequences over a wide range of expression levels are described in U.S. Patent Application Serial Number 10/032,393, filed December 21, 2001. Temperature activated promoters, such as promoters regulated by temperature sensitive repressors, such as the lambda C₁₀₅₇ repressor, are also envisioned. Although the insert nucleic acids may be derived from the chromosome

of the cell or microorganism into which the expression vector is to be introduced, because the insert is not in its natural chromosomal location, the insert nucleic acid is an exogenous nucleic acid for the purposes of the discussion herein. The term "expression" is defined as the production of a sense or antisense RNA molecule from a gene, gene fragment, genomic fragment, chromosome, operon or
5 portion thereof. Expression can also be used to refer to the process of peptide or polypeptide synthesis. An expression vector is defined as a vehicle by which a ribonucleic acid (RNA) sequence is transcribed from a nucleic acid sequence carried within the expression vehicle. The expression vector can also contain features that permit translation of a protein product from the transcribed RNA message expressed from the exogenous nucleic acid sequence carried by the expression vector. Accordingly, an
10 expression vector can produce an RNA molecule as its sole product or the expression vector can produce a RNA molecule that is ultimately translated into a protein product.

Once generated, the expression library containing the exogenous nucleic acid sequences is introduced into a population of cells (such as the organism from which the exogenous nucleic acid sequences were obtained) to search for genes that are required for bacterial proliferation. Because the
15 library molecules are foreign, in context, to the population of cells, the expression vectors and the nucleic acid segments contained therein are considered exogenous nucleic acid.

Expression of the exogenous nucleic acid fragments in the test population of cells containing the expression library is then activated. Activation of the expression vectors consists of subjecting the cells containing the vectors to conditions that result in the expression of the exogenous nucleic acid
20 sequences carried by the expression library. The test population of cells is then assayed to determine the effect of expressing the exogenous nucleic acid fragments on the test population of cells. Those expression vectors that negatively impact the growth of the cells upon induction of expression of the random sequences contained therein are identified, isolated, and purified for further study.

In some embodiments, vectors which comprises a regulatable fusion promoter selected
25 from a suite of fusion promoters, wherein the promoter suite is useful for modulating both the basal and maximal levels of transcription of a nucleic acid over a wide dynamic range thus allowing the desired level of production of a transcript, can be used to express exogenous nucleic acids, including the nucleic acids of the present invention. Such promoters are described in U.S. Patent Application Serial Number 10/032,393, filed December 21, 2001, the disclosure of which is
30 incorporated herein by reference in its entirety.

In some other embodiments, vectors useful for the production of stabilized mRNA having an increased lifetime (including antisense RNA) in Gram negative organisms are described in U.S. Provisional Patent Application Serial Number 60/343,512, filed December 21, 2001. Briefly, the stabilized antisense RNA may comprise an antisense RNA which was identified as inhibiting
35 proliferation as described above which has been engineered to contain at least one stem loop flanking each end of the antisense nucleic acid. In some embodiments, the at least one stem-loop structure formed at the 5' end of the stabilized antisense nucleic acid comprises a flush, double stranded 5' end. In some embodiments, one or more of the stem loops comprises a rho independent

terminator. In additional embodiments, the stabilized antisense RNA lacks a ribosome binding site. In further embodiments, the stabilized RNA lacks sites which are cleaved by one or more RNases, such as RNase E or RNase III. In some embodiments, the stabilized antisense RNA may be transcribed in a cell which the activity of at least one enzyme involved in RNA degradation has been reduced. For example, the activity of an enzyme such as RNase E, RNase II, RNase III, polynucleotide phosphorylase, and poly(A) polymerase, RNA helicase, enolase or an enzyme having similar functions may be reduced in the cell.

Alternatively, genes required for proliferation may be identified by replacing the natural promoter for the proliferation required gene with a regulatable promoter as described above. The growth of such strains under conditions in which the promoter is active or non-repressed is compared to the growth under conditions in which the promoter is inactive or repressed. If the strains fail to grow or grow at a substantially reduced rate under conditions in which the promoter is inactive or repressed but grow normally under conditions in which the promoter is active or non-repressed, then the gene which is operably linked to the regulatable promoter encodes a gene product required for proliferation. For example, proliferation-required genes and gene products identified using promoter replacement are described in U.S. Patent Application Serial Number 09/948,993.

For example, in some embodiments, the natural promoter may be replaced using techniques which employ homologous recombination to exchange a promoter present on the chromosome of the cell with the desired promoter. In such methodology, a nucleic acid comprising a promoter replacement cassette is introduced into the cell. As illustrated in Figure 1A, the promoter replacement cassette comprises a 5' region homologous to the sequence which is 5' of the natural promoter in the chromosome, the promoter which is to replace the chromosomal promoter and a 3' region which is homologous to sequences 3' of the natural promoter in the chromosome. In some embodiments, the promoter replacement cassette may also include a nucleic acid encoding an identifiable or selectable marker disposed between the 5' region which is homologous to the sequence 5' of the natural promoter and the promoter which is to replace the chromosomal promoter. If desired, the promoter replacement cassette may also contain a transcriptional terminator 3' of the gene encoding an identifiable or selectable marker, as illustrated in Figure 1B. As illustrated in Figure 1A and 1B, homologous recombination is allowed to occur between the chromosomal region containing the natural promoter and the promoter replacement cassette. Cells in which the promoter replacement cassette has integrated into the chromosome are identified or selected. To confirm that homologous recombination has occurred, the chromosomal structure of the cells may be verified by Southern analysis or PCR.

In some embodiments, the promoter replacement cassette may be introduced into the cell as a linear nucleic acid, such a PCR product or a restriction fragment. Alternatively, the promoter replacement may be introduced into the cell on a plasmid. Figures 1A and 1B illustrates the

replacement of a chromosomal promoter with a desired promoter through homologous recombination.

In some embodiments, the cell into which the promoter replacement cassette is introduced may carry mutations which enhance its ability to be transformed with linear DNA or which enhance the frequency of homologous recombination. For example, if the cell is an *Escherichia coli* cell it may have a mutation in the gene encoding Exonuclease V of the RecBCD recombination complex. If the cell is an *Escherichia coli* cell it may have a mutation that activates the RecET recombinase of the λ prophage and/or a mutation that enhances recombination through the RecF pathway. For example, the *Escherichia coli* cells may be RecB or RecC mutants carrying an sbcA or sbcB mutation. Alternatively, the *Escherichia coli* cells may be recD mutants. In other embodiments the *Escherichia coli* cells may express the λ Red recombination genes. For example, *Escherichia coli* cells suitable for use in techniques employing homologous recombination have been described in Datsenko, K.A. and Wanner, B.L., PNAS 97:6640-6645 (2000); Murphy, K.C., J. Bact 180: 2053-2071 (1998); Zhang, Y., et al., Nature Genetics 20: 123-128 (1998); and Muyrers, J.P.P. et al., Genes & Development 14: 1971-1982 (2000). It will be appreciated that cells carrying mutations in similar genes may be constructed in organisms other than *Escherichia coli*.

In some embodiments of the present invention, a regulatable fusion promoter selected from a suite of fusion promoters, wherein the promoter suite is useful for modulating both the basal and maximal levels of transcription of a nucleic acid over a wide dynamic range thus allowing the desired level of production of a transcript, is with the promoter replacement methods described above. Such promoters are described in U.S. Patent Application Serial Number 10/032,393, filed December 21, 2001, the disclosure of which is incorporated herein by reference in its entirety.

A variety of assays are contemplated to identify nucleic acid sequences that negatively impact growth upon expression. In one embodiment, growth in cultures expressing exogenous nucleic acid sequences and growth in cultures not expressing these sequences is compared. Growth measurements are assayed by examining the extent of growth by measuring optical densities. Alternatively, enzymatic assays can be used to measure bacterial growth rates to identify exogenous nucleic acid sequences of interest. Colony size, colony morphology, and cell morphology are additional factors used to evaluate growth of the host cells. Those cultures that fail to grow or grow at a reduced rate under expression conditions are identified as containing an expression vector encoding a nucleic acid fragment that negatively affects a proliferation-required gene.

Once exogenous nucleic acids of interest are identified, they are analyzed. The first step of the analysis is to acquire the nucleotide sequence of the nucleic acid fragment of interest. To achieve this end, the insert in those expression vectors identified as containing a nucleotide sequence of interest is sequenced, using standard techniques well known in the art. The next step of the process is to determine the source of the nucleotide sequence. As used herein "source" means the genomic region containing the cloned fragment.

Determination of the gene(s) corresponding to the nucleotide sequence is achieved by comparing the obtained sequence data with databases containing known protein and nucleotide sequences from various microorganisms. Thus, initial gene identification is made on the basis of significant sequence similarity or identity to either characterized or predicted *Escherichia coli*,
 5 *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, and *Salmonella typhimurium* genes or their encoded proteins and/or homologues in other species.

The number of nucleotide and protein sequences available in database systems has been growing exponentially for years. For example, the complete nucleotide sequences of *Caenorhabditis elegans* and several bacterial genomes, including *E. coli*, *Aeropyrum pernix*, *Aquifex aeolicus*,
 10 *Archaeoglobus fulgidus*, *Bacillus subtilis*, *Borrelia burgdorferi*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium tetani*, *Corynebacterium diphtheria*, *Deinococcus radiodurans*, *Haemophilus influenzae*, *Helicobacter pylori* 26695, *Helicobacter pylori* J99, *Methanobacterium thermoautotrophicum*, *Methanococcus jannaschii*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Pseudomonas aeruginosa*, *Pyrococcus abyssi*, *Pyrococcus*
 15 *horikoshii*, *Rickettsia prowazekii*, *Synechocystis PCC6803*, *Thermotoga maritima*, *Treponema pallidum*, *Bordetella pertussis*, *Campylobacter jejuni*, *Clostridium acetobutylicum*, *Mycobacterium tuberculosis* CSU#93, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pseudomonas aeruginosa*, *Pyrobaculum aerophilum*, *Pyrococcus furiosus*, *Rhodobacter capsulatus*, *Salmonella typhimurium*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Ureaplasma urealyticum* and *Vibrio cholera* are
 20 available. This nucleotide sequence information is stored in a number of databanks, such as GenBank, the National Center for Biotechnology Information (NCBI), the Genome Sequencing Center (<http://genome.wustl.edu/gsc/salmonella.shtml>), and the Sanger Centre (http://www.sanger.ac.uk/projects/S_typhi) which are publicly available for searching. A variety of computer programs are available to assist in the analysis of the sequences stored within these
 25 databases. FASTA, (W. R. Pearson (1990) "Rapid and Sensitive Sequence Comparison with FASTP and FASTA" Methods in Enzymology 183:63- 98), Sequence Retrieval System (SRS), (Etzold & Argos, SRS an indexing and retrieval tool for flat file data libraries. Comput. Appl. Biosci. 9:49-57, 1993) are two examples of computer programs that can be used to analyze sequences of interest. In one embodiment of the present invention, the BLAST family of computer
 30 programs, which includes BLASTN version 2.0 with the default parameters, or BLASTX version 2.0 with the default parameters, is used to analyze nucleotide sequences.

BLAST, an acronym for "Basic Local Alignment Search Tool," is a family of programs for database similarity searching. The BLAST family of programs includes: BLASTN, a nucleotide sequence database searching program, BLASTX, a protein database searching program where the input
 35 is a nucleic acid sequence; and BLASTP, a protein database searching program. BLAST programs embody a fast algorithm for sequence matching, rigorous statistical methods for judging the significance of matches, and various options for tailoring the program for special situations. Assistance

in using the program can be obtained by e-mail at blast@ncbi.nlm.nih.gov. tBLASTX can be used to translate a nucleotide sequence in all three potential reading frames into an amino acid sequence.

Bacterial genes are often transcribed in polycistronic groups. These groups comprise operons, which are a collection of genes and intergenic sequences under common regulation. The genes of an operon are transcribed on the same mRNA and are often related functionally. Given the nature of the screening protocol, it is possible that the identified exogenous nucleic acid corresponds to a gene or portion thereof with or without adjacent noncoding sequences, an intragenic sequence (i.e. a sequence within a gene), an intergenic sequence (i.e. a sequence between genes), a nucleotide sequence spanning at least a portion of two or more genes, a 5' noncoding region or a 3' noncoding region located upstream or downstream from the actual nucleotide sequence that is required for bacterial proliferation. Accordingly, it is often desirable to determine which gene(s) that is encoded within the operon is individually required for proliferation.

In one embodiment of the present invention, an operon is identified and then dissected to determine which gene or genes are required for proliferation. Operons can be identified by a variety of means known to those in the art. For example, the RegulonDB DataBase described by Huerta et al. (*Nucl. Acids Res.* 26:55-59, 1998), which may also be found on the website http://www.cifn.unam.mx/Computational_Biology/regulondb/, provides information about operons in *Escherichia coli*. The Subtilist database (<http://bioweb.pasteur.fr/GenoList/SubtiList>), (Moszer, I., Glaser, P. and Danchin, A. (1995) *Microbiology* 141: 261-268 and Moszer, I (1998) *FEBS Letters* 430: 28-36, may also be used to predict operons. This database lists genes from the fully sequenced, Gram positive bacteria, *Bacillus subtilis*, together with predicted promoters and terminator sites. This information can be used in conjunction with the *Staphylococcus aureus* genomic sequence data to predict operons and thus produce a list of the genes affected by the antisense nucleic acids of the present invention. The *Pseudomonas aeruginosa* web site (<http://www.pseudomonas.com>) can be used to help predict operon organization in this bacterium. The databases available from the Genome Sequencing Center (<http://genome.wustl.edu/gsc/salmonella.shtml>), and the Sanger Centre (http://www.sanger.ac.uk/projects/S_typhi) may be used to predict operons in *Salmonella typhimurium*. The TIGR microbial database has an incomplete version of the *E. faecalis* genome http://www.tigr.org/cgi-bin/BlastSearch/blast.cgi?organism=e_faecalis. One can take a nucleotide sequence and BLAST it for homologs.

A number of techniques that are well known in the art can be used to dissect the operon. Analysis of RNA transcripts by Northern blot or primer extension techniques are commonly used to analyze operon transcripts. In one aspect of this embodiment, gene disruption by homologous recombination is used to individually inactivate the genes of an operon that is thought to contain a gene required for proliferation.

Several gene disruption techniques have been described for the replacement of a functional gene with a mutated, non-functional (null) allele. These techniques generally involve the use of

homologous recombination. One technique using homologous recombination in *Staphylococcus aureus* is described in Xia et al. 1999, Plasmid 42: 144-149. This technique uses crossover PCR to create a null allele with an in-frame deletion of the coding region of a target gene. The null allele is constructed in such a way that nucleotide sequences adjacent to the wild type gene are retained.

- 5 These homologous sequences surrounding the deletion null allele provide targets for homologous recombination so that the wild type gene on the *Staphylococcus aureus* chromosome can be replaced by the constructed null allele. This method can be used with other bacteria as well, including *Salmonella* and *Klebsiella* species. Similar gene disruption methods that employ the counter selectable marker *sacB* (Schweizer, H. P., Klassen, T. and Hoang, T. (1996) Mol. Biol. of
- 10 *Pseudomonas*. ASM press, 229-237, are available for *Pseudomonas*, *Salmonella* and *Klebsiella* species. *E. faecalis* genes can be disrupted by recombining in a non-replicating plasmid that contains an internal fragment to that gene (Leboeuf, C., L. Leblanc, Y. Auffray and A. Hartke. 2000. J. Bacteriol. 182:5799-5806.

- The crossover PCR amplification product is subcloned into a suitable vector having a
- 15 selectable marker, such as a drug resistance marker. In some embodiments the vector may have an origin of replication which is functional in *E. coli* or another organism distinct from the organism in which homologous recombination is to occur, allowing the plasmid to be grown in *E. coli* or the organism other than that in which homologous recombination is to occur, but may lack an origin of replication functional in *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella*
- 20 *pneumoniae*, *Pseudomonas aeruginosa*, *Salmonella typhimurium*, *Acinetobacter baumannii*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Corynebacterium diphtheriae*, *Enterobacter cloacae*, *Enterococcus faecium*,
- 25 *Haemophilus influenzae*, *Helicobacter pylori*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella multocida*, *Proteus mirabilis*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella paratyphi*, *Salmonella typhi*, *Staphylococcus*
- 30 *epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus mutans*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae* or *Yersinia pestis* such that selection of the selectable marker requires integration of the vector into the homologous region of the *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Salmonella typhimurium*, *Acinetobacter*
- 35 *baumannii*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Corynebacterium diphtheriae*, *Enterobacter cloacae*, *Enterococcus*

faecium, *Haemophilus influenzae*, *Helicobacter pylori*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella multocida*, *Proteus mirabilis*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella paratyphi*, *Salmonella typhi*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus mutans*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae* or *Yersinia pestis* chromosome. Usually a single crossover event is responsible for this integration event such that the *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Salmonella typhimurium*, *Acinetobacter baumannii*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Corynebacterium diphtheriae*, *Enterobacter cloacae*, *Enterococcus faecium*, *Haemophilus influenzae*, *Helicobacter pylori*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella multocida*, *Proteus mirabilis*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella paratyphi*, *Salmonella typhi*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus mutans*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae* or *Yersinia pestis* chromosome now contains a tandem duplication of the target gene consisting of one wild type allele and one deletion null allele separated by vector sequence. Subsequent resolution of the duplication results in both removal of the vector sequence and either restoration of the wild type gene or replacement by the in-frame deletion. The latter outcome will not occur if the gene should prove essential. A more detailed description of this method is provided in Example 10 below. It will be appreciated that this method may be practiced with any of the nucleic acids or organisms described herein.

Recombinant DNA techniques can be used to express the entire coding sequences of the gene identified as required for proliferation, or portions thereof. The over-expressed proteins can be used as reagents for further study. The identified exogenous sequences are isolated, purified, and cloned into a suitable expression vector using methods well known in the art. If desired, the nucleic acids can contain the nucleotide sequences encoding a signal peptide to facilitate secretion of the expressed protein.

Expression of fragments of the bacterial genes identified as required for proliferation is also contemplated by the present invention. The fragments of the identified genes can encode a polypeptide comprising at least 5, at least 10, at least 15, at least 20, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, at least 55, at least 60, at least 65, at least 75, or more than 75 consecutive amino

acids of a gene complementary to one of the identified sequences of the present invention. The nucleic acids inserted into the expression vectors can also contain endogenous sequences upstream and downstream of the coding sequence.

When expressing the encoded protein of the identified nucleic acid required for bacterial proliferation or a fragment thereof, the nucleic acid to be expressed is operably linked to a promoter in an expression vector using conventional cloning technology. The expression vector can be any of the bacterial, insect, yeast, or mammalian expression systems known in the art. Commercially available vectors and expression systems are available from a variety of suppliers including Genetics Institute (Cambridge, MA), Stratagene (La Jolla, California), Promega (Madison, Wisconsin), and Invitrogen (San Diego, California). If desired, to enhance expression and facilitate proper protein folding, the codon usage and codon bias of the sequence can be optimized for the particular expression organism in which the expression vector is introduced, as explained by Hatfield, et al., U.S. Patent No. 5,082,767, incorporated herein by this reference. Fusion protein expression systems are also contemplated by the present invention.

Following expression of the protein encoded by the identified exogenous nucleic acid, the protein may be purified. Protein purification techniques are well known in the art. Proteins encoded and expressed from identified exogenous nucleic acids can be partially purified using precipitation techniques, such as precipitation with polyethylene glycol. Alternatively, epitope tagging of the protein can be used to allow simple one step purification of the protein. In addition, chromatographic methods such as ion-exchange chromatography, gel filtration, use of hydroxyapatite columns, immobilized reactive dyes, chromatofocusing, and use of high-performance liquid chromatography, may also be used to purify the protein. Electrophoretic methods such as one-dimensional gel electrophoresis, high-resolution two-dimensional polyacrylamide electrophoresis, isoelectric focusing, and others are contemplated as purification methods. Also, affinity chromatographic methods, comprising antibody columns, ligand presenting columns and other affinity chromatographic matrices are contemplated as purification methods in the present invention.

The purified proteins produced from the gene encoding sequences identified as required for proliferation can be used in a variety of protocols to generate useful antimicrobial reagents. In one embodiment of the present invention, antibodies are generated against the proteins expressed from the identified exogenous nucleic acids. Both monoclonal and polyclonal antibodies can be generated against the expressed proteins. Methods for generating monoclonal and polyclonal antibodies are well known in the art. Also, antibody fragment preparations prepared from the produced antibodies discussed above are contemplated.

In addition, the purified protein, fragments thereof, or derivatives thereof may be administered to an individual in a pharmaceutically acceptable carrier to induce an immune response against the protein. Preferably, the immune response is a protective immune response which protects the individual. Methods for determining appropriate dosages of the protein and pharmaceutically acceptable carriers may be determined empirically and are familiar to those skilled in the art.

Another application for the purified proteins of the present invention is to screen small molecule libraries for candidate compounds active against the various target proteins of the present invention. Advances in the field of combinatorial chemistry provide methods, well known in the art, to produce large numbers of candidate compounds that can have a binding, or otherwise inhibitory effect on a target protein. Accordingly, the screening of small molecule libraries for compounds with binding affinity or inhibitory activity for a target protein produced from an identified gene is contemplated by the present invention.

In some embodiments of the present invention, a cell sensitized by expressing an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, an antisense nucleic acid comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a nucleic acid complementary to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397, a nucleic acid complementary to a nucleic acid comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397, a nucleic acid complementary to a nucleic acid which encodes a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42398-78581, a nucleic acid complementary to a nucleic acid which encodes at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids of a polypeptide sequence selected from the group consisting of SEQ ID NOs.: 42398-78581, a homologous antisense nucleic acid, an antisense nucleic acid comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of a homologous nucleic acid, a nucleic acid complementary to a homologous coding nucleic acid, a nucleic acid complementary to at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of a homologous coding nucleic acid, a nucleic acid complementary to a nucleic acid which encodes a homologous polypeptide, or a nucleic acid complementary to a nucleic acid which encodes at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids of a homologous polypeptide, is contacted with one or more candidate compounds from a small molecule library. Candidate compounds which further inhibit the proliferation of the sensitized cell may be identified as possessing inhibitory activity for a target protein or product produced by the gene to which the antisense sequence is complementary.

A number of vectors useful in the above methods are described in U.S. Patent Application Serial Number 10/032,393, filed December 21, 2001.

In some embodiments of the present invention, the methods for the production of stabilized RNA, as described in U.S. Patent Application Serial Number 60/343,512, can be used for the production of a stabilized transcript, which corresponds to a nucleic acid described herein, having an increased lifetime in Gram-negative organisms. Briefly, the stabilized antisense RNA may comprise an antisense RNA which was identified as inhibiting proliferation as described above

which has been engineered to contain at least one stem loop flanking each end of the antisense nucleic acid. In some embodiments, the at least one stem-loop structure formed at the 5' end of the stabilized antisense nucleic acid comprises a flush, double stranded 5' end. In some embodiments, one or more of the stem loops comprises a rho independent terminator. In additional embodiments, the stabilized antisense RNA lacks a ribosome binding site. In further embodiments, the stabilized RNA lacks sites which are cleaved by one or more RNAses, such as RNase E or RNase III. In some embodiments, the stabilized antisense RNA may be transcribed in a cell which the activity of at least one enzyme involved in RNA degradation has been reduced. For example, the activity of an enzyme such as RNase E, RNase II, RNase III, polynucleotide phosphorylase, and poly(A) polymerase, RNA helicase, enolase or an enzyme having similar functions may be reduced in the cell.

The present invention further contemplates utility against a variety of other pathogenic microorganisms in addition to *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Salmonella typhimurium*, *Acinetobacter baumannii*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Corynebacterium diphtheriae*, *Enterobacter cloacae*, *Enterococcus faecium*, *Haemophilus influenzae*, *Helicobacter pylori*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella multocida*, *Proteus mirabilis*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella paratyphi*, *Salmonella typhi*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus mutans*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae* and *Yersinia pestis*. For example, homologous coding nucleic acids, homologous antisense nucleic acids or homologous polypeptides from other pathogenic microorganisms (including nucleic acids homologous to the nucleic acids of SEQ ID NOs.: 6214-42397, nucleic acids homologous to the antisense nucleic acids of SEQ ID NOs.: 1-6213, and polypeptides homologous to the polypeptides of SEQ ID NOs.: 42398-78581) may be identified using methods such as those described herein. The homologous coding nucleic acids, homologous antisense nucleic acids or homologous polypeptides may be used to identify compounds which inhibit the proliferation of these other pathogenic microorganisms using methods such as those described herein.

For example, the proliferation-required nucleic acids, antisense nucleic acids, and polypeptides from *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Salmonella typhimurium*, *Acinetobacter baumannii*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Chlamydia*

pneumoniae, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Corynebacterium diphtheriae*, *Enterobacter cloacae*, *Enterococcus faecium*, *Haemophilus influenzae*, *Helicobacter pylori*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*,
 5 *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella multocida*, *Proteus mirabilis*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella paratyphi*, *Salmonella typhi*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus mutans*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae* or
 10 *Yersinia pestis* described herein (including the nucleic acids of SEQ ID NOs.: 6214-42397, the antisense nucleic acids of SEQ ID NOs.: 1-6213, and the polypeptides of SEQ ID NOs.: 42398-78581) may be used to identify homologous coding nucleic acids, homologous antisense nucleic acids or homologous polypeptides required for proliferation in prokaryotes and eukaryotes. For example, nucleic acids or polypeptides required for the proliferation of protists, such as *Plasmodium* spp.;
 15 plants; animals, such as *Entamoeba* spp. and *Contracaecum* spp; and fungi including *Candida* spp., (e.g., *Candida albicans*), *Cryptococcus neoformans*, and *Aspergillus fumigatus* may be identified. In one embodiment of the present invention, monera, specifically bacteria, including both Gram positive and Gram negative bacteria, are probed in search of novel gene sequences required for proliferation. Likewise, homologous antisense nucleic acids which may be used to inhibit growth of these organisms.
 20 or to identify antibiotics may also be identified. These embodiments are particularly important given the rise of drug resistant bacteria.

The number of bacterial species that are becoming resistant to existing antibiotics is growing. A partial list of these microorganisms includes: *Escherichia* spp., such as *E. coli*, *Enterococcus* spp., such as *E. faecalis*; *Pseudomonas* spp., such as *P. aeruginosa*, *Clostridium* spp., such as *C.*
 25 *botulinum*, *Haemophilus* spp., such as *H. influenzae*, *Enterobacter* spp., such as *E. cloacae*, *Vibrio* spp., such as *V. cholera*; *Moraxella* spp., such as *M. catarrhalis*; *Streptococcus* spp., such as *S. pneumoniae*, *Neisseria* spp., such as *N. gonorrhoeae*; *Mycoplasma* spp., such as *Mycoplasma pneumoniae*; *Salmonella typhimurium*; *Helicobacter pylori*; *Escherichia coli*; and *Mycobacterium tuberculosis*. The genes and polypeptides identified as required for the proliferation of *Escherichia*
 30 *coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Salmonella typhimurium*, *Acinetobacter baumannii*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Corynebacterium*
 35 *diphtheriae*, *Enterobacter cloacae*, *Enterococcus faecium*, *Haemophilus influenzae*, *Helicobacter pylori*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella*

multocida, *Proteus mirabilis*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella paratyphi*,
Salmonella typhi, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus*
mutans, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma*
urealyticum, *Vibrio cholerae* or *Yersinia pestis* (including the nucleic acids of SEQ ID NOs.: 6214-
5 42397, the sequences complementary to the nucleic acids of SEQ ID NOs.: 6214-42397, and the
polypeptides of SEQ ID NOs.: 42398-78581) can be used to identify homologous coding nucleic
acids or homologous polypeptides required for proliferation from these and other organisms using
methods such as nucleic acid hybridization and computer database analysis. Likewise, the
antisense nucleic acids which inhibit proliferation of *Escherichia coli*, *Staphylococcus aureus*,
10 *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Salmonella typhimurium*,
Acinetobacter baumannii, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia*
burgdorferi, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter*
jejuni, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium*
botulinum, *Clostridium difficile*, *Corynebacterium diphtheriae*, *Enterobacter cloacae*, *Enterococcus*
15 *faecium*, *Haemophilus influenzae*, *Helicobacter pylori*, *Legionella pneumophila*, *Listeria*
monocytogenes, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*,
Mycobacterium leprae, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma*
pneumoniae, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella multocida*, *Proteus*
mirabilis, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella paratyphi*, *Salmonella typhi*,
20 *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus mutans*, *Streptococcus*
pneumoniae, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio*
cholerae or *Yersinia pestis* (including the antisense nucleic acids of SEQ ID NOs.: 1-6213 or the
sequences complementary thereto) may also be used to identify antisense nucleic acids which
inhibit proliferation of these and other microorganisms or cells using nucleic acid hybridization or
25 computer database analysis.

In one embodiment of the present invention, the nucleic acid sequences from *Escherichia coli*,
Staphylococcus aureus, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*,
Salmonella typhimurium, *Acinetobacter baumannii*, *Bacillus anthracis*, *Bacteroides fragilis*,
Bordetella pertussis, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*,
30 *Burkholderia mallei*, *Campylobacter jejuni*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*,
Clostridium acetobutylicum, *Clostridium botulinum*, *Clostridium difficile*, *Corynebacterium*
diphtheriae, *Enterobacter cloacae*, *Enterococcus faecium*, *Haemophilus influenzae*, *Helicobacter*
pylori, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium*
avium, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma*
35 *genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella*
multocida, *Proteus mirabilis*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella paratyphi*,
Salmonella typhi, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus*
mutans, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma*

urealyticum, *Vibrio cholerae* or *Yersinia pestis* (including the nucleic acids of SEQ ID NOs.: 6214-42397 and the antisense nucleic acids of SEQ ID NOs. 1-6213) are used to screen genomic libraries generated from *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Salmonella typhimurium*, *Acinetobacter baumannii*,
5 *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Corynebacterium diphtheriae*, *Enterobacter cloacae*, *Enterococcus faecium*, *Haemophilus influenzae*, *Helicobacter pylori*, *Legionella pneumophila*, *Listeria monocytogenes*,
10 *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella multocida*, *Proteus mirabilis*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella paratyphi*, *Salmonella typhi*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus mutans*, *Streptococcus pneumoniae*,
15 *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Yersinia pestis* and other bacterial species of interest. For example, the genomic library may be from Gram positive bacteria, Gram negative bacteria or other organisms including *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*,
25 *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*,
30 *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*,
35 *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* or any species falling within the genera of any of the above species, including coagulase negative species of *Staphylococcus*. In some embodiments, the genomic

library may be from an organism other than *E. coli*. Standard molecular biology techniques are used to generate genomic libraries from various cells or microorganisms. In one aspect, the libraries are generated and bound to nitrocellulose paper. The identified exogenous nucleic acid sequences of the present invention can then be used as probes to screen the libraries for homologous sequences.

5 For example, the libraries may be screened to identify homologous coding nucleic acids or homologous antisense nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213, nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500
10 consecutive nucleotides of one of SEQ ID NOs. 1-6213, nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a nucleic acid complementary to one of SEQ ID NOs. 1-6213, nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of the sequence complementary to one of SEQ ID NOs. 1-
15 6213, nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a nucleic acid selected from the group consisting of SEQ ID NOS.: 6214-42397, nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of one of SEQ ID NOS.: 6214-42397, nucleic acids comprising nucleotide sequences
20 which hybridize under stringent conditions to a nucleic acid complementary to one of SEQ ID NOS.: 6214-42397, nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of the sequence complementary to one of SEQ ID NOS.: 6214-42397.

25 The libraries may also be screened to identify homologous nucleic coding nucleic acids or homologous antisense nucleic acids comprising nucleotide sequences which hybridize under moderate conditions to a nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213, nucleic acids comprising nucleotide sequences which hybridize under moderate conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500
30 consecutive nucleotides of one of SEQ ID NOs. 1-6213, nucleic acids comprising nucleotide sequences which hybridize under moderate conditions to a nucleic acid complementary to one of SEQ ID NOs. 1-6213, nucleic acids comprising nucleotide sequences which hybridize under moderate conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of the sequence complementary to one of SEQ ID
35 NOs. 1-6213, nucleic acids comprising nucleotide sequences which hybridize under moderate conditions to a nucleic acid selected from the group consisting of SEQ ID NOS.: 6214-42397, nucleic acids comprising nucleic acid sequences which hybridize under moderate conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500

consecutive nucleotides of one of SEQ ID NOS.: 6214-42397, nucleic acids comprising nucleotide sequences which hybridize under moderate conditions to a nucleic acid complementary to one of SEQ ID NOS.: 6214-42397 and nucleic acids comprising nucleotide sequences which hybridize under moderate conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100,
5 150, 200, 300, 400, or 500 consecutive nucleotides of the sequence complementary to one of SEQ ID NOS.: 6214-42397.

The homologous coding nucleic acids, homologous antisense nucleic acids or homologous polypeptides identified as above can then be used as targets or tools for the identification of new, antimicrobial compounds using methods such as those described herein. In some embodiments, the
10 homologous coding nucleic acids, homologous antisense nucleic acids, or homologous polypeptides may be used to identify compounds with activity against more than one microorganism. [Placeholder]

For example, the preceding methods may be used to isolate homologous coding nucleic acids or homologous antisense nucleic acids comprising a nucleotide sequence with at least 97%, at least 95%, at least 90%, at least 85%, at least 80%, or at least 70% nucleotide sequence identity to a
15 nucleotide sequence selected from the group consisting of one of the sequences of SEQ ID NOS. 1-6213, fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides thereof, and the sequences complementary thereto. The preceding methods may also be used to isolate homologous coding nucleic acids or homologous antisense nucleic acids comprising a nucleotide sequence with at least 97%, at least 95%, at least 90%, at least 85%, at
20 least 80%, or at least 70% nucleotide sequence identity to a nucleotide sequence selected from the group consisting of one of the nucleotide sequences of SEQ ID NOS.: 6214-42397, fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides thereof, and the sequences complementary thereto. Identity may be measured using BLASTN version 2.0 with the default parameters. (Altschul, S.F. et al. Gapped BLAST and PSI-
25 BLAST: A New Generation of Protein Database Search Programs, Nucleic Acid Res. 25: 3389-3402 (1997). For example, the homologous polynucleotides may comprise a coding sequence which is a naturally occurring allelic variant of one of the coding sequences described herein. Such allelic variants may have a substitution, deletion or addition of one or more nucleotides when compared to the nucleic acids of SEQ ID NOS: 1-6213, SEQ ID NOS.: 6214-42397 or the
30 nucleotide sequences complementary thereto.

Additionally, the above procedures may be used to isolate homologous coding nucleic acids which encode polypeptides having at least 99%, 95%, at least 90%, at least 85%, at least 80%, at least 70%, at least 60%, at least 50%, at least 40% or at least 25% amino acid identity or similarity to a polypeptide comprising the sequence of one of SEQ ID NOS: 42398-78581 or to a polypeptide
35 whose expression is inhibited by a nucleic acid of one of SEQ ID NOS: 1-6213 or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof as determined using the FASTA version 3.0t78 algorithm with the default parameters. Alternatively, protein identity or similarity may be identified using BLASTP with the default

parameters, BLASTX with the default parameters, or TBLASTN with the default parameters. (Altschul, S.F. et al. Gapped BLAST and PSI-BLAST: A New Generation of Protein Database Search Programs, *Nucleic Acid Res.* 25: 3389-3402 (1997).

Alternatively, homologous coding nucleic acids, homologous antisense nucleic acids or homologous polypeptides may be identified by searching a database to identify sequences having a desired level of nucleotide or amino acid sequence homology to a nucleic acid or polypeptide involved in proliferation or an antisense nucleic acid to a nucleic acid involved in microbial proliferation. A variety of such databases are available to those skilled in the art, including GenBank and GenSeq. In some embodiments, the databases are screened to identify nucleic acids with at least 97%, at least 95%, at least 90%, at least 85%, at least 80%, or at least 70% nucleotide sequence identity to a nucleic acid required for proliferation, an antisense nucleic acid which inhibits proliferation, or a portion of a nucleic acid required for proliferation or a portion of an antisense nucleic acid which inhibits proliferation. For example, homologous coding sequences may be identified by using a database to identify nucleic acids homologous to one of SEQ ID Nos. 1-6213, homologous to fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides thereof, nucleic acids homologous to one of SEQ ID NOS.: 6214-42397, homologous to fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of one of SEQ ID NOS.: 6214-42397, nucleic acids homologous to one of SEQ ID Nos. 1-6213, homologous to fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides thereof or nucleic acids homologous to the sequences complementary to any of the preceding nucleic acids. In other embodiments, the databases are screened to identify polypeptides having at least 99%, 95%, at least 90%, at least 85%, at least 80%, at least 70%, at least 60%, at least 50%, at least 40% or at least 25% amino acid sequence identity or similarity to a polypeptide involved in proliferation or a portion thereof. For example, the database may be screened to identify polypeptides homologous to a polypeptide comprising one of SEQ ID NOs: 42398-78581, a polypeptide whose expression is inhibited by a nucleic acid of one of SEQ ID NOs: 1-6213 or homologous to fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids of any of the preceding polypeptides. In some embodiments, the database may be screened to identify homologous coding nucleic acids, homologous antisense nucleic acids or homologous polypeptides from cells or microorganisms other than the *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Salmonella typhimurium*, *Acinetobacter baumannii*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Corynebacterium diphtheriae*, *Enterobacter cloacae*, *Enterococcus faecium*, *Haemophilus influenzae*, *Helicobacter pylori*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*,

Mycobacterium leprae, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella multocida*, *Proteus mirabilis*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella paratyphi*, *Salmonella typhi*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus mutans*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae* or *Yersinia pestis* species from which they were obtained. For example the database may be screened to identify homologous coding nucleic acids, homologous antisense nucleic acids or homologous polypeptides from microorganisms such as *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* or any species falling within the genera of any of the above species, including coagulase negative *Staphylococcus*. In some embodiments, the homologous coding nucleic acids, homologous antisense nucleic acids, or homologous polypeptides are from an organism other than *E. coli*.

In another embodiment, gene expression arrays and microarrays can be employed. Gene expression arrays are high density arrays of DNA samples deposited at specific locations on a glass chip, nylon membrane, or the like. Such arrays can be used by researchers to quantify relative gene expression under different conditions. Gene expression arrays are used by researchers to help identify optimal drug targets, profile new compounds, and determine disease pathways. An example of this technology is found in U.S. Patent No. 5,807,522.

It is possible to study the expression of all genes in the genome of a particular microbial organism using a single array. For example, the arrays may consist of 12 x 24 cm nylon filters containing PCR products corresponding to ORFs from *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Salmonella typhimurium*,
 5 *Acinetobacter baumannii*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Corynebacterium diphtheriae*, *Enterobacter cloacae*, *Enterococcus faecium*, *Haemophilus influenzae*, *Helicobacter pylori*, *Legionella pneumophila*, *Listeria*
 10 *monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella multocida*, *Proteus mirabilis*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella paratyphi*, *Salmonella typhi*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus mutans*, *Streptococcus*
 15 *pneumoniae*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae* or *Yersinia pestis* (including the nucleic acids of SEQ ID NOs.: 6214-42397) . 10 ngs of each PCR product are spotted every 1.5 mm on the filter. Single stranded labeled cDNAs are prepared for hybridization to the array (no second strand synthesis or amplification step is done) and placed in contact with the filter. Thus the labeled cDNAs are of "antisense" orientation.
 20 Quantitative analysis is done by phosphorimager.

Hybridization of cDNA made from a sample of total cell mRNA to such an array followed by detection of binding by one or more of various techniques known to those in the art results in a signal at each location on the array to which cDNA hybridized. The intensity of the hybridization signal obtained at each location in the array thus reflects the amount of mRNA for that specific
 25 gene that was present in the sample. Comparing the results obtained for mRNA isolated from cells grown under different conditions thus allows for a comparison of the relative amount of expression of each individual gene during growth under the different conditions.

Gene expression arrays may be used to analyze the total mRNA expression pattern at various time points after induction of an antisense nucleic acid complementary to a proliferation-
 30 required gene. Analysis of the expression pattern indicated by hybridization to the array provides information on other genes whose expression is influenced by antisense expression. For example, if the antisense is complementary to a gene for ribosomal protein L7/L12 in the 50S subunit, levels of other mRNAs may be observed to increase, decrease or stay the same following expression of antisense to the L7/L12 gene. If the antisense is complementary to a different 50S subunit
 35 ribosomal protein mRNA (e.g. L25), a different mRNA expression pattern may result. Thus, the mRNA expression pattern observed following expression of an antisense nucleic acid comprising a nucleotide sequence complementary to a proliferation required gene may identify other proliferation-required nucleic acids. In addition, the mRNA expression patterns observed when the

bacteria are exposed to candidate drug compounds or known antibiotics may be compared to those observed with antisense nucleic acids comprising a nucleotide sequence complementary to a proliferation-required nucleic acid. If the mRNA expression pattern observed with the candidate drug compound is similar to that observed with the antisense nucleic acid, the drug compound may be a promising therapeutic candidate. Thus, the assay would be useful in assisting in the selection of promising candidate drug compounds for use in drug development.

In cases where the source of nucleic acid deposited on the array and the source of the nucleic acid being hybridized to the array are from two different cells or microorganisms, gene expression arrays can identify homologous nucleic acids in the two cells or microorganisms.

The present invention also contemplates additional methods for screening other microorganisms for proliferation-required genes. In one aspect of this embodiment, an antisense nucleic acid comprising a nucleotide sequence complementary to the proliferation-required sequences from *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Salmonella typhimurium*, *Acinetobacter baumannii*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Corynebacterium diphtheriae*, *Enterobacter cloacae*, *Enterococcus faecium*, *Haemophilus influenzae*, *Helicobacter pylori*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella multocida*, *Proteus mirabilis*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella paratyphi*, *Salmonella typhi*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus mutans*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae* or *Yersinia pestis*, or a portion thereof, is transcribed in an antisense orientation in such a way as to alter the level or activity of a nucleic acid required for proliferation of an autologous or heterologous cell or microorganism. For example, the antisense nucleic acid may be a homologous antisense nucleic acid such as an antisense nucleic acid homologous to the nucleotide sequence complementary to one of SEQ ID NOs.: 6214-42397, an antisense nucleic acid comprising a nucleotide sequence homologous to one of SEQ ID NOs.: 1-6213, or an antisense nucleic acid comprising a nucleotide sequence complementary to a portion of any of the preceding nucleic acids. The cell or microorganism transcribing the homologous antisense nucleic acid may be used in a cell-based assay, such as those described herein, to identify candidate antibiotic compounds. In another embodiment, the conserved portions of nucleotide sequences identified as proliferation-required can be used to generate degenerate primers for use in the polymerase chain reaction (PCR). The PCR technique is well known in the art. The successful production of a PCR product using degenerate primers generated from the nucleotide sequences identified herein indicates the presence of a homologous gene sequence in the species being screened.

This homologous gene is then isolated, expressed, and used as a target for candidate antibiotic compounds. In another aspect of this embodiment, the homologous gene (for example a homologous coding nucleic acid) thus identified, or a portion thereof, is transcribed in an autologous cell or microorganism or in a heterologous cell or microorganism in an antisense orientation in such a way as to alter the level or activity of a homologous gene required for proliferation in the autologous or heterologous cell or microorganism. Alternatively, a homologous antisense nucleic acid may be transcribed in an autologous or heterologous cell or microorganism in such a way as to alter the level or activity of a gene product required for proliferation in the autologous or heterologous cell or microorganism.

The nucleic acids homologous to the genes required for the proliferation of *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Salmonella typhimurium*, *Acinetobacter baumannii*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Corynebacterium diphtheriae*, *Enterobacter cloacae*, *Enterococcus faecium*, *Haemophilus influenzae*, *Helicobacter pylori*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella multocida*, *Proteus mirabilis*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella paratyphi*, *Salmonella typhi*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus mutans*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae* or *Yersinia pestis* or the sequences complementary thereto may be used to identify homologous coding nucleic acids or homologous antisense nucleic acids from cells or microorganisms other than *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Salmonella typhimurium*, *Acinetobacter baumannii*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Corynebacterium diphtheriae*, *Enterobacter cloacae*, *Enterococcus faecium*, *Haemophilus influenzae*, *Helicobacter pylori*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella multocida*, *Proteus mirabilis*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella paratyphi*, *Salmonella typhi*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus mutans*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae* or *Yersinia pestis* to inhibit the proliferation of cells or microorganisms other than

Escherichia coli, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*,
Pseudomonas aeruginosa, *Salmonella typhimurium*, *Acinetobacter baumannii*, *Bacillus anthracis*,
Bacteroides fragilis, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*,
Burkholderia fungorum, *Burkholderia mallei*, *Campylobacter jejuni*, *Chlamydia pneumoniae*,
5 *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*,
Corynebacterium diphtheriae, *Enterobacter cloacae*, *Enterococcus faecium*, *Haemophilus*
influenzae, *Helicobacter pylori*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella*
catarrhalis, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium*
tuberculosis, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria*
10 *meningitidis*, *Pasteurella multocida*, *Proteus mirabilis*, *Pseudomonas putida*, *Pseudomonas*
syringae, *Salmonella paratyphi*, *Salmonella typhi*, *Staphylococcus epidermidis*, *Staphylococcus*
haemolyticus, *Streptococcus mutans*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*,
Treponema pallidum, *Ureaplasma urealyticum*, *Vibrio cholerae* or *Yersinia pestis* by inhibiting the
activity or reducing the amount of the identified homologous coding nucleic acid or homologous
15 polypeptide in the cell or microorganism other than *Escherichia coli*, *Staphylococcus aureus*,
Enterococcus faecalis, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Salmonella typhimurium*,
Acinetobacter baumannii, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia*
burgdorferi, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter*
jejuni, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium*
20 *botulinum*, *Clostridium difficile*, *Corynebacterium diphtheriae*, *Enterobacter cloacae*, *Enterococcus*
faecium, *Haemophilus influenzae*, *Helicobacter pylori*, *Legionella pneumophila*, *Listeria*
monocytogenes, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*,
Mycobacterium leprae, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma*
pneumoniae, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella multocida*, *Proteus*
25 *mirabilis*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella paratyphi*, *Salmonella typhi*,
Staphylococcus epidermidis, *Staphylococcus haemolyticus*, *Streptococcus mutans*, *Streptococcus*
pneumoniae, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio*
cholerae or *Yersinia pestis* or to identify compounds which inhibit the growth of cells or
microorganisms other than *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*,
30 *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Salmonella typhimurium*, *Acinetobacter*
baumannii, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*,
Burkholderia cepacia, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*,
Chlamydia pneumoniae, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium*
botulinum, *Clostridium difficile*, *Corynebacterium diphtheriae*, *Enterobacter cloacae*, *Enterococcus*
35 *faecium*, *Haemophilus influenzae*, *Helicobacter pylori*, *Legionella pneumophila*, *Listeria*
monocytogenes, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*,
Mycobacterium leprae, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma*
pneumoniae, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella multocida*, *Proteus*

mirabilis, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella paratyphi*, *Salmonella typhi*,
Staphylococcus epidermidis, *Staphylococcus haemolyticus*, *Streptococcus mutans*, *Streptococcus*
pneumoniae, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio*
cholerae or *Yersinia pestis* as described below. For example, the nucleic acids homologous to
5 proliferation-required genes from *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*,
Klebsiella pneumoniae, *Pseudomonas aeruginosa*, *Salmonella typhimurium*, *Acinetobacter*
baumannii, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*,
Burkholderia cepacia, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*,
Chlamydia pneumoniae, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium*
10 *botulinum*, *Clostridium difficile*, *Corynebacterium diphtheriae*, *Enterobacter cloacae*, *Enterococcus*
faecium, *Haemophilus influenzae*, *Helicobacter pylori*, *Legionella pneumophila*, *Listeria*
monocytogenes, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*,
Mycobacterium leprae, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma*
pneumoniae, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella multocida*, *Proteus*
15 *mirabilis*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella paratyphi*, *Salmonella typhi*,
Staphylococcus epidermidis, *Staphylococcus haemolyticus*, *Streptococcus mutans*, *Streptococcus*
pneumoniae, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio*
cholerae or *Yersinia pestis* or the sequences complementary thereto may be used to identify
compounds which inhibit the growth of *Acinetobacter baumannii*, *Anaplasma marginale*,
20 *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia*
burgdorferi, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter*
jejuni, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*,
Candida parapsilosis, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida*
pseudotropicalis), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*,
25 *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*,
Coccidioides immitis, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter*
cloacae, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*,
Helicobacter pylori, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*,
Listeria monocytogenes, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*,
30 *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma*
pneumoniae, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella*
haemolytica, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*,
Pseudomonas aeruginosa, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*,
Salmonella choleraesuis, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella*
35 *typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*,
Staphylococcus aureus, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus*
pneumoniae, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma*
urealyticum, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*,

Yersinia pestis or any species falling within the genera of any of the above species. In some embodiments of the present invention, the nucleic acids homologous to proliferation-required sequences from *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Salmonella typhimurium*, *Acinetobacter baumannii*,
5 *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Corynebacterium diphtheriae*, *Enterobacter cloacae*, *Enterococcus faecium*, *Haemophilus influenzae*, *Helicobacter pylori*, *Legionella pneumophila*, *Listeria monocytogenes*,
10 *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella multocida*, *Proteus mirabilis*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella paratyphi*, *Salmonella typhi*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus mutans*, *Streptococcus pneumoniae*,
15 *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae* or *Yersinia pestis* (including nucleic acids homologous to one of SEQ ID NOs.: 6214-42397) or the sequences complementary thereto (including nucleic acids homologous to one of SEQ ID NOs.: 1-6213) are used to identify proliferation-required sequences in an organism other than *E. coli*.

In another embodiment of the present invention, antisense nucleic acids complementary to the sequences identified as required for proliferation or portions thereof (including antisense nucleic acids comprising a nucleotide sequence complementary to one of SEQ ID NOs.: 6214-42397 or portions thereof, such as the nucleic acids of SEQ ID NOs.: 1-6213) are transferred to vectors capable of function within a species other than the species from which the sequences were obtained. For example, the vector may be functional in *Acinetobacter baumannii*, *Anaplasma marginale*,
20 *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*,
25 *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*,
30 *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*,

Salmonella choleraesuis, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* or any species falling within the genera of any of the above species. In some embodiments of the present invention, the vector may be functional in an organism other than *E. coli*. As would be appreciated by one of ordinary skill in the art, vectors may contain certain elements that are species specific. These elements can include promoter sequences, operator sequences, repressor genes, origins of replication, ribosomal binding sequences, termination sequences, and others. To use the antisense nucleic acids, one of ordinary skill in the art would know to use standard molecular biology techniques to isolate vectors containing the sequences of interest from cultured bacterial cells, isolate and purify those sequences, and subclone those sequences into a vector adapted for use in the species of bacteria to be screened.

Vectors for a variety of other species are known in the art. For example, numerous vectors which function in *E. coli* are known in the art. Also, Pla et al. have reported an expression vector that is functional in a number of relevant hosts including: *Salmonella typhimurium*, *Pseudomonas putida*, and *Pseudomonas aeruginosa*. *J. Bacteriol.* 172(8):4448-55 (1990). Brunschwig and Darzins (Gene (1992) 111:35-4, described a shuttle expression vector for *Pseudomonas aeruginosa*. Vectors useful for the production of stabilized mRNA having an increased lifetime (including antisense RNA) in Gram negative organisms are described in U.S. Provisional Patent Application Serial Number 60/343,512, filed December 21, 2001. Similarly many examples exist of expression vectors that are freely transferable among various Gram positive microorganisms. Expression vectors for *Enterococcus faecalis* may be engineered by incorporating suitable promoters into a pAK80 backbone (Israelsen, H., S. M. Madsen, A. Vrang, E. B. Hansen and E. Johansen. 1995. *Appl. Environ. Microbiol.* 61:2540-2547. A number of vectors useful for nucleic acid expression (including antisense nucleic acid expression) in *Enterococcus faecalis*, *Staphylococcus aureus* as well as other Gram positive organisms are described in U.S. Patent Application Serial Number 10/032,393, filed December 21, 2001.

Following the subcloning of the antisense nucleic acids complementary to proliferation-required sequences from *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Salmonella typhimurium*, *Acinetobacter baumannii*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Corynebacterium diphtheriae*, *Enterobacter cloacae*, *Enterococcus faecium*, *Haemophilus influenzae*, *Helicobacter pylori*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*,

Mycobacterium leprae, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella multocida*, *Proteus mirabilis*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella paratyphi*, *Salmonella typhi*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus mutans*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae* or *Yersinia pestis* or portions thereof into a vector functional in a second cell or microorganism of interest (i.e. a cell or microorganism other than the one from which the identified nucleic acids were obtained), the antisense nucleic acids are conditionally transcribed to test for bacterial growth inhibition. The nucleotide sequences of the nucleic acids from *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Salmonella typhimurium*, *Acinetobacter baumannii*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Corynebacterium diptheriae*, *Enterobacter cloacae*, *Enterococcus faecium*, *Haemophilus influenzae*, *Helicobacter pylori*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella multocida*, *Proteus mirabilis*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella paratyphi*, *Salmonella typhi*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus mutans*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae* or *Yersinia pestis* that, when transcribed, inhibit growth of the second cell or microorganism are compared to the known genomic sequence of the second cell or microorganism to identify the homologous gene from the second organism. If the homologous sequence from the second cell or microorganism is not known, it may be identified and isolated by hybridization to the proliferation-required *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Salmonella typhimurium*, *Acinetobacter baumannii*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Corynebacterium diptheriae*, *Enterobacter cloacae*, *Enterococcus faecium*, *Haemophilus influenzae*, *Helicobacter pylori*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella multocida*, *Proteus mirabilis*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella paratyphi*, *Salmonella typhi*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus mutans*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio*

cholerae or *Yersinia pestis* sequence of interest or by amplification using PCR primers based on the proliferation-required nucleotide sequence of interest as described above. In this way, sequences which may be required for the proliferation of the second cell or microorganism may be identified. For example, the second microorganism may be *Acinetobacter baumannii*, *Anaplasma marginale*,
 5 *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*,
 10 *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*,
 15 *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*,
 20 *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* or any species falling within the genera of any of the above species. In some
 25 embodiments of the present invention, the second microorganism is an organism other than *E. coli*.

The homologous nucleic acid sequences from the second cell or microorganism which are identified as described above may then be operably linked to a promoter, such as an inducible promoter, in an antisense orientation and introduced into the second cell or microorganism. The techniques described herein for identifying *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus*
 30 *faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Salmonella typhimurium*, *Acinetobacter baumannii*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Corynebacterium diphtheriae*, *Enterobacter cloacae*, *Enterococcus*
 35 *faecium*, *Haemophilus influenzae*, *Helicobacter pylori*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella multocida*, *Proteus*

mirabilis, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella paratyphi*, *Salmonella typhi*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus mutans*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae* or *Yersinia pestis* genes required for proliferation may thus be employed to determine
5 whether the identified nucleotide sequences from a second cell or microorganism inhibit the proliferation of the second cell or microorganism. For example, the second microorganism may be *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* or any species falling within the genera of any of the above species. In some
25 embodiments of the present invention, the second microorganism may be an organism other than *E. coli*.

30 Antisense nucleic acids required for the proliferation of microorganisms other than *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Salmonella typhimurium*, *Acinetobacter baumannii*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Chlamydia pneumoniae*,
35 *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Corynebacterium diphtheriae*, *Enterobacter cloacae*, *Enterococcus faecium*, *Haemophilus influenzae*, *Helicobacter pylori*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium*

tuberculosis, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella multocida*, *Proteus mirabilis*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella paratyphi*, *Salmonella typhi*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus mutans*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*,
5 *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae* or *Yersinia pestis* or the genes corresponding thereto, may also be hybridized to a microarray containing the *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Salmonella typhimurium*, *Acinetobacter baumannii*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*,
10 *Burkholderia mallei*, *Campylobacter jejuni*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Corynebacterium diphtheriae*, *Enterobacter cloacae*, *Enterococcus faecium*, *Haemophilus influenzae*, *Helicobacter pylori*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella multocida*, *Proteus mirabilis*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella paratyphi*, *Salmonella typhi*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus mutans*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae* or *Yersinia pestis* (including the nucleic acids of SEQ ID NOs.: 6214-
20 42397) to gauge the homology between the *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Salmonella typhimurium*, *Acinetobacter baumannii*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Corynebacterium diphtheriae*, *Enterobacter cloacae*, *Enterococcus faecium*, *Haemophilus influenzae*, *Helicobacter pylori*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella multocida*, *Proteus mirabilis*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella paratyphi*, *Salmonella typhi*,
30 *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus mutans*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae* or *Yersinia pestis* sequences and the proliferation-required nucleic acids from other cells or microorganisms. For example, the proliferation-required nucleic acid may be from
35 *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida*

guilliermondii, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*,
 5 *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella*
 10 *haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus*
 15 *pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* or any species falling within the genera of any of the above species. In some embodiments of the present invention, the proliferation-required nucleotide sequences from
Escherichia coli, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*,
 20 *Pseudomonas aeruginosa*, *Salmonella typhimurium*, *Acinetobacter baumannii*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Corynebacterium diphtheriae*, *Enterobacter cloacae*, *Enterococcus faecium*, *Haemophilus*
 25 *influenzae*, *Helicobacter pylori*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella multocida*, *Proteus mirabilis*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella paratyphi*, *Salmonella typhi*, *Staphylococcus epidermidis*, *Staphylococcus*
 30 *haemolyticus*, *Streptococcus mutans*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae* or *Yersinia pestis* or homologous nucleic acids are used to identify proliferation-required sequences in an organism other than *E. coli*. In some embodiments of the present invention, the proliferation-required sequences may be from an organism other than *E. coli*. The proliferation-required nucleic acids from a cell or microorganism
 35 other than *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Salmonella typhimurium*, *Acinetobacter baumannii*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Chlamydia pneumoniae*,

Chlamydia trachomatis, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Corynebacterium diphtheriae*, *Enterobacter cloacae*, *Enterococcus faecium*, *Haemophilus influenzae*, *Helicobacter pylori*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella multocida*, *Proteus mirabilis*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella paratyphi*, *Salmonella typhi*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus mutans*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae* or *Yersinia pestis* may be hybridized to the array under a variety of conditions which permit hybridization to occur when the probe has different levels of homology to the nucleotide sequence on the microarray. This would provide an indication of homology across the cells or microorganisms as well as clues to other possible essential genes in these cells or microorganisms.

In some embodiments of the present invention, the essential gene products described herein are used in methods of identifying a target on which a compound that inhibits cellular proliferation acts. Such methods are described in the U.S. Patent Application entitled METHODS FOR IDENTIFYING THE TARGET OF A COMPOUND WHICH INHIBITS CELLULAR PROLIFERATION, filed February 8, 2002. As employed herein, some embodiments of methods used to identify a target on which a compound that inhibits cellular proliferation acts utilize collections or cultures of strains comprising strains which either overexpress a different gene product which is required for cellular proliferation (such as the gene products described herein) or underexpress a different gene product (such as the gene products described herein) which is required for cellular proliferation (i.e. at least some of the strains in the culture overexpress or underexpress a gene product required for cellular proliferation). In some embodiments, the present invention uses collections or cultures of strains comprising both strains which overexpress gene products required for cellular proliferation and strains which underexpress the same gene products required for cellular proliferation. Preferably, each of the strains present in the culture or collection either overexpresses or underexpresses a different gene product which is required for cellular proliferation (i.e. all of the strains in the culture overexpress or underexpress a gene product required for cellular proliferation). However, in some embodiments, the culture or collection may include one or more strains which do not overexpress or underexpress a gene product which is required for proliferation. The gene product which is overexpressed or underexpressed in each strain may be any gene product which is required for cellular proliferation, including a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397, a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42398-78581, a gene product whose activity or level is inhibited by a homologous

antisense nucleic acid, a gene product encoded by a homologous coding nucleic acid, and a gene product comprising a homologous polypeptide.

As used herein the term "culture" refers to a plurality of strains growing in a single aliquot of a liquid growth medium and the term "collection" refers to a plurality of strains each of which is
5 growing in a separate aliquot of liquid growth medium or a different location on a solid growth medium.

In some embodiments, if desired, one or more of the strains in the culture or collection of strains may overexpress or underexpress more than one gene product described herein which is required for cellular proliferation. In this embodiment, the gene products which are overexpressed
10 or underexpressed in one or more of the strains may be functionally related or functionally unrelated. This may facilitate the identification of compounds when two or more gene products share similar functions in the cell or where the cell has multiple biochemical pathways which lead to a particular end product.

Alternatively, if the gene product described herein to be overexpressed or underexpressed is
15 encoded by a gene which is part of an operon containing a plurality of genes, the desired gene may be overexpressed or underexpressed while the remaining genes in the operon are expressed at levels where they do not impact the ability of the cell to grow in the presence of a particular compound. For example, the desired gene may be placed under the control of a regulatable promoter, a transcriptional terminator may be placed 3' of the desired gene and a promoter, preferably a
20 constitutive promoter, may be placed 3' of the transcriptional terminator and 5' of the remaining genes in the operon.

In some embodiments, the culture or collection of strains may comprise a strain which overexpresses or underexpresses a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 1-6213.
25 In some embodiments, the culture or collection of strains may comprise strains which in aggregate overexpress or underexpress at least two gene products whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOS.: 1-6213, at least 10 gene products whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOS.: 1-6213, at least 20 gene products whose activity or level is inhibited by a nucleic acid
30 selected from the group consisting of SEQ ID NOS.: 1-6213, at least 30 gene products whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOS.: 1-6213, at least 50 gene products whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOS.: 1-6213, at least 100 gene products whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOS.: 1-6213, at least 300
35 gene products whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOS.: 1-6213 or more than 300 gene products whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOS.: 1-6213, wherein each strain in the culture or collection of strains overexpresses or underexpresses a single gene

product whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs. 1-6213. Alternatively, if desired, one or more of the strains in the culture or collection of strains may overexpress or underexpress more than one gene product whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs. 1-6213.

5 In other embodiments, the culture or collection of strains may comprise a strain which overexpresses or underexpresses a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397. In some embodiments, the culture or collection of strains may comprise strains which in aggregate overexpress or underexpress at least two gene products encoded by a nucleic acid comprising a nucleotide
10 sequence selected from the group consisting of SEQ ID NOs.: 6214-42397, at least 10 gene products encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397, at least 20 gene products encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397, at least 30 gene products encoded by a nucleic acid comprising a nucleotide sequence selected from
15 the group consisting of SEQ ID NOs.: 6214-42397, at least 50 gene products encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397, at least 100 gene products encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397, at least 300 gene products encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of
20 SEQ ID NOs.: 6214-42397 or more than 300 gene products encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397, wherein each strain in the culture or collection of strains overexpresses or underexpresses a single gene product encoded by a nucleic acid selected from the group consisting of SEQ ID NOs. 6214-42397. Alternatively, if desired, one or more strains in the culture or collection of strains may overexpress
25 or underexpress more than one gene product encoded by a nucleic acid selected from the group consisting of SEQ ID NOs. 6214-42397.

In some embodiments the culture or collection of strains comprises a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42938-78581 is overexpressed or underexpressed. In some embodiments, the culture or collection
30 of strains may comprise strains which in aggregate overexpress or underexpress at least two gene products comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42938-78581, at least 10 gene products comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42938-78581, at least 20 gene products comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42938-78581, at least 30 gene
35 products comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42938-78581, at least 50 gene products comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42938-78581, at least 100 gene products comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42938-78581, at least 300 gene

products comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42938-78581 or more than 300 gene products comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42938-78581, wherein each strain in the culture or collection of strains overexpresses or underexpresses a single gene product selected from the group consisting of SEQ ID NOs. 42938-78581. Alternatively, if desired one or more of the strains in the culture or collection of strains may overexpress or underexpress more than one gene product selected from the group consisting of SEQ ID NOs. 42938-78581.

In other embodiments, the culture or collection of strains comprises a strain in which at least one of the gene products encoded by a homologous coding nucleic acid as defined above is overexpressed or underexpressed. In some embodiments, the culture or collection of strains may comprise strains which in aggregate overexpress or underexpress at least 2, at least 10, at least 20, at least 30, at least 50, at least 100, at least 300 or more than 300 gene products encoded by a homologous coding nucleic acid as defined above. If desired the culture or collection of strains may comprise one or more strains which overexpress or underexpress more than one gene product encoded by a homologous coding nucleic acid. In further embodiments, the culture or collection of strains comprises a strain in which at least one, at least 10, at least 20, at least 30, at least 50, at least 100, at least 300 or more than 300 homologous polypeptides as defined above is overexpressed or underexpressed. If desired the culture or collection of strains may comprise one or more strains which overexpress or underexpress more than one homologous polypeptide.

For example, in some embodiments, the culture or collection of strains comprises a strain in which at least one gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 is overexpressed or underexpressed, wherein each strain overexpresses or underexpresses one gene product. In some

embodiments, the culture or collection of strains may comprise strains in which in aggregate at least 2, at least 10, at least 20, at least 30, at least 50, at least 100, at least 300, or more than 300 gene products selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 is overexpressed or underexpressed, wherein each strain overexpresses or underexpresses one gene product.

If desired, one or more of the strains in the culture or collection of strains may overexpress or underexpress more than one gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213.

In further embodiments, the culture or collection of strains comprises a strain in which at least one gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate conditions is overexpressed or underexpressed, wherein each strain overexpresses or underexpresses one gene product. In some embodiments, the culture or collection of strains comprises a strain or a group of strains in which in aggregate at least 2, at least 10, at least 20, at least 30, at least 50, at least 100, at least 300, or more than 300 gene products encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate conditions is overexpressed or underexpressed, wherein each strain overexpresses or underexpresses one gene product.

If desired, one or more of the strains in the culture or collection of strains may overexpress or underexpress more than one gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 6214-42397 under moderate conditions.

In additional embodiments, the culture or collection of strains comprises a strain in which at least one gene product comprising a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOS.: 42938-78581 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOS.: 42938-78581 is overexpressed or underexpressed, wherein each strain overexpresses or underexpresses one gene product. In some embodiments, the culture or collection of strains comprises a strain or a group of strains in which in aggregate at least 2, at least 10, at least 20, at

least 30, at least 50, at least 100, at least 300, or more than 300 gene products comprising a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 42938-78581 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 42938-78581 is overexpressed or underexpressed, wherein each strain overexpresses or underexpresses one gene product.

If desired, one or more of the strains in the culture or collection of strains may overexpress or underexpress more than one polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 42938-78581 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 42938-78581.

The methods of the present invention may be used to identify the targets of compounds which inhibit the proliferation of any desired cell or organism. In some embodiments, these methods are employed to identify the targets of compounds which inhibit the proliferation of bacteria, fungi, or protozoans. In further embodiments, these methods are employed to identify the targets of compounds which inhibit the growth of an organism selected from the group consisting of *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* or any species falling within the genera of any of the above species.

Overexpression may be obtained using a variety of techniques familiar to those skilled in the art. For example, overexpression may be obtained by operably linking a gene encoding a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397, a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42398-78581, a gene product whose activity or level is inhibited by a homologous antisense nucleic acid, a gene product encoded by a homologous coding nucleic acid, or a gene product comprising a homologous polypeptide to a promoter which transcribes a higher level of mRNA encoding or comprising the gene product than does a wild type cell.

A variety of promoters may be used to overexpress the gene product described herein, including a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397, a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42398-78581, a gene product whose activity or level is inhibited by a homologous antisense nucleic acid, a gene product encoded by a homologous coding nucleic acid, and a gene product comprising a homologous polypeptide. The promoters used to overexpress the gene product may be relatively strong promoters, promoters which possess a moderate level of activity, or relatively weak promoters and may be either constitutive or regulatable promoters. In some embodiments, several strains, each of which overexpresses the gene product to a different extent, may be used in order to optimize the degree of overexpression of the gene product.

In some embodiments, each of the gene products required for proliferation may be placed under the control of several different promoters of varying strengths to create several different strains which express the gene product at varying levels. The level of expression of the gene product in each of the strains is compared to that in wild type cells in order to identify a promoter which provides a desired level of expression relative to wild type cells (i.e. a desired level of overexpression or underexpression). The strain having the desired level of expression is then included in a culture or collection of strains to be contacted with a test compound as discussed below. Examples of suites of regulatable promoters having varying strengths that are useful for the expression of gene products at varying levels are described in U.S. Patent Application Serial Number 10/032,393, filed on December 21, 2002.

The promoter is selected to be active in the type of cell in which the gene product is to be expressed. For example, for overexpression of the gene product in mammalian cells, the gene encoding the gene product may be operably linked to promoters such as the SV40 promoter, the metallothionein promoter, the MMTV promoter, the RSV promoter, the tetP promoter, the adenovirus major late promoter or other promoters known to those skilled in the art. In yeast, the gene encoding the gene product may be operably linked to promoters such as the CYC1, ADHI,

ADHII, GAL1, GAL10, PHO5, PGK or other promoters used in the art. Similarly, in bacteria, the gene encoding the gene product may be operably linked to the , SP6, T3, trc promoter, lac promoter, temperature regulated lambda promoters, the *Bacillus* aprE and nprE promoters (U.S. Patent No. 5,387,521), the bacteriophage lambda P_L and P_R promoters (Renaut, et al., (1981) Gene 15: 81) the trp promoter (Russell, et al., (1982) Gene 20: 23), the tac promoter (de Boer et al., (1983) Proc. Natl. Acad. Sci. USA 80: 21), *B. subtilis* alkaline protease promoter (Stahl et al., (1984) J. Bacteriol. 158, 411-418) alpha amylase promoter of *B. subtilis* (Yang et al., (1983) Nucleic Acids Res. 11, 237-249) or *B. amyloliquefaciens* (Tarkinen, et al, (1983) J. Biol. Chem. 258, 1007-1013), the neutral protease promoter from *B. subtilis* (Yang et al, (1984) J. Bacteriol. 160, 15-21), T7 RNA polymerase promoter (Studier and Moffatt (1986) J Mol Biol. 189(1):113-30), *B. subtilis* xyl promoter or mutant tetR promoter active in bacilli (Geissendorfer & Hillen (1990) Appl. Microbiol. Biotechnol. 33:657-663), Staphylococcal enterotoxin D promoter (Zhang and Stewart (2000) J. Bacteriol. 182(8):2321-5), cap8 operon promoter from *Staphylococcus aureus* (Ouyang et al., (1999) J. Bacteriol. 181(8):2492-500), the lactococcal nisA promoter (Eichenbaum (1998) Appl Environ Microbiol. 64(8):2763-9), promoters from in *Acholeplasma laidlawii* (Jarhede et al., (1995) Microbiology 141 (Pt 9):2071-9), porA promoter of *Neisseria meningitidis* (Sawaya et al., (1999) Gene 233:49-57), the fbpA promoter of *Neisseria gonorrhoeae* (Forng et al., (1997) J. Bacteriol. 179:3047-3052), *Corynebacterium diphtheriae* toxin gene promoter (Schmitt and Holmes (1994) J. Bacteriol. 176(4):1141-9), the hasA operon promoter from Group A Streptococci (Alberti et al., (1998) Mol Microbiol 28(2):343-53), the rpoS promoter of *Pseudomonas putida* (Kojic and Venturi (2001) J. Bacteriol. 183:3712-3720), the *Acinetobacter baumannii* phosphate regulated *ppk* gene promoter (Gavigan et al., Microbiology 145:2931-7 (1999)); the *Acinetobacter baumannii* *adhC1* promoter which is induced under iron limitation and repressed when the cells are cultured in the presence of free inorganic iron (Echenique et al., Microbiology 147:2805-15 (2001)); the *flaB* promoter of pGK12 active in *Borrelia burgdorferi* (Sartakova et al., Proc Natl Acad Sci U S A. 97(9):4850-5 (2000)); the use of Ptrc promoter results in strong inducer-dependent expression in *Burkholderia spp* (Santos et al., FEMS Microbiol Lett 195(1):91-6 (2001)); the iron regulated *sodA* promoter of *Bordetella pertussis* (Graeff-Wohlleben et al., J Bacteriol 179(7):2194-201 (1997)); UV-inducible bcn and uviAB promoters in *Clostridia spp* (Garnier and Cole Mol Microbiol 2(5):607-14 (1988)); the heat-inducible *clpB* promoter of *Campylobacter jejuni* (Thies et al., Gene 230(1):61-7 (1999)); promoters carrying bacteriophage C1 operator sites in *Klebsiella pneumoniae* (Schoefield et al, J Bacteriol 183(23):6947-50 (2001)); the *Proteus mirabilis* *ureR* promoter (Poore et al., J Bacteriol 183(15):4526-35 (2001)); and the heat-inducible *groESL* promoter in *Listeria monocytogenes*, and the IPTG inducible promoter in pLEX5BA (Krause et al., J. Mol. Biol. 274: 365 (1997). In another embodiment, which may be useful in *Staphylococcus aureus*, the promoter is a novel inducible promoter system, XylT5, comprising a modified T5 promoter fused to the *xylO* operator from the *xylA* promoter of *Staphylococcus aureus*. This promoter is described in U.S. Patent Application Serial Number 10/032,393. In another embodiment the promoter may be a two-

component inducible promoter system in which the T7 RNA polymerase gene is integrated on the chromosome and is regulated by *lacUV5/ lacO* (Brunschwig, E. and Darzins, A. 1992. Gene 111:35-41, and a T7 gene 10 promoter, which is transcribed by T7 RNA polymerase, is fused with a *lacO* operator. In another embodiment the promoter may be the promoters from the plasmids pEPEF3 or pEPEF14, which harbor xylose inducible promoters functional in *E. faecalis*, described in U.S. Patent Application Serial No. 10/032,393. Other promoters which may be used are familiar to those skilled in the art. In fungi, the gene encoding the gene product may be operably linked to the CaACT1 promoter (Morschhauser, Mol. Gen. Genet. 257: 412-420 (1998), or other promoters familiar to those skilled in the art. It will be appreciated that other combinations of organisms and promoters may also be used in the present invention.

In some embodiments, overexpression may be achieved by using homologous recombination to replace the natural promoter which drives expression of the proliferation-required genes described herein with a regulatable promoter. For example, the methods described in U.S. Patent Application 09/948,993 may be used to place the gene required for proliferation under the control of a regulatable promoter. Examples of gene products, which are encoded by genes that can be overexpressed by regulatable promoters introduced by such promoter replacement methods include a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397, a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42398-78581, a gene product whose activity or level is inhibited by a homologous antisense nucleic acid, a gene product encoded by a homologous coding nucleic acid, and a gene product comprising a homologous polypeptide.

Briefly, in some embodiments of these methods in which natural promoters are replaced by regulatable promoters, the cells may be haploid, such as bacterial cells. Regulatable promoters that are useful for promoter replacement in bacterial cells include, but are not limited to, the promoters described in U.S. Patent Application Serial Number 10/032,393 filed December 21, 2001. A linear promoter replacement cassette comprising a regulatable promoter flanked by nucleotide sequences having homology to the natural promoter is introduced into the cell. In some embodiments, the cassette also comprises a nucleotide sequence encoding a selectable marker or a marker whose expression is readily identified. The cassette may be a double stranded nucleic acid or a single stranded nucleic acid as described in U.S. Patent Application Serial Number 09/948,993. Upon homologous recombination, the natural promoter is replaced with the regulatable promoter, leaving the gene required for proliferation under the control of the regulatable promoter. Strains in which the gene required for proliferation is under control of the regulatable promoter are grown under conditions in which the regulatable promoter provides a level of the proliferation-required gene product which is above the level in a wild type cell. For example, the strains may be grown in the

presence of an inducer which induces expression from the regulatable promoter, or under conditions in which the action of a repressor on the regulatable promoter is reduced or eliminated.

Alternatively, rather than replacing the native promoters of each of the genes encoding a proliferation-required gene product described herein with a single desired replacement promoter, a plurality of replacement promoters which provide desired expression levels for the gene products to be overexpressed or underexpressed are used. The method is performed as described above except that rather than using a single labeled primer complementary to a nucleotide sequence within the single replacement promoter, a plurality of labeled primers complementary to suitable nucleotide sequences in the plurality of replacement promoters are used.

Alternatively, in embodiments in which the level or activity of proliferation-required gene products described herein is reduced by transcribing an antisense nucleic acid complementary to at least a portion of the genes encoding such gene products, the strains may be designed such that the length of the nucleotide sequence encoding the antisense nucleic acid is different for each gene. Amplification reactions are performed as described above using primers at each end of the gene encoding the antisense nucleic acid such that the amplification product corresponding to each gene has a unique length or a dye which allows it to be distinguished from other amplification products of the same length. Alternatively, the lengths of the nucleotide sequences encoding the antisense nucleic acids may not be unique for each gene, but the primers used in the amplification reaction may be selected such that the length of the amplification product corresponding to each gene is unique.

In another embodiment, the native promoters may be replaced with promoters which include therein or adjacent thereto a unique nucleotide sequence which is distinct from that present in the other replacement promoters in the strains in the culture or collection of strains. In this embodiment, each promoter includes or has adjacent thereto a unique "tag" which may be used to identify strains which proliferate more rapidly or more slowly in the culture or collection of strains. The tag may be detected using hybridization based methods or amplification based methods, including the amplification method which generates amplification products having a unique size for each proliferation required gene described above.

Alternatively, the native promoter which directs the transcription of the proliferation-required genes described herein may be rendered regulatable by inserting a regulatory element into the chromosome of the cell via homologous recombination such that the regulatory element regulates the level of transcription from the promoter. Examples of gene products, which are encoded by genes that have promoters which can be rendered regulatable by regulatory elements inserted by such methods include a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397, a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42398-78581, a gene product whose activity or

level is inhibited by a homologous antisense nucleic acid, a gene product encoded by a homologous coding nucleic acid, and a gene product comprising a homologous polypeptide.

A variety of regulatory elements may be used to regulate the expression of essential gene products described herein. The regulatory element may be an operator which is recognized by a repressor (e.g. lac, tet, araBAD repressors) or a nucleotide sequence which is recognized by a transcriptional activator. In some embodiments, the regulatory element may be a transcriptional terminator, a nucleotide sequence which introduces a bend in the DNA or an upstream activating sequence. A linear regulatory element insertion cassette comprising a regulatory element flanked by nucleotide sequences having homology to the natural promoter is introduced into the cell. In some embodiments, the cassette also comprises a nucleotide sequence encoding a selectable marker or a marker whose expression is readily identified. The cassette may be a double stranded nucleic acid or a single stranded nucleic acid as described in U.S. Patent Application Serial Number 09/948,993. Upon homologous recombination, the regulatory element is inserted into the chromosome, leaving the gene required for proliferation under the control of the regulatory element. Strains in which the gene required for proliferation is under control of the regulatory element are grown under conditions in which the regulatable promoter provides a level of the proliferation-required gene product which is above the level in a wild type cell. For example, the strains may be grown in the presence of an inducer which induces expression from the promoter, or under conditions in which the action of a repressor on the promoter is reduced or eliminated. It will be appreciated that the amplification method which generates amplification products having a unique size for each proliferation required gene may be used to detect strains which are overrepresented or underrepresented in the culture or collection of strains. For example, if desired, primers complementary to a nucleotide sequence within the regulatory element may be used in the amplification reaction.

The promoter replacement cassette or regulatory element insertion cassette may be a double stranded nucleic acid, such as an amplicon generated through PCR or other amplification methods, or a single stranded nucleic acid, such as an oligonucleotide. For example, single stranded nucleic acids may be introduced into the chromosome using the methods described in Ellis et al., PNAS 98: 6742-6746, 2001.

In some embodiments, the cell into which the promoter replacement cassette or regulatory element insertion cassette is introduced has an enhanced frequency of recombination. For example, the cells may lack or have a reduced level or activity of one or more exonucleases which would ordinarily degrade the DNA to be inserted into the chromosome. In further embodiments, the cells may both lack or have reduced levels of exonucleases and express or overexpress proteins involved in mediating homologous recombination. For example, if the methods are performed in *Escherichia coli* or other enteric prokaryotes, cells in which the activity of exonuclease V of the RecBCD recombination pathway, which degrades linear nucleic acids, has been reduced or eliminated, such as recB, recC, or recD mutants may be used. In some embodiments, the cells have

mutations in more than one of the *recB*, *recC*, and *recD* genes which enhance the frequency of homologous recombination. For example the cells may have mutations in both the *recB* and *recC* genes.

The promoter replacement or regulatory element insertion methods may also be performed in *Escherichia coli* cells in which the activity of the RecET recombinase system of the Rac prophage has been activated, such as cells which carry an *sbcA* mutation. The *RecE* gene of the rac prophage encodes ExoVIII a 5'-3' exonuclease, while the *RecT* gene of the Rac prophage encodes a single stranded DNA binding protein which facilitates renaturation and D-loop formation. Thus, the gene products of the *RecE* and *RecT* genes or proteins with analogous functions facilitate homologous recombination. The *RecE* and *RecT* genes lie in the same operon but are normally not expressed. However, *sbcA* mutants activate the expression the *RecE* and *RecT* genes. In some embodiments, the methods may be performed in cells which carry mutations in the *recB* and *recC* genes as well as the *sbcA* mutation. The *RecE* and *RecT* gene may be constitutively or conditionally expressed. For example, the methods may be performed in *E. coli* strain JC8679, which carries the *sbcA23*, *recB21* and *recC22* mutations.

In some embodiments, the methods may be performed in *Escherichia coli* cells in which recombination via the *RecF* pathway has been enhanced, such as cells which carry an *sbcB* mutation.

It will be appreciated that the *RecE* and *RecT* gene products, or proteins with analogous functions may be conditionally or constitutively expressed in prokaryotic organisms other than *E. coli*. In some embodiments, these proteins may be conditionally or constitutively expressed in *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*,

Staphylococcus aureus, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* or any species falling within the genera of any of the above species. For example, plasmids encoding these gene products may be introduced into the organism. If desired, the coding sequences encoding these gene products may be optimized to reflect the codon preferences of the organism in which they are to be expressed. Similarly, in some embodiments, the organism may contain mutations analogous to the *recB*, *recC*, *recD*, *sbcA* or *sbcB* mutations which enhance the frequency of homologous recombination.

In further embodiments, the promoter replacement or regulatory element insertion methods may be conducted in cells which utilize the Red system of bacteriophage lambda (λ) or analogous systems from other phages to enhance the frequency of homologous recombination. The Red system contains three genes, (γ , β and *exo* whose products are the Gam, Bet and Exo proteins (see Ellis et al. PNAS 98:6742-6746, 2001. The Gam protein inhibits the RecBCD exonuclease V, thus permitting Beta and Exo to gain access to the ends of the DNA to be integrated and facilitating homologous recombination. The Beta protein is a single stranded DNA binding protein that promotes the annealing of a single stranded nucleic acid to a complementary single stranded nucleic acid and mediates strand exchange. The Exo protein is a double-stranded DNA dependent 5'-3' exonuclease that leaves 3' overhangs that can act as substrates for recombination. Thus, constitutive or conditional expression of the λ Red proteins or proteins having analogous functions facilitates homologous recombination.

It will be appreciated that the λ Beta, Gam and Exo proteins, or proteins with analogous functions may be expressed constitutively or conditionally in prokaryotic organisms other than *E. coli*. In some embodiments, these proteins may be conditionally or constitutively expressed in *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*,

Pseudomonas aeruginosa, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* or any species falling within the genera of any of the above species. For example, plasmids encoding these gene products may be introduced into the organism. If desired, the coding sequences encoding these gene products may be optimized to reflect the codon preferences of the organism in which they are to be expressed.

In some embodiments, the cells may have an increased frequency of homologous recombination as a result of more than one of the aforementioned characteristics. In some embodiments, the enhanced frequency of recombination may be a conditional characteristic of the cells which depends on the culture conditions in which the cells are grown. For example, in some embodiments, expression of the λ Red Gam, Exo, and Beta proteins or recE and recT proteins may be regulated. Thus, the cells may have an increased frequency of homologous recombination as a result of any combination of the aforementioned characteristics. For example, in some embodiments, the cell may carry the sbcA and recBC mutations.

In some embodiments, a linear double stranded DNA to be inserted into the chromosome of the organism is introduced into an organism constitutively or conditionally expressing the recE and recT or the λ Beta, Gam and Exo proteins or proteins with analogous functions as described above. In some embodiments, the organism may be *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*,

Staphylococcus aureus, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* or any species falling within the genera of any of the above species. In some
 5 embodiments, the double stranded DNA may be introduced into an organism having the recBC and sbcA mutations or analogous mutations.

In other embodiments, a single stranded DNA to be inserted into the chromosome of the organism is introduced into an organism expressing the λ Beta protein or a protein with an analogous function. In some embodiments the single stranded DNA is introduced into an organism
 10 expressing both the λ Beta and Gam proteins or proteins with analogous functions. In further embodiments, the single stranded DNA is introduced into an organism expressing the λ Beta, Gam and Exo proteins or proteins with analogous functions. The λ proteins or analogous proteins may be expressed constitutively or conditionally. In some embodiments, the organism may be *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*,
 15 *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*,
 20 *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*,
 25 *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*,
 30 *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* or any species falling within the genera of any of the above species.

35 In some embodiments, the linear nucleic acid may be introduced into the chromosome of a first organism which has an enhanced frequency of homologous recombination and then transferred to a second organism which is less amenable to direct application of the present methods. For example, the linear nucleic acid may be introduced into the chromosome of *E. coli* and transferred

into a second organism via conjugation or transduction. After introduction into the second organism, the nucleic acid is inserted into the chromosome of the second organism via homologous recombination, thereby effectively transferring the regulatory element from the chromosome of the first organism into the corresponding location in the chromosome of the second organism.

5 In other embodiments, the cells may be diploid cells, such as fungal cells. In some embodiments, one copy of the gene encoding the proliferation-required gene product may be disrupted, rendering it inactive. In further embodiments, one copy of the gene encoding the proliferation-required gene product may be disrupted and the other copy of the gene encoding the proliferation-required gene product may be placed under the control of a regulatable promoter.

10 Such strains may be generated by disrupting the first copy of the gene encoding the proliferation-required gene product by homologous recombination using a disruption cassette comprising a nucleotide sequence encoding an expressible dominant selectable marker flanked on each side by nucleic acids homologous to the target sequence to be disrupted. The second copy of the gene encoding the proliferation-required gene product may be placed under the control of a regulatable

15 promoter by homologous recombination using a promoter replacement cassette comprising a regulatable promoter flanked on each side by nucleic acids homologous to the natural promoter for the proliferation-required gene. The promoter replacement cassette may also include a nucleotide sequence encoding a selectable marker located 5' of the regulatable promoter but between the nucleic acids homologous to the natural promoter.

20 In other embodiments, overexpression may be achieved by operably linking a proliferation-required gene product described herein to a desired promoter in a vector. The vector may be a vector which replicates extrachromosomally or a vector which integrates into the chromosome. For example, if the vector is to be used in bacterial cells, the vector may be a pBR322 based vector or a bacteriophage based vector such as P1 or lambda. If the vector is to be used in *Saccharomyces*

25 *cerevisiae*, it may be a vector based on the 2 micron circle or a vector incorporating a yeast chromosomal origin of replication. If the vector is to be used in mammalian cells, it may be a retroviral vector, SV40 based vector, a vector based on bovine papilloma virus, a vector based on adenovirus, or a vector based on adeno-associated virus. If the vector is to be used in *Candida albicans* it may be a vector comprising a promoter selected from the group consisting of the

30 CaPCK1, MET25, MAL2, PHO5, GAL1,10, STE2 or STE3 promoters. In some embodiments, the vectors described in the following publications may be used: CIp10, an efficient and convenient integrating vector for *Candida albicans*. Murad et al., Yeast 16(4):325-7 (2000); Transforming vector pCPW7, Kvaal et al., : Infect Immun 67(12):6652-62 (1999); Transforming vector pCWOP16, Kvaal et al., : Infect Immun 65(11):4668-75 (1997); double-ARS vector, pRM1, to be

35 used for direct cloning in Ca by complementation of the histidine auxotrophy of strain CA9, Pla et al., Gene 165(1):115-20 (1995); pMK16, that was developed for the transformation of *C. albicans* and carries an ADE2 gene marker and a *Candida* autonomously replicating sequence (CARS) element promoting autonomous replication (cited in Sanglard and Fiechter Yeast 8(12):1065-75

(1992); A plasmid vector (denoted pRC2312) was constructed, which replicates autonomously in *Escherichia coli*, *Saccharomyces cerevisiae* and *Candida albicans*. It contains LEU2, URA3 and an autonomously replicating sequence (ARS) from *C. albicans*, Cannon et al., Mol Gen Genet 235(2-3):453-7 (1992); Expression vector (CIp10-MAL2p) for use in *Candida albicans* has been
 5 constructed in which a gene of interest can be placed under the control of the CaMAL2 maltase promoter and stably integrated at the CaRP10 locus (Backen et al., Yeast 16(12):1121-9 (2000)); (Volker, R. S., A. Sonneborn, C. E. Leuker, and J. F. Ernst. 1997. Efg1p, an essential regulator of morphogenesis of the human pathogen *Candida albicans*, is a member of a conserved class of bHLH proteins regulating morphogenetic processes in fungi. EMBO 16:1982-1991.); and a *C.*
 10 *albicans* transformation vector containing the *C. albicans* URA3 gene, a Candida ARS sequence, and a portion of the *Saccharomyces cerevisiae* 2 microns circle containing the replication origin was constructed. Goshorn et al., Infect Immun 60(3):876-84 (1992). A variety of other vectors suitable for use in foregoing organisms or in any other organism in which the present invention is to be practiced are familiar to those skilled in the art.

15 Underexpression of a proliferation-required gene product described herein may be obtained in a variety of ways. For example, in one embodiment underexpression of the proliferation-required gene product may be achieved by providing an agent, such as an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, an antisense nucleic acid comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400,
 20 or 500 consecutive nucleotides of a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a nucleic acid complementary to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397, a nucleic acid complementary to a nucleic acid comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of a nucleotide sequence selected from the group consisting of SEQ ID
 25 NOs.: 6214-42397, a nucleic acid complementary to a nucleic acid which encodes a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42398-78581, a nucleic acid complementary to a nucleic acid which encodes at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids of a polypeptide sequence selected from the group consisting of SEQ ID NOs.: 42398-78581, a homologous antisense nucleic acid, an antisense
 30 nucleic acid comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of a homologous nucleic acid, a nucleic acid complementary to a homologous coding nucleic acid, a nucleic acid complementary to at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of a homologous coding nucleic acid, a nucleic acid complementary to a nucleic acid which encodes a homologous polypeptide, or a
 35 nucleic acid complementary to a nucleic acid which encodes at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids of a homologous polypeptide, which reduces the level or activity of the gene product within the cell. In one embodiment, the agent may comprise an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ

ID NOs.: 1-6213 which is complementary to a nucleic acid encoding the proliferation-required gene product or complementary to a portion of a nucleic acid encoding the proliferation-required gene product.

5 In one example of antisense-inhibition-based underexpression, a nucleic acid which encodes the antisense nucleic acid may be operably linked to a regulatable promoter. When grown under appropriate conditions, such as media containing an inducer of transcription or an agent which alleviates repression of transcription, the antisense nucleic acid is expressed in the cell, thereby reducing the level or activity of the gene product within the cell. In some embodiments, the concentration of the inducer of transcription or the agent which alleviates repression of transcription
10 may be varied to provide optimal results. Such methods have been described previously herein and in U.S. Patent Application Serial Number 09/815,242, U.S. Patent Application Serial Number 09/492,709, U.S. Patent Application Serial Number 09/711,164, or U.S. Patent Application Serial Number 09/741,669.

Alternatively, underexpression of a proliferation-required gene product described herein
15 may be achieved by constructing strains in which the expression of the gene product is under the control of a constitutive or regulatable promoter using methods such as those described above with respect to methods in which the gene product is overexpressed. To provide cells which underexpress the gene product, the cells are grown under conditions in which the gene product is expressed at a level lower than that of a wild type cell. For example, the cells may be grown under
20 conditions in which a repressor reduces the level of transcription from the regulatable promoter.

In other embodiments, underexpression may be achieved by operably linking the gene required for proliferation to a desired promoter in a vector as described above with respect to
embodiments in which gene products required for proliferation are overexpressed. In some
embodiments, the vector may be present in cells in which the chromosomal copy or copies of the
25 gene has been disrupted.

Examples of gene products, which are encoded by genes that can be underexpressed using methods such as those described above with respect to methods in which the gene product is overexpressed include a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a
30 gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397, a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42398-78581, a gene product whose activity or level is inhibited by a homologous antisense nucleic acid, a gene product encoded by a homologous coding nucleic acid, and a gene product comprising a homologous polypeptide.

35 One embodiment of the invention includes a method for identifying a gene product described herein on which a compound which inhibits the proliferation of an organism acts. The method employs a culture which comprises a mixture of strains of the organism. At least some of the strains in the culture overexpress a different gene product which is required for the proliferation

of the organism. Preferably, each of the strains in the culture overexpresses a different gene product which is required for proliferation of the organism (i.e. all of the strains in the culture overexpress a gene product which is required for proliferation of the organism). For example, the gene product which is overexpressed in each strain may be a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397, a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42398-78581, a gene product whose activity or level is inhibited by a homologous antisense nucleic acid, a gene product encoded by a homologous coding nucleic acid, and a gene product comprising a homologous polypeptide.

Strains that overexpress the proliferation-required gene product may be obtained using the methods described above. The culture may comprise any number of strains which overexpress a gene product required for proliferation. For example the culture may comprise at least two strains, at least 10 strains, at least 20 strains, at least 30, strains, at least 50 strains, at least 100 strains, at least 300 strains or more than 300 strains which overexpress a gene product required for proliferation. In some embodiments, the culture may comprise strains which in aggregate overexpress all or most of the gene products required for proliferation of the organism.

The culture is contacted with a compound which inhibits proliferation of the organism. The compound may be a candidate drug compound obtained from any source. For example, the compound may be a compound generated using combinatorial chemistry, a compound from a natural product library, or an impure or partially purified compound, such as a compound in a partially purified natural extract. The culture is contacted with a sufficient concentration of the compound to inhibit the proliferation of strains of the organism in the culture which do not overexpress the gene product on which the compound acts, such that strains which overexpress said gene product on which the compound acts proliferate more rapidly in the culture than strains which do not overexpress said gene product on which said compound acts. Thus, after a sufficient period of time, the strain which overexpresses the gene product on which the compound acts will be more prevalent in the culture than strains which do not overexpress the gene product on which the compound acts. In a preferred embodiment, the growth conditions and incubation period are selected so that only one strain, the strain overexpressing the target of the compound, is recovered from the culture. Thus, in one embodiment, a plurality of cultures containing a plurality of strains each of which overexpresses a different proliferation-required gene product may be grown in the presence of varying concentrations of the compound. In addition to varying the compound concentrations, in embodiments where expression of the proliferation-required gene product is under the control of a regulatable promoter, the plurality of cultures may be grown at varying concentrations of an agent which regulates the level of expression from the promoter, such as an inducer or an agent which reduces the effect of a repressor on transcription from the promoter. It

will be appreciated, that the cultures may be grown in liquid medium in the presence of the compound whose target is to be identified (and where appropriate in the presence of an agent which regulates the level of expression from the promoter) or alternatively, a liquid culture comprising the strains which overexpress the proliferation-required gene products may be grown in the absence of the compound whose target is to be identified and then introduced onto a solid medium containing the compound (and, where appropriate, also containing an agent which regulates the level of expression from the promoter).

The identity of the overexpressed gene product which is the target of the compound may be determined using a variety of methods. For example, in some embodiments of the present invention, the nucleic acids present in the culture or collection of strains which was contacted with the compound may be compared to the nucleic acids present in a control culture or collection of strains which was not contacted with the compound to identify nucleic acids which are overrepresented in the culture or collection of strains contacted with the test compound relative to the control culture or collection of strains. Alternatively, in some embodiments, the nucleic acids present in a culture or collection of strains contacted with the test compound may be analyzed to identify those nucleic acids which are present without comparison to a control culture or collection of strains.

In some embodiments, the strains which proliferated more rapidly in the culture or collection of strains, i.e. strains having an enhanced ability to proliferate in the presence of a test compound relative to other strains in the culture or collection of strains, are identified as follows. Amplification products which are correlated with each of the overexpressed genes and which are distinguishable from one another are obtained from a culture or collection grown in the presence of a test compound. The amplification products are distinguished from one another to determine whether a particular amplification product is overrepresented in the culture or collection of strains. In some embodiments, the amplification products corresponding to each of the gene products have lengths which permit them to be distinguished from one another. In another embodiment, one or more of the amplification products have similar or identical lengths but are distinguishable from one another based on a detectable agent, such as a dye, attached thereto. In some embodiments, amplification products which are overrepresented are identified by comparing the amplification products from the culture or collection of strains which was contacted with the test compound to the amplification products from a culture or collection of strains which was not contacted with the test compound. Alternatively, amplification products which are overrepresented may be identified by simply identifying the amplification products obtained from the culture or collection of strains contacted with the test compound (for example, only one or a few strains may have proliferated in the presence of the test compound). The above methods for generating distinguishable amplification products may be used in conjunction with any of the methods for generating strains which overexpress gene products required for proliferation described herein in order to facilitate the

identification of strains which proliferate more rapidly or more slowly in the presence of a test compound.

For example, in some embodiments of the present invention, each of the native promoters of each of the genes encoding gene product required for proliferation are replaced by a single
5 desired replacement promoter. After growth of the culture or collection of strains containing the strains in which the promoters have been replaced in the presence of a test compound for a desired period of time, an amplification reaction is performed on nucleic acids obtained from the culture as follows.

The nucleic acids from the culture or collection of strains may be divided into at least two
10 aliquots if desired. In a preferred embodiment the nucleic acids from the culture or collection of strains are divided into four aliquots. A single primer complementary to a nucleotide sequence within the replacement promoter, within the proliferation required genes, or within nucleic acid sequences adjacent to the promoter or proliferation required genes is divided into at least two portions, one portion for each aliquot of nucleic acids. Each portion of the primer is labeled with a
15 distinct detectable dye, such as the 6FAMTM, TETTM, VICTM, HEXTM, NEDTM, and PETTM dyes obtainable from Applied Biosystems (Foster City, CA). For example, the DS-31 or DS-33 dye sets available from Applied Biosystems (Foster City, CA) may be used to label the primers. Alternatively, the HEXTM, NED, JOE, TMR and TETTM dyes available from Amersham Biosciences may be used. Thus, if the nucleic acids from the culture are not divided into aliquots, a
20 single primer labeled with a single dye may be used. If the nucleic acids from the culture are divided into aliquots, at least 2, at least 3, at least 4 or more than 4 primers labeled with distinguishable dyes may be used. Each of the portions of labeled primers are added to each of the aliquots of the nucleic acids from the culture or collection of strains such that each aliquot of nucleic acid receives a single labeled primer with a single detectable dye thereon. In some
25 embodiments, the primers are divided into 3 portions, 4 portions or more than 4 portions, with each portion having a dye which is distinguishable from the dyes on the other portions thereon.

Each of the aliquots of nucleic acids also receives a set of unlabeled primers, with each of the unlabeled primers being complementary to a nucleotide sequence within the promoter, within a nucleotide sequence which is unique to one of the genes encoding gene products required for
30 proliferation which were placed under the control of the replacement promoter, or within nucleotide sequences adjacent to the promoter or proliferation required genes. Each of the aliquots receives primers unique to 1/N proliferation required genes which were placed under the control of the replacement promoter, where N is the number of aliquots (i.e. if the culture or collection of strains consisted of 100 strains in which a gene required for proliferation was placed under the control of
35 the replacement promoter and was divided into four aliquots, then each of the four aliquots of nucleic acids from the culture or collection of strains would receive primers complementary to 25 of the genes). The unlabeled primers are selected so that each will yield an amplification product having a length distinguishable from the length of the amplification product produced with the other

unlabeled primers. Preferably, the amplification products are between about 100-about 400 nucleotides in length, but any lengths which may be distinguished from each other may be used. In addition, in some of the embodiments some of the amplification products may have identical or very similar lengths but be distinguishable from one another due to labeling with distinguishable dyes.

A nucleic acid amplification reaction is conducted on each of the nucleic acid aliquots. The amplification products are then separated by length to identify amplification products having increased representation in the culture or collection of strains (i.e. amplification products derived from cells which proliferated more rapidly in the culture or collection of strains). The amplification products are then correlated with the corresponding genes to determine which strains proliferated more rapidly in the culture or collection of strains. If desired, amplification products having increased representation in the culture may be identified by comparing the amplification products obtained from a culture or collection of strains which was contacted with the compound to amplification products obtained from a control culture or collection of strains which was not contacted with the compound. Alternatively, if desired, the amplification products which are obtained from a culture which was contacted with the compound may be directly identified without comparison to a control culture which was not contacted with the compound.

For example, in some embodiments, the amplification products from each of the nucleic acid aliquots are pooled and subjected to capillary electrophoresis. The amplification products are detected by detecting the fluorescent dyes attached thereto and their lengths are determined to identify those amplification products having increased or decreased representation in the culture or collection of strains. Figures 2A and 2B illustrate one embodiment of this method in which the absence of an amplification product from an amplification reaction performed on a culture comprising a plurality of strains underexpressing genes required for proliferation indicates that a test compound acts on the gene corresponding to the missing amplification product. It will be appreciated that the method may also be used to identify an amplification product which is overrepresented in an amplification reaction conducted on a culture or collection of strains overexpressing genes required for proliferation because the test compound acted on the corresponding gene.

Alternatively, in another embodiment, a first amplification reaction is performed on nucleic acids obtained from a culture or collection of strains which was contacted with the compound using a first primer complementary to a nucleotide sequence present upstream or downstream of all of the overexpressed genes (such as a primer complementary to a nucleotide sequence in a replacement promoter upstream of all of the overexpressed genes) and a set of primers complementary to a nucleotide sequence unique to each of the strains (such as a primer complementary to a nucleotide sequence within each of the proliferation-required genes). One of the two amplification primers for each of the proliferation required genes is labeled with a dye as described above. Preferably, the common primer complementary to a nucleotide sequence upstream or downstream of all of the

overexpressed genes is labeled with the dye. The primers used in the amplification reaction are designed so that the amplification product corresponding to each proliferation-required gene has a unique length or a dye which allows it to be distinguished from other amplification products of the same length. A second amplification reaction is conducted on a control culture or collection of strains which was not contacted with the compound using the same primers as in the first amplification reaction. The amplification products from the first amplification reaction are compared to those from the second amplification reaction to identify one or more amplification products which are overrepresented in the culture or collection of strains. For example, the amplification products from the first amplification reaction may be run in a separate lane of a polyacrylamide gel or a separate capillary than the amplification products from the second amplification reaction and the two lanes or capillaries are compared to one another. If desired, in the embodiment where the amplification products from the first amplification reaction are run in a different lane or capillary than the amplification products from the second amplification reaction, the same dye may be used to label the primers in the first and second amplification reactions. Alternatively, if desired, different dyes may be used to label the primers in the first and second amplification reactions. If desired, in the embodiment where the amplification products from the first amplification reaction are run in a different lane or capillary than the amplification products from the second amplification reaction, the same dye may be used to label the primers in the first and second amplification reactions. Alternatively, if desired, different dyes may be used to label the primers in the first and second amplification reactions.

Alternatively, in some embodiments, the primers in the second amplification reaction are labeled with a different dye which is distinguishable from the dye used in the first amplification reaction. In this embodiment, the amplification reactions may be pooled and run in the same lane on a polyacrylamide gel or in the same capillary and the products from each amplification reaction are compared by comparing the amount of each dye present for each amplification product. Figures 3A and 3B illustrate one embodiment of this method in which the absence of an amplification product from the amplification reaction performed on a culture comprising a plurality of strains underexpressing genes required for proliferation which was contacted with the compound indicates that a test compound acts on the gene corresponding to the missing amplification product. It will be appreciated that the method may also be used to identify an amplification product which is overrepresented in an amplification reaction conducted on a culture or collection of strains overexpressing genes required for proliferation because the test compound acted on the corresponding gene.

If desired, rather than dividing the culture into aliquots, individual amplification reactions may be conducted on nucleic acids obtained from the culture or collection of strains. Each amplification reaction contains primers which will yield an amplification product specific for only one of the proliferation required genes. The resulting amplification products from each of the

individual amplification reactions are pooled and amplification products having increased representation in the culture are identified as described above.

In another embodiment, a culture or collection of strains in which gene products required for proliferation are overexpressed from regulatable promoters which replaced the native promoters of the genes encoding these gene products is allowed to grow in the presence of a test compound for a desired number of generations. Preferably, the culture or collection of strains is allowed to grow in the presence of the test compound for at least 20 generations. Nucleic acids are isolated from the culture or collection of strains and an amplification reaction is performed using a primer which is complementary to a nucleotide sequence within the replacement promoter(s) or a nucleotide sequence adjacent to the a 5' end thereof and primers which are complementary to a nucleotide sequence within the proliferation required genes or nucleotide sequences adjacent thereto. The resulting amplification product(s) is directly sequenced using a primer complementary to a nucleotide sequence within the replacement promoter.

In one embodiment of the present invention, the vector containing the nucleotide sequence encoding the proliferation-required gene product is obtained from a strain which proliferated more rapidly in the culture using methods such as plasmid preparation techniques. Nucleic acid sequencing techniques are then employed to determine the nucleotide sequence of the gene which was overexpressed.

Alternatively, the identity of the overexpressed gene product which is the target of the compound may be determined by performing a nucleic acid amplification reaction, such as a polymerase chain reaction (PCR), to identify the nucleotide sequence of the gene which was overexpressed. For example, aliquots of a nucleic acid preparation, such as a purified plasmid, from the strain which is recovered from the culture may each be contacted with pairs of PCR primers which would amplify a different proliferation-required gene to determine which pair of primers yields an amplification product.

An alternative method for determining the identity of the gene product described herein which is the target of the compound involves obtaining a nucleic acid array, such as a DNA chip, which contains each of the proliferation-required genes which were overexpressed in the strains in the culture. Each proliferation-required gene occupies a known location in the array. A nucleic acid preparation, such as a plasmid preparation, from the recovered strain is labeled with a detectable agent, such as radioactive or fluorescent moiety, and placed in contact with the nucleic acid array under conditions which permit the labeled nucleic acid to hybridize to complementary nucleic acids on the array. The location on the array to which the labeled nucleic acids hybridize is determined to identify the gene which was overexpressed in the recovered strain. If desired the hybridized nucleic acids from a culture which was contacted with the compound may be compared to the hybridized nucleic acids from a control culture which was not contacted with the compound. Alternatively, the hybridized nucleic acids from a culture which was contacted with the compound may be directly identified without comparison to nucleic acids from a control culture.

In some instances, more than one strain may proliferate more rapidly in the presence of the compound. This may result from a variety of causes. For example, the concentration of the compound may not have been high enough to restrict proliferation only to cells which overexpress one gene product (i.e. the target gene product). While strains which overexpress the target gene product will be the most prevalent strain in the culture, other strains may also have proliferated. In such instances, the identity of the gene product in the strain which is most prevalent in the culture may be identified by quantitating the levels of each of the genes encoding proliferation-required proteins in the culture. This may be accomplished by quantitative PCR, DNA sequencing, hybridization, or array technology as described above.

In other instances, multiple strains will exhibit more rapid proliferation in the culture as a result of a common functional attribute. For example, the strains which proliferate more rapidly may each overexpress a gene product with a common enzymatic activity, such as serine protease activity for example. Alternatively, the strains which proliferate more rapidly may each overexpress a gene product with a common functional domain, such as a cAMP binding domain. In such instances, the common attribute of the strains which proliferate more rapidly may provide information as to the mode of action of the compound or the biochemical activity of the target of the compound. For example, if all of the overexpressed genes in the strains which proliferated more rapidly are serine proteases, the compound acts by inhibiting serine protease activity and the target protein is a serine protease. If desired, the compound may be derivatized and the efficacy of the derivatized compound against each of the strains which proliferated more rapidly may be assessed as described herein in order to identify derivatives which are capable of interacting with a wide range of targets sharing a common activity or binding site (i.e. derivatives which have a greater ability to inhibit the proliferation of all the strains than the original compound) or to identify derivatives having greater specificity for a desired target (i.e. derivatives which have a greater specificity for one of the strains than the original compound). For example, it is possible that a nonessential gene product expressed in the cell might also bind to the initial test compound in addition to the gene product required for proliferation. In such an instance, it is desirable to obtain a derivative of the initial test compound which is specific for the gene product required for proliferation. In addition, it is possible that two gene products required for proliferation might bind to the initial test compound but specificity for one of the gene products is desired.

Rather than employing a single culture which contains multiple strains each of which overexpresses a proliferation-required gene product described herein, the methods of the present invention may be performed using an array of individual strains (i.e. a collection of strains) each of which overexpresses a different proliferation-required gene product. For example, individual strains each overexpressing a different proliferation-required gene product may be grown in different wells of a multiwell plate. Each well is contacted with the compound (and, where appropriate an agent which regulates the level of expression from the promoter). The level of proliferation of the strains in each of the wells is determined to identify a strain which proliferated

more rapidly. The identity of the overexpressed gene product in the strain that proliferated more rapidly is determined as described above.

In another embodiment, individual strains each overexpressing a different proliferation-required gene product (i.e. a collection of strains) are grown at different locations on a solid medium, such as an agar plate. The medium contains the compound and where appropriate an agent which regulates the level of expression from the promoter). The level of proliferation of each of the strains is determined to identify a strain which proliferated more rapidly. The identity of the overexpressed gene product in the strain that proliferated more rapidly is determined as described above.

The above methods may be used to prioritize compound development or to determine whether the compound has been previously identified or whether the target of the compound is the target of a previously identified drug. In particular, if the product is a natural product, it is advantageous to determine whether it has been previously identified prior to investing significant effort in developing it. Thus, in some embodiments of the present invention, the target of a partially purified or purified natural product or a compound produced by combinatorial chemistry is identified using the methods described above and compared to the targets of known drugs. If the target is identical to that of a known drug, further development of the compound is halted.

Alternatively, an array of strains each of which overexpresses a different gene product described herein (i.e. a collection of strains) is grown on solid medium containing a compound to be evaluated. The location of each strain in the array and the gene product overexpressed by that strain is known. The pattern of colonies which grow in the presence of the compound is evaluated and compared to the pattern of colonies which grow in the presence of previously identified drugs. If the pattern of colonies which grow in the presence of the compound being evaluated is the same as the pattern of colonies which grow in the presence of a previously identified drug, further development of the compound is halted.

Additionally in some embodiments, the sequence of the gene product in a strain which proliferated more rapidly in the assays described above is compared to the sequence of gene products from heterologous organisms to determine the likely spectrum of species whose growth would be inhibited by the compound. If the gene product has a high degree of homology to gene products from heterologous species, it is likely that the compound would also inhibit the growth of these heterologous species. Homology may be determined using any of a variety of methods familiar to those skilled in the art. For example, homology may be determined using a computer program such as BLASTP or FASTA. The ability of the compound to inhibit the growth of the heterologous species may then be confirmed by comparing the growth of cells of the heterologous species in the presence and absence of the compound.

Current methods for identifying the target of compounds which inhibit cellular proliferation are laborious and time consuming. The above methods may be employed to allow the targets of a large number of compounds to be rapidly identified. In such methods, the methods described above

are simultaneously performed for each of a large number of compounds. For example, the compounds may be members of a library of compounds generated using combinatorial chemistry or members of a natural product library. In such methods, a plurality of cultures each comprising a plurality of strains each of which overexpresses a different gene product required for proliferation
5 or a plurality of collections of individual strains each of which overexpresses a different gene product required for proliferation is obtained. Each culture or collection of strains is contacted with a different compound in the library and the target of the compound is identified as described above.

In another embodiment, the gene product described herein on which a compound which inhibits the proliferation of an organism acts is identified using a culture which comprises a mixture
10 of strains of the organism including strains which underexpress a different gene product which is required for proliferation of the organism (i.e. at least some of the strains in the culture underexpress a gene product which is required for proliferation of the organism). Preferably, each of the strains in the culture underexpress a different a gene product which is required for the proliferation of the organism (i.e. all of the strains in the culture underexpress a gene product which
15 is required for the proliferation of the organism). In some embodiments, the culture comprises at least one strain which underexpresses a gene product selected from the group consisting of a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-
20 42397, a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42398-78581, a gene product whose activity or level is inhibited by a homologous antisense nucleic acid, a gene product encoded by a homologous coding nucleic acid, and a gene product comprising a homologous polypeptide.

Strains underexpressing the proliferation-required gene products described herein may be
25 obtained using the methods described above. The culture may comprise any number of strains. For example the culture may comprise at least two strains, at least 10 strains, at least 20 strains, at least 30, strains, at least 50 strains, at least 100 strains, at least 300 strains or more than 300 strains which underexpress a gene product required for proliferation. In some embodiments, the strains in the culture in aggregate may underexpress all or most of the gene products required for proliferation of
30 the organism.

The culture is contacted with a compound which inhibits proliferation of the organism. The compound may be a candidate drug compound obtained from any source. For example, the compound may be a compound generated using combinatorial chemistry, a compound from a natural product library, or an impure or partially purified compound, such as a compound in a
35 partially purified natural extract. The culture is contacted with a sufficient concentration of the compound to inhibit the proliferation of strains of the organism in the culture which underexpress the gene product on which the compound acts, such that strains which do not underexpress the gene product on which the compound acts proliferate more rapidly in the culture than strains which do

underexpress said gene product on which said compound acts. Thus, after a sufficient period of time, the strain which underexpresses the gene product on which the compound acts will be less prevalent in the culture than strains which do not underexpress the gene product on which the compound acts. In one embodiment, the growth conditions and incubation period are selected so that only one strain, the strain underexpressing the target of the compound, proliferates at a reduced rate in the culture. In another embodiment, the growth conditions may be selected so that the strain underexpressing the target of the compound is not recovered from the culture. Thus, in one embodiment, a plurality of cultures containing a plurality of strains each of which underexpresses a different proliferation-required gene product may be grown in the presence of varying concentrations of the compound. In addition to varying the compound concentrations, in embodiments where expression of the proliferation-required gene product is under the control of a regulatable promoter, the plurality of cultures may be grown at varying concentrations of an agent which regulates the level of expression from the promoter, such as an inducer or an agent which reduces the effect of a repressor on transcription from the promoter. It will be appreciated, that the cultures may be grown in liquid medium in the presence of the compound whose target is to be identified (and where appropriate in the presence of an agent which regulates the level of expression from the promoter) or alternatively, a liquid culture comprising the strains which underexpress the proliferation-required gene products may be grown in the absence of the compound whose target is to be identified and then introduced onto a solid medium containing the compound (and, where appropriate, also containing an agent which regulates the level of expression from the promoter).

The identity of the underexpressed gene product which is the target of the compound may be determined using a variety of methods. For example, in some embodiments of the present invention, the nucleic acids present in the culture or collection of strains which was contacted with the compound may be compared to the nucleic acids present in a control culture or collection of strains which was not contacted with the compound to identify nucleic acids which are underrepresented in the culture or collection of strains contacted with the test compound relative to the control culture or strains. Alternatively, in some embodiments, the nucleic acids present in a culture or collection of strains contacted with the test compound may be analyzed to identify those nucleic acids which are missing or present at reduced levels without comparison to a control culture or collection of strains.

In some embodiments of the present invention, the strains which proliferated more slowly in the culture or collection of strains, i.e. strains having an decreased ability to proliferate in the presence of a test compound or which do not proliferate in the presence of a test compound, are identified as follows. Amplification products which are correlated with each of the underexpressed genes and which are distinguishable from one another are obtained from a culture or collection grown in the presence of a test compound. The amplification products are distinguished from one another to determine whether a particular amplification product is underrepresented in the culture or collection of strains. In some embodiments, the amplification products corresponding to each of the

gene products have lengths which permit them to be distinguished from one another. In another embodiment, one or more of the amplification products have similar or identical lengths but are distinguishable from one another based on a detectable agent, such as a dye, attached thereto. In some embodiments, amplification products which are underrepresented are identified by comparing
5 the amplification products from the culture or collection of strains which was contacted with the test compound to the amplification products from a culture or collection of strains which was not contacted with the test compound. Alternatively, amplification products which are underrepresented in the culture or collection of strains may be identified simply by determining which amplification products are missing or present at reduced levels in the culture or collection of
10 strains. The above methods for generating distinguishable amplification products may be used in conjunction with any of the methods for generating strains which underexpress gene products required for proliferation described herein in order to facilitate the identification of strains which proliferate more slowly in the presence of a test compound.

For example, in some embodiments of the present invention, each of the native promoters of each
15 of the genes encoding gene product required for proliferation are replaced by a single desired replacement promoter. After growth of the culture or collection of strains containing the strains in which the promoters have been replaced in the presence of a test compound for a desired period of time, an amplification reaction is performed on nucleic acids obtained from the culture as follows.

The nucleic acids from the culture or collection of strains are divided into at least two
20 aliquots. In a preferred embodiment the nucleic acids from the culture or collection of strains are divided into four aliquots. A single primer complementary to a nucleotide sequence within the replacement promoter, within the proliferation required genes, or within nucleic acid sequences adjacent to the promoter or proliferation required genes is divided into four groups. Each group is labeled with a distinct detectable dye, such as the 6FAM™, TET™, VIC™, HEX™, NED™, and
25 PET™ dyes obtainable from Applied Biosystems (Foster City, CA). For example, the DS-31 or DS-33 dye sets available from Applied Biosystems (Foster City, CA) may be used to label the primers. Each of the groups of labeled primers are added to each of the aliquots of the nucleic acids from the culture or collection of strains such that each aliquot of nucleic acid receives a single labeled primer with a single detectable dye thereon.

Each of the aliquots of nucleic acids also receives a set of unlabeled primers, with each of
30 the unlabeled primers being complementary to a nucleotide sequence within the promoter, within a nucleotide sequence which is unique to one of the genes encoding gene products required for proliferation which were placed under the control of the replacement promoter, or within nucleotide sequences adjacent to the promoter or proliferation required genes. Each of the aliquots receives
35 primers unique to 1/N proliferation required genes which were placed under the control of the replacement promoter, where N is the number of aliquots (i.e. if the culture or collection of strains consisted of 100 strains in which a gene required for proliferation was placed under the control of the replacement promoter and was divided into four aliquots, then each of the four aliquots of

nucleic acids from the culture or collection of strains would receive primers complementary to 25 of the genes). The unlabeled primers are selected so that each will yield an amplification product having a length distinguishable from the length of the amplification product produced with the other unlabeled primers. Preferably, the amplification products are between about 100-about 400
5 nucleotides in length, but any lengths which may be distinguished from each other may be used. In addition, in some of the embodiments some of the amplification products may have identical or very similar lengths but be distinguishable from one another due to labeling with distinguishable dyes.

A nucleic acid amplification reaction is conducted on each of the nucleic acid aliquots. The
10 amplification products are then separated by length to identify amplification products decreased representation or which are absent in the culture or collection of strains. The amplification products are then correlated with the corresponding genes to determine which strains proliferated more slowly in the culture or collection of strains. If desired, amplification products having decreased representation in the culture may be identified by comparing the amplification products obtained
15 from a culture or collection of strains which was contacted with the compound to amplification products obtained from a control culture or collection of strains which was not contacted with the compound. Alternatively, if desired, the amplification products which are missing or present at reduced levels in a culture which was contacted with the compound may be directly identified without comparison to a control culture which was not contacted with the compound.

For example, in some embodiments, the amplification products from each of the nucleic
20 acid aliquots are pooled and subjected to capillary electrophoresis. The amplification products are detected by detecting the fluorescent dyes attached thereto and their lengths are determined to identify those amplification products having decreased representation in the culture or collection of strains. Figures 2A and 2B illustrate one embodiment of this method in which the absence of an
25 amplification product from an amplification reaction performed on a culture comprising a plurality of strains underexpressing genes required for proliferation indicates that a test compound acts on the gene corresponding to the missing amplification product.

Alternatively, in another embodiment, a first amplification reaction is performed on nucleic
acids obtained from a culture or collection of strains which was contacted with the compound using
30 a first primer complementary to a nucleotide sequence present upstream or downstream of all of the overexpressed genes (such as a primer complementary to a nucleotide sequence in a replacement promoter upstream of all of the overexpressed genes) and a set of primers complementary to a nucleotide sequence unique to each of the strains (such as a primer complementary to a nucleotide sequence within each of the proliferation-required genes). One of the two amplification primers for
35 each of the proliferation required genes is labeled with a dye as described above. Preferably, the common primer complementary to a nucleotide sequence upstream or downstream of all of the overexpressed genes is labeled with the dye. The primers used in the amplification reaction are designed so that the amplification product corresponding to each proliferation-required gene has a

unique length. A second amplification reaction is conducted on a control culture or collection of strains which was not contacted with the compound using the same primers as in the first amplification reaction. The amplification products from the first amplification reaction are compared to those from the second amplification reaction to identify one or more amplification products which are underrepresented in the culture or collection of strains. For example, the amplification products from the first amplification reaction may be run in a separate lane of a polyacrylamide gel or a separate capillary than the amplification products from the second amplification reaction and the two lanes or capillaries are compared to one another.

Alternatively, in some embodiments, the primers in the second amplification reaction are labeled with a different dye which is distinguishable from the dye used in the first amplification reaction. In this embodiment, the amplification reactions may be pooled and run in the same lane on a polyacrylamide gel or in the same capillary and the products from each amplification reaction are compared by comparing the amount of each dye present for each amplification product. Figures 3A and 3B illustrate one embodiment of this method in which the absence of an amplification product from the amplification reaction performed on a culture comprising a plurality of strains underexpressing genes required for proliferation which was contacted with the compound indicates that a test compound acts on the gene corresponding to the missing amplification product.

If desired, rather than dividing the culture into aliquots, individual amplification reactions may be conducted on nucleic acids obtained from the culture or collection of strains. Each amplification reaction contains primers which will yield an amplification product specific for only one of the proliferation required genes. The resulting amplification products from each of the individual amplification reactions are pooled and amplification products having decreased representation in the culture are identified as described above.

In an alternative embodiment, the representation of each strain in the culture may be assessed by hybridizing detectably labeled nucleic acids encoding the proliferation-required gene products, or portions thereof, obtained from the culture to an array comprising nucleic acids encoding the gene products required for proliferation or portions thereof. Each nucleic acid encoding a gene product required for proliferation or portion thereof occupies a known location on the array. The signal from each location on the array is quantitated to identify those nucleic acids encoding a proliferation-required gene product which are underrepresented in the culture. If desired the hybridized nucleic acids from a culture which was contacted with the compound may be compared to the hybridized nucleic acids from a control culture which was not contacted with the compound. Alternatively, the hybridized nucleic acids from a culture which was contacted with the compound may be directly analyzed without comparison to nucleic acids from a control culture.

In another alternative, each strain underexpressing a gene product required for proliferation may be constructed to contain a unique nucleic acid sequence (referred to herein as a "tag"). The tag may be included in the chromosome of each strain or in an extrachromosomal vector. For example, the tag could be included in a vector encoding an antisense nucleic acid complementary to

a gene encoding a gene product required for proliferation or a portion of such a gene or the tag may be included in the antisense nucleic acid itself. The representation of each strain in the culture may be assessed by performing an amplification reaction using primers complementary to each of the tags and quantitating the levels of the resulting amplification products to identify a tag which is underrepresented or absent from the culture. Since each tag corresponds to one strain, the strain which is underrepresented or absent from the culture may be identified. If desired the tags present in a culture which was contacted with the compound may be compared to the tags present in a control culture which was not contacted with the compound. Alternatively, the tags present in a culture which was contacted with the compound may be analyzed without comparison to a control culture.

It will be appreciated that, if desired, unique tags may also be used in embodiments in which gene products required for proliferation are overexpressed. In some aspects of such embodiments, the tags may be within or adjacent to the promoter which drives expression of the gene encoding the gene product. In such embodiments, the gene product which is overexpressed in strains which proliferate more rapidly in the culture may be identified by detecting the presence or amount of the unique tag corresponding to that gene product in the culture.

In some instances, more than one strain may proliferate less rapidly in the presence of the compound. This may result from a variety of causes. For example, the concentration of the compound may not have been high enough to reduce the proliferation only in cells which underexpress one gene product (i.e. the target gene product). While strains which underexpress the target gene product will be the least prevalent strain in the culture, other strains may also be underrepresented. In such instances, the identity of the gene product in the strain which is least prevalent in the culture (or not recovered from the culture) may be identified by quantitating the levels of each of the genes encoding proliferation-required proteins in the culture. This may be accomplished by quantitative PCR, DNA sequencing, hybridization, or array technology as described above.

In other instances, multiple strains will exhibit less rapid proliferation in the culture as a result of a common functional attribute. For example, the strains which proliferate less rapidly (or the strains which are not recovered from the culture) may each underexpress a gene product with a common enzymatic activity, such as serine protease activity for example. Alternatively, the strains which proliferate less rapidly (or the strains which are not recovered from the culture) may each underexpress a gene product with a common functional domain, such as a cAMP binding domain. In such instances, the common attribute of the strains which proliferate less rapidly (or the strains which are not recovered from the culture) may provide information as to the mode of action of the compound or the biochemical activity of the target of the compound. For example, if all of the underexpressed genes in the strains which proliferated less rapidly are serine proteases, the compound acts by inhibiting serine protease activity and the target protein is a serine protease. If desired, the compound may be derivatized and the efficacy of the derivatized compound against

each of the strains which proliferated more rapidly may be assessed as described herein in order to identify derivatives which are capable of interacting with a wide range of targets sharing a common activity or binding site (i.e. derivatives which have a greater ability to inhibit the proliferation of all the strains than the original compound) or to identify derivatives having greater specificity for a
5 desired target (i.e. derivatives which have a greater specificity for one of the strains than the original compound).

Rather than employing a single culture which contains multiple strains each of which underexpresses a proliferation-required gene product described herein, the methods of the present invention may be performed using an array of individual strains (i.e. a collection of strains) each of
10 which underexpresses a different proliferation-required gene product. For example, individual strains each underexpressing a different proliferation-required gene product may be grown in different wells of a multiwell plate. Each well is contacted with the compound (and, where appropriate an agent which regulates the level of expression from the promoter). The level of proliferation of the strains in each of the wells is determined to identify a strain which proliferated
15 less rapidly or which did not proliferate at all. The identity of the underexpressed gene product in the strain that proliferated less rapidly or which did not proliferate at all is determined as described above.

In another embodiment, individual strains each underexpressing a different proliferation-required gene product (i.e. a collection of strains) are grown at different locations on a solid
20 medium, such as an agar plate. The medium contains the compound and, where appropriate, an agent which regulates the level of expression from the promoter. The level of proliferation of each of the strains is determined to identify a strain which proliferated less rapidly (or a strain which is not recovered from the culture). The identity of the underexpressed gene product in the strain that proliferated less rapidly (or the strain which is not recovered from the culture) is determined as
25 described above.

The above methods may be used to prioritize compound development or to determine whether the compound has been previously identified or whether the target of the compound is the target of a previously identified drug. In particular, if the product is a natural product is advantageous to determine whether it has been previously identified prior to investing significant
30 effort in developing it. Thus, in some embodiments of the present invention, the target of a partially purified or purified natural product or a compound produced by combinatorial chemistry is identified using the methods described above and compared to the targets of known drugs. If the target is identical to that of a known drug, further development of the compound is halted.

Alternatively, an array of strains each of which underexpresses a different gene product
35 described herein (i.e. a collection of strains) is grown on solid medium containing a compound to be evaluated. The location of each strain in the array and the gene product underexpressed by that strain is known. The pattern of colonies which grow less rapidly or fail to grow in the presence of the compound is evaluated and compared to the pattern of colonies which grow less rapidly or fail

to grow in the presence of previously identified drugs. If the pattern of colonies which grow less rapidly or fail to grow in the presence of the compound being evaluated is the same as the pattern of colonies which grow less rapidly or fail to grow in the presence of a previously identified drug, further development of the compound is halted.

5 Additionally, the nucleotide sequence of the gene product described herein in a strain which proliferated less rapidly (or a strain which was not recovered from the culture) in the assays described above is compared to the nucleotide sequence of gene products from heterologous organisms to determine the likely spectrum of species whose growth would be inhibited by the compound. If the gene product has a high degree of homology to gene products from heterologous
10 species, it is likely that the compound would also inhibit the growth of these heterologous species. Homology may be determined using any of a variety of methods familiar to those skilled in the art. For example, homology may be determined using a computer program such as BLASTP or FASTA. The ability of the compound to inhibit the growth of the heterologous species may then be confirmed by comparing the growth of cells of the heterologous species in the presence and absence
15 of the compound.

 In other embodiments, the present invention uses collections or cultures of strains comprising both strains which overexpress gene products described herein required for cellular proliferation and strains which underexpress the same gene products required for cellular proliferation. The gene product which is overexpressed or underexpressed in each strain may be a
20 gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 1-6213, a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 6214-42397, a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 42398-78581, a gene product whose activity or level is inhibited by a homologous
25 antisense nucleic acid, a gene product encoded by a homologous coding nucleic acid, and a gene product comprising a homologous polypeptide.

 The culture or collection of strains is contacted with a compound and the nucleic acids present in the culture or collection of strains are analyzed. Preferably, nucleic acids derived from overexpressing strains can be distinguished from those derived from underexpressing strains. For
30 example, the overexpressing strains may be obtained using promoter replacement as described above while the underexpressing strains may be obtained by expressing antisense nucleic acids. Accordingly, in one embodiment, amplification primers may be designed which will uniquely amplify nucleic acids from the overexpressing strains or the underexpressing strains. If a compound acts on a gene product which was overexpressed and underexpressed in the culture, then
35 the amplification product obtained from the strain in the culture or collection which overexpressed gene product will be overrepresented in the culture or collection while the amplification product obtained from the strain which underexpressed the gene product will be underrepresented in the culture or collection. If desired, nucleic acids from a culture or collection which was contacted with

the compound may be compared to nucleic acids from a control culture or collection which was not contacted with the compound. Alternatively, nucleic acids from a culture or collection which was contacted with the compound may be directly analyzed without comparison to a control culture or collection.

5 In some embodiments, strains are constructed in which a nucleic acid complementary to a gene encoding a gene product described herein required for proliferation or a portion thereof is operably linked to a regulatable promoter. For example, in some embodiments, the strains may transcribe an antisense nucleic acid selected from the group consisting of SEQ ID NOs.: 1-6213 or fragments thereof which inhibit proliferation or reduce the activity or level of the gene product
10 encoded by the gene comprising a nucleotide sequence complementary to the antisense nucleic acid or homologous antisense nucleic acids or fragments thereof. In other embodiments, the strains may transcribe an antisense nucleic acid which reduces the activity or level of a gene product encoded by SEQ ID NOs.: 6214-42397, the polypeptides of SEQ ID NOs.: 42398-78581, homologous coding nucleic acids or homologous polypeptides. A culture comprising a plurality of such strains
15 wherein each strain expresses an antisense nucleic acid against a different gene product required for proliferation is grown in the presence of varying levels of a compound which inhibits proliferation and in the presence of varying levels of an agent which regulates the level of transcription from the regulatable promoter. Nucleic acids samples are obtained from the culture, detectably labeled and hybridized to a solid support comprising nucleic acids containing the genes encoding the
20 proliferation-required gene products or a portion thereof. The level of hybridization is quantitated for each nucleic acid encoding each of the proliferation-required gene products to determine the rate at which each of the strains proliferated in the culture. If the antisense nucleic acid expressed by a strain in the culture is not complementary to all or a portion of the gene encoding the target of the compound (i.e. a nonspecific strain), then the hybridization intensity for that strain will not be
25 correlated with the concentration of the compound (See Figure 4), while if the antisense nucleic acid expressed by a strain in the culture is complementary to all or a portion of the gene encoding the target of the compound, the hybridization intensity for that strain will be intimately correlated with the concentration of the compound (See Figure 5). In this manner, the target of the compound may be identified. It will be appreciated that, as described above, rather than growing the strains in
30 a single culture, each strain may be grown in a different location on a solid medium or in a different well of a multiwell plate.

 The methods described above can be simultaneously performed for each of a large number of compounds. For example, the compounds may be members of a library of compounds generated using combinatorial chemistry or members of a natural product library. In such methods, a plurality
35 of cultures each comprising a plurality of strains each of which overexpresses or underexpresses a different gene product required for proliferation or a plurality of collections of individual strains each of which overexpresses or underexpresses a different gene product required for proliferation is

obtained. Each culture or collection of strains is contacted with a different compound in the library and the target of the compound is identified as described above.

In still another embodiment, the antisense nucleic acids of the present invention (including the antisense nucleic acids of SEQ ID NOs. 1-6213 fragments thereof or homologous antisense nucleic acids or fragments thereof) that inhibit bacterial growth or proliferation can be used as antisense therapeutics for killing bacteria. The antisense sequences can be complementary to one of SEQ ID NOs.: 6214-42397 or fragments thereof, homologous coding nucleic acids or fragments thereof. Alternatively, antisense therapeutics can be complementary to operons in which proliferation-required genes reside (i.e. the antisense nucleic acid may hybridize to a nucleotide sequence of any gene in the operon in which the proliferation-required genes reside). Further, antisense therapeutics can be complementary to a proliferation-required gene or portion thereof with or without adjacent noncoding sequences, an intragenic sequence (i.e. a sequence within a gene), an intergenic sequence (i.e. a sequence between genes), a sequence spanning at least a portion of two or more genes, a 5' noncoding region or a 3' noncoding region located upstream or downstream from the actual sequence that is required for bacterial proliferation or an operon containing a proliferation-required gene.

In addition to therapeutic applications, the present invention encompasses the use of nucleic acids complementary to nucleic acids required for proliferation as diagnostic tools. For example, nucleic acid probes comprising nucleotide sequences complementary to proliferation-required sequences that are specific for particular species of cells or microorganisms can be used as probes to identify particular microorganism species or cells in clinical specimens. This utility provides a rapid and dependable method by which to identify the causative agent or agents of a bacterial infection. This utility would provide clinicians the ability to accurately identify the species responsible for the infection and administer a compound effective against it. In an extension of this utility, antibodies generated against proteins translated from mRNA transcribed from proliferation-required sequences can also be used to screen for specific cells or microorganisms that produce such proteins in a species-specific manner.

Other embodiments of the present invention include methods of identifying compounds which inhibit the activity of gene products required for cellular proliferation using rational drug design. As discussed in more detail below, in such methods, the structure of the gene product is determined using techniques such as x-ray crystallography or computer modeling. Compounds are screened to identify those which have a structure which would allow them to interact with the gene product or a portion thereof to inhibit its activity. The compounds may be obtained using any of a variety of methods familiar to those skilled in the art, including combinatorial chemistry. In some embodiments, the compounds may be obtained from a natural product library. In some embodiments, compounds having a structure which allows them to interact with the active site of a gene product, such as the active site of an enzyme, or with a portion of the gene product which interacts with another biomolecule to form a complex are identified. If desired, lead compounds may be identified and further optimized to provide compounds which are highly effective against the gene product.

The following examples teach the genes of the present invention and a subset of uses for the genes identified as required for proliferation. These examples are illustrative only and are not intended to limit the scope of the present invention.

EXAMPLES

5 The following examples are directed to the identification and exploitation of genes required for proliferation. Methods of gene identification are discussed as well as a variety of methods to utilize the identified sequences. It will be appreciated that any of the antisense nucleic acids, proliferation-
 10 required genes or proliferation-required gene products described herein, or portions thereof, may be used in the procedures described below, including the antisense nucleic acids of SEQ ID NOS.: 1-6213, the nucleic acids of SEQ ID NOS.: 6214-42397, or the polypeptides of SEQ ID NOS.: 42398-78581. Likewise, homologous antisense nucleic acids, homologous coding nucleic acids, homologous polypeptides or portions of any of the above-mentioned nucleic acids or polypeptides, may be used in any of the procedures described below.

15 **Genes Identified as Required for Proliferation of *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* and *Salmonella typhimurium*.**

Genomic fragments were operably linked to an inducible promoter in a vector and assayed for growth inhibition activity. Example 1 describes the examination of a library of genomic fragments cloned into vectors comprising inducible promoters. Upon induction with xylose or IPTG, the vectors
 20 produced an RNA molecule corresponding to the subcloned genomic fragments. In those instances where the genomic fragments were in an antisense orientation with respect to the promoter, the transcript produced was complementary to at least a portion of an mRNA (messenger RNA) encoding a *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* or *Salmonella typhimurium* gene product such that they interacted with
 25 sense mRNA produced from various *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* or *Salmonella typhimurium* genes and thereby decreased the translation efficiency or the level of the sense messenger RNA thus decreasing production of the protein encoded by these sense mRNA molecules. In cases where the sense mRNA encoded a protein required for proliferation, bacterial cells containing a vector from which transcription
 30 from the promoter had been induced failed to grow or grew at a substantially reduced rate. Additionally, in cases where the transcript produced was complementary to at least a portion of a non-translated RNA and where that non-translated RNA was required for proliferation, bacterial cells containing a vector from which transcription from the promoter had been induced also failed to grow or grew at a substantially reduced rate. In contrast, cells grown under non-inducing conditions grow at a
 35 normal rate.

The above method was used to identify genes required for cellular proliferation in *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* and *Salmonella typhimurium*. Additionally, a number of genes required for cellular

proliferation in *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* and *Salmonella typhimurium*, which have been described in the following U.S. Patent Applications: U.S. Patent Application Serial Number 09/492,709, filed January 27, 2000; U.S. Patent Application Serial Number 09/711,164, filed November 9, 2000; 5 U.S. Patent Application Serial Number 09/741,669, filed December 19, 2000 and U.S. Patent Application Serial Number 09/815,242 filed March 21, 2001, U.S. Provisional Patent Application Serial Number 60/342,923, filed October 25, 2001, have been previously identified using the above method.

EXAMPLE 1

10 Inhibition of Bacterial Proliferation after Induction of Antisense Expression

To identify genes required for proliferation of *E. coli*, random genomic fragments were cloned into the IPTG-inducible expression vector pLEX5BA (Krause et al., J. Mol. Biol. 274: 365 (1997) or a modified version of pLEX5BA, pLEX5BA-3' in which a synthetic linker containing a T7 terminator was ligated between the PstI and HindIII sites of pLEX5BA. In particular, to 15 construct pLEX5BA-3', the following oligonucleotides were annealed and inserted into the PstI and HindIII sites of pLEX5BA:

5' -GTCTAGCATAACCCCTTGGGGCTCTAAACGGGTCCTTGAGGGGTTTTTGA-3' (SEQ ID NO: 78584)
 5' -AGCTTCAAAAAACCCCTCAAGGACCCGTTTAGAGGCCCAAGGGTTAT
 20 GCTAGACTGCA-3' (SEQ ID NO: 78585)

Random fragments of *E. coli* genomic DNA were generated by DNaseI digestion or sonication, filled in with T4 polymerase, and cloned into the SmaI site of pLEX5BA or pLEX5BA-3'. Upon activation or induction, the promoter transcribed the random genomic fragments.

A number of vectors which allow the production of transcripts which have an extended 25 lifetime in *E. coli* as well as other Gram negative bacteria can also be utilized in conjunction with these antisense inhibition experiments. Such vectors are described in U.S. Provisional Patent Application Serial Number 60/343,512, filed December 21, 2001. Briefly, the stabilized antisense RNA may comprise an antisense RNA which was identified as inhibiting proliferation as described above which has been engineered to contain at least one stem loop flanking each end of the 30 antisense nucleic acid. In some embodiments, the at least one stem-loop structure formed at the 5' end of the stabilized antisense nucleic acid comprises a flush, double stranded 5' end. In some embodiments, one or more of the stem loops comprises a rho independent terminator. In additional embodiments, the stabilized antisense RNA lacks a ribosome binding site. In further embodiments, the stabilized RNA lacks sites which are cleaved by one or more RNases, such as RNase E or 35 RNase III. In some embodiments, the stabilized antisense RNA may be transcribed in a cell which the activity of at least one enzyme involved in RNA degradation has been reduced. For example, the activity of an enzyme such as RNase E, RNase II, RNase III, polynucleotide phosphorylase, and poly(A) polymerase, RNA helicase, enolase or an enzyme having similar functions may be reduced in the cell.

To study the effects of transcriptional induction in liquid medium, growth curves were carried out by back diluting cultures 1:200 into fresh media with or without 1 mM IPTG and measuring the OD₄₅₀ every 30 minutes (min). To study the effects of transcriptional induction on solid medium, 10², 10³, 10⁴, 10⁵, 10⁶, 10⁷ and 10⁸ fold dilutions of overnight cultures were prepared. Aliquots of from 0.5
5 to 3 µl of these dilutions were spotted on selective agar plates with or without 1 mM IPTG. After overnight incubation, the plates were compared to assess the sensitivity of the clones to IPTG.

Of the numerous clones tested, some clones were identified as containing a sequence that inhibited *E. coli* growth after IPTG induction. Accordingly, the gene to which the inserted nucleic acid sequence corresponds, or a gene within the operon containing the inserted nucleic acid, is required for
10 proliferation in *E. coli*.

Nucleic acids involved in proliferation of *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* and *Salmonella typhimurium* were identified as follows. Randomly generated fragments of *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* or *Salmonella typhimurium* genomic DNA were
15 transcribed from inducible promoters.

In the case of *Staphylococcus aureus*, a novel inducible promoter system, XylT5, comprising a modified T5 promoter fused to the *xylO* operater from the *xylA* promoter of *Staphylococcus aureus* was used. The promoter is described in U.S. Patent Application Serial Number 10/032,393, filed December 21, 2001. Transcription from this hybrid promoter is
20 inducible by xylose.

Randomly generated fragments of *Salmonella typhimurium* genomic DNA were transcribed from an IPTG inducible promoter in pLEX5BA (Krause et al., J. Mol. Biol. 274: 365 (1997) or a derivative thereof. Randomly generated fragementts of *Klebsiella pneumoniae* genomic DNA were expressed from an IPTG inducible promoter in pLEX5BA-Kan. To construct
25 pLEX5BA-kan, pLEX5BA was digested to completion with *ClaI* in order to remove the *bla* gene. Then the plasmid was treated with a partial *NotI* digestion and blunted with T4 DNA polymerase. A 3.2 kbp fragment was then gel purified and ligated to a blunted 1.3 kbp kan gene from pKan π . Kan resistant transformants were selected on Kan plates. Orientation of the kan gene was checked by *SmaI* digestion. A clone, which had the kan gene in the same orientation as the *bla* gene, was used
30 to identify genes required for proliferation of *Klebsiella pneumoniae*. Randomly generated fragments of *Pseudomonas aeruginosa* genomic DNA were trancribed from a two-component inducible promoter system. Integrated on the chromosome was the T7 RNA polymerase gene regulated by *lacUV5/ lacO* (Brunschwig, E. and Darzins, A. 1992. Gene 111:35-41. On a separate plasmid, a T7 gene 10 promoter, which is transcribed by T7 RNA polymerase, was fused with a
35 *lacO* operator followed by a multiple cloning site.

Should the genomic DNA downstream of the promoter contain, in an antisense orientation, at least a portion of an mRNA or a non-translated RNA encoding a gene product involved in proliferation, then induction of transcription from the promoter will result in detectable inhibition of proliferation.

5 In the case of *Staphylococcus aureus*, a shotgun library of *Staphylococcus aureus* genomic fragments was cloned into the vector pXyIT5-P15a, which harbors the XyIT5 inducible promoter. The vector was linearized at a unique *Bam*HI site immediately downstream of the XyIT5 promoter/operator. The linearized vector was treated with shrimp alkaline phosphatase to prevent reclosure of the linearized ends. Genomic DNA isolated from *Staphylococcus aureus* strain RN450
10 was fully digested with the restriction enzyme *Sau*3A, or, alternatively, partially digested with DNase I and "blunt-ended" by incubating with T4 DNA polymerase. Random genomic fragments between 200 and 800 base pairs in length were selected by gel purification. The size-selected genomic fragments were added to the linearized and dephosphorylated vector at a molar ratio of 0.1 to 1, and ligated to form a shotgun library.

15 The ligated products were transformed into electrocompetent *E. coli* strain XL1-Blue MRF' (Stratagene) and plated on LB medium with supplemented with carbenicillin at 100 µg/ml. Resulting colonies numbering 5×10^5 or greater were scraped and combined, and were then subjected to plasmid purification.

 The purified library was then transformed into electrocompetent *Staphylococcus aureus*
20 RN4220. Resulting transformants were plated on agar containing LB + 0.2% glucose (LBG medium) + chloramphenicol at 15 µg/ml (LBG+CM15 medium) in order to generate 100 to 150 platings at 500 colonies per plating. The colonies were subjected to robotic picking and arrayed into wells of 384 well culture dishes. Each well contained 100µl of LBG + CM15 liquid medium. Inoculated 384 well dishes were incubated 16 hours at 37°C, and each well was robotically gridded
25 onto solid LBG + CM15 medium with or without 2% xylose. Gridded plates were incubated 16 hours at 37°C, and then manually scored for arrayed colonies that were growth-compromised in the presence of xylose.

 Arrayed colonies that were growth-sensitive on medium containing 2% xylose, yet were able to grow on similar medium lacking xylose, were subjected to further growth sensitivity
30 analysis as follows: Colonies from the plate lacking xylose were manually picked and inoculated into individual wells of a 96 well culture dish containing LBG + CM15, and were incubated for 16 hours at 37°C. These cultures were robotically diluted 1/100 into fresh medium and allowed to incubate for 4 hours at 37°C, after which they were subjected to serial dilutions in a 384 well array and then gridded onto media containing 2% xylose or media lacking xylose. After growth for 16
35 hours at 37°C, the arrays that resulted on the two media were compared to each other. Clones that grew similarly at all dilutions on both media were scored as a negative and were no longer considered. Clones that grew on xylose medium but failed to grow at the same serial dilution on the non-xylose plate were given a score based on the differential, i.e. should the clone grow at a

serial dilution of 10^4 or less on the xylose plate and grow at a serial dilution of 10^8 or less on the non-xylose plate, then the corresponding clone received a score of "4" representing the log difference in growth observed.

For *Salmonella typhimurium* and *Klebsiella pneumoniae* growth curves were carried out by back diluting cultures 1:200 into fresh media containing 1 mM IPTG or media lacking IPTG and measuring the OD₄₅₀ every 30 minutes (min). To study the effects of transcriptional induction on solid medium, 10^2 , 10^3 , 10^4 , 10^5 , 10^6 , 10^7 and 10^8 fold dilutions of overnight cultures were prepared. Aliquots of from 0.5 to 3 μ l of these dilutions were spotted on selective agar plates with or without 1 mM IPTG. After overnight incubation, the plates were compared to assess the sensitivity of the clones to IPTG.

Nucleic acids involved in proliferation of *Pseudomonas aeruginosa* were identified as follows. Randomly generated fragments of *Pseudomonas aeruginosa* genomic DNA were transcribed from a two-component inducible promoter system. Integrated on the chromosome was the T7 RNA polymerase gene regulated by *lacUV5/lacO* (Brunschwig, E. and Darzins, A. 1992. Gene 111:35-41). On an expression plasmid there was a T7 gene 10 promoter, which is transcribed by T7 RNA polymerase, fused with a *lacO* operator followed by a multiple cloning site. Transcription from this hybrid promoter is inducible by IPTG. Should the genomic DNA downstream of the promoter contain, in an antisense orientation, at least a portion of an mRNA encoding a gene product involved in proliferation, then induction of expression from the promoter will result in detectable inhibition of proliferation.

A shotgun library of *Pseudomonas aeruginosa* genomic fragments was cloned into the vectors pEP5, pEP5S, or other similarly constructed vectors which harbor the T7*lacO* inducible promoter. The vector was linearized at a unique *Sma*I site immediately downstream of the T7*lacO* promoter/operator. The linearized vector was treated with shrimp alkaline phosphatase to prevent reclosure of the linearized ends. Genomic DNA isolated from *Pseudomonas aeruginosa* strain PAO1 was partially digested with DNase I and "blunt-ended" by incubating with T4 DNA polymerase. Random genomic fragments between 200 and 800 base pairs in length were selected by gel purification. The size-selected genomic fragments were added to the linearized and dephosphorylated vector at a molar ratio of 2 to 1, and ligated to form a shotgun library.

The ligated products were transformed into electrocompetent *E. coli* strain XL1-Blue MRF' (Stratagene) and plated on LB medium with carbenicillin at 100 μ g/ml or Streptomycin 100 μ g/ml. Resulting colonies numbering 5×10^5 or greater were scraped and combined, and were then subjected to plasmid purification.

The purified library was then transformed into electrocompetent *Pseudomonas aeruginosa* strain PAO1. Resulting transformants were plated on LB agar with carbenicillin at 100 μ g/ml or Streptomycin 40 μ g/ml in order to generate 100 to 150 platings at 500 colonies per plating. The colonies were subjected to robotic picking and arrayed into wells of 384 well culture dishes. Each well contained 100 μ l of LB + CB 100 or Streptomycin 40 liquid medium. Inoculated 384 well

dishes were incubated 16 hours at room temperature, and each well was robotically gridded onto solid LB + CB100 or Streptomycin 40 medium with or without 1 mM IPTG. Gridded plates were incubated 16 hours at 37°C, and then manually scored for arrayed colonies that were growth-compromised in the presence of IPTG.

5 Arrayed colonies that were growth-sensitive on medium containing 1 mM IPTG, yet were able to grow on similar medium lacking IPTG, were subjected to further growth sensitivity analysis as follows: Colonies from the plate lacking IPTG were manually picked and inoculated into individual wells of a 96 well culture dish containing LB + CB100 or Streptomycin 40, and were incubated for 16 hours at 30°C. These cultures were robotically diluted 1/100 into fresh medium
10 and allowed to incubate for 4 hours at 37°C, after which they were subjected to serial dilutions in a 384 well array and then gridded onto media with and without 1 mM IPTG. After growth for 16 hours at 37°C, the arrays of serially diluted spots that resulted were compared between the two media. Clones that grew similarly at all dilutions on both media were scored as a negative and were no longer considered. Clones that grew on IPTG medium but failed to grow at the same serial
15 dilution on the non-IPTG plate were given a score based on the differential, i.e. should the clone grow at a serial dilution of 10^4 or less on the IPTG plate and grow at a serial dilution of 10^8 or less on the IPTG plate, then the corresponding clone received a score of "4" representing the log difference in growth observed.

 Following the identification of those vectors that, upon induction, negatively impacted
20 *Pseudomonas aeruginosa* growth or proliferation, the inserts or nucleic acid fragments contained in those vectors were isolated for subsequent characterization. Vectors of interest were subjected to nucleic acid sequence determination.

 Nucleic acids involved in proliferation of *E. faecalis* were identified as follows. Randomly generated fragments of genomic DNA were expressed from the vectors pEPEF3 or pEPEF14,
25 which contain the CP25 or P59 promoter, respectively, regulated by the xyl operator/repressor. These plasmids as well as other vectors useful for the expression of nucleic acids in *Enterococcus faecalis* and other Gram positive organisms are described in U.S. Patent Application Serial Number 10/032,393, filed December 21, 2001, the disclosure of which is incorporated herein by reference in its entirety. Should the genomic DNA downstream of the promoter contain, in an antisense
30 orientation, at least a portion of a mRNA encoding a gene product involved in proliferation, then induction of expression from the promoter will result in detectable inhibition of proliferation.

 A shotgun library of *E. faecalis* genomic fragments was cloned into the vector pEPEF3 or pEPEF14, which harbor xylose inducible promoters. The vector was linearized at a unique *Sma*I site immediately downstream of the promoter/operator. The linearized vector was treated with
35 alkaline phosphatase to prevent reclosure of the linearized ends. Genomic DNA isolated from *E. faecalis* strain OG1RF was partially digested with DNase I and "blunt-ended" by incubating with T4 DNA polymerase. Random genomic fragments between 200 and 800 base pairs in length were

selected by gel purification. The size-selected genomic fragments were added to the linearized and dephosphorylated vector at a molar ratio of 2 to 1, and ligated to form a shotgun library.

The ligated products were transformed into electrocompetent *E. coli* strain TOP10 cells (Invitrogen) and plated on LB medium with erythromycin (Erm) at 150 µg/ml. Resulting colonies numbering 5 x 10⁵ or greater were scraped and combined, and were then subjected to plasmid purification.

The purified library was then transformed into electrocompetent *E. faecalis* strain OG1RF. Resulting transformants were plated on Todd-Hewitt (TH) agar with erythromycin at 10 µg/ml in order to generate 100 to 150 platings at 500 colonies per plating. The colonies were subjected to robotic picking and arrayed into wells of 384 well culture dishes. Each well contained 100 µl of THB + Erm 10 µg/ml. Inoculated 384 well dishes were incubated 16 hours at room temperature, and each well was robotically gridded onto solid TH agar + Erm with or without 5% xylose. Gridded plates were incubated 16 hours at 37°C, and then manually scored for arrayed colonies that were growth-compromised in the presence of xylose.

Arrayed colonies that were growth-sensitive on medium containing 5% xylose, yet were able to grow on similar medium lacking xylose, were subjected to further growth sensitivity analysis. Colonies from the plate lacking xylose were manually picked and inoculated into individual wells of a 96 well culture dish containing THB + Erm 10, and were incubated for 16 hours at 30°C. These cultures were robotically diluted 1/100 into fresh medium and allowed to incubate for 4 hours at 37°C, after which they were subjected to serial dilution on plates containing 5% xylose or plates lacking xylose. After growth for 16 hours at 37°C, the arrays of serially diluted spots that resulted were compared between the two media. Colonies that grew similarly on both media were scored as a negative and corresponding colonies were no longer considered. Colonies on xylose medium that failed to grow to the same serial dilution compared to those on the non-xylose plate were given a score based on the differential. For example, colonies on xylose medium that only grow to a serial dilution of -4 while they were able to grow to -8 on the non-xylose plate, then the corresponding transformant colony received a score of "4" representing the log difference in growth observed.

Following the identification of those vectors that, upon induction, negatively impacted *E. faecalis* growth or proliferation, the inserts or nucleic acid fragments contained in those expression vectors were isolated for subsequent characterization. The inserts in the vectors of interest were subjected to nucleotide sequence determination.

It will be appreciated that other restriction enzymes and other endonucleases or methodologies may be used to generate random genomic fragments. In addition, random genomic fragments may be generated by mechanical shearing. Sonication and nebulization are two such techniques commonly used for mechanical shearing of DNA.

EXAMPLE 2

Nucleotide Sequence Determination of Identified Clones Transcribing Nucleic Acid Fragments with Detrimental Effects on *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* or *Salmonella typhimurium* Proliferation

5 Plasmids from clones that received a dilution plating score of "2" or greater were isolated to obtain the genomic DNA insert responsible for growth inhibition as follows.

The nucleotide sequences of the nucleic acid sequences which inhibited the growth of *Escherichia coli* were determined using plasmid DNA isolated using QIAPREP (Qiagen, Valencia, CA) and methods supplied by the manufacturer. The primers used for sequencing the inserts were 5' -
 10 TGTTTATCAGACCGCTT - 3' (SEQ ID NO: 78586) and 5' - ACAATTTACACAGCCTC - 3' (SEQ ID NO: 78587). These sequences flank the polylinker in pLEX5BA.

The nucleotide sequences of the nucleic acid sequences which inhibited the growth of *Staphylococcus aureus* were determined as follows. *Staphylococcus aureus* were grown in standard laboratory media (LB or TB with 15 ug/ml Chloramphenicol to select for the plasmid). Growth
 15 was carried out at 37°C overnight in culture tubes or 2 ml deep well microtiter plates.

Lysis of *Staphylococcus aureus* was performed as follows. Cultures (2-5 ml) were centrifuged and the cell pellets resuspended in 1.5 mg/ml solution of lysostaphin (20 µl/ml of original culture) followed by addition of 250 µl of resuspension buffer (Qiagen). Alternatively, cell pellets were resuspended directly in 250 µl of resuspension buffer (Qiagen) to which 5-20 µl of a 1
 20 mg/ml lysostaphin solution were added.

DNA was isolated using Qiagen miniprep kits or Wizard (Qiagen) miniprep kits according to the instructions provided by the manufacturer.

The genomic DNA inserts were amplified from the purified plasmids by PCR as follows.

1 µl of Qiagen purified plasmid was put into a total reaction volume of 25 µl Qiagen Hot
 25 Start PCR mix. For *Staphylococcus aureus*, the following primers were used in the PCR reaction:
 pXyIT5F: CAGCAGTCTGAGTTATAAAATAG (SEQ ID NO: 78588)
 LexL TGTTTTATCAGACCGCTT (SEQ ID NO: 78589)

Similar methods were conducted for *Salmonella typhimurium* and *Klebsiella pneumoniae*. For *Salmonella typhimurium* and *Klebsiella pneumoniae* the following primers were used:
 30 5' - TGTTTTATCAGACCGCTT - 3' (SEQ ID NO: 78589) and
 5'-ACAATTTACACAGCCTC-3' (SEQ ID NO: 78587)

PCR was carried out in a PE GenAmp with the following cycle times:

- Step 1. 95° C 15 min
- Step 2. 94° C 45 sec
- 35 Step 3. 54° C 45 sec
- Step 4. 72° C 1 minute
- Step 5. Return to step 2, 29 times
- Step 6. 72° C 10 minutes

Step 7. 4° C hold

The PCR products were cleaned using Qiagen Qiaquick PCR plates according to the manufacturer's instructions.

For *Pseudomonas aeruginosa*, plasmids from transformant colonies that received a dilution
5 plating score of "2" or greater were isolated to obtain the genomic DNA insert responsible for
growth inhibition as follows. *Pseudomonas aeruginosa* were grown in standard laboratory media
(LB with carbenicillin at 100 µg/ml or Streptomycin 40 µg/ml to select for the plasmid). Growth
was carried out at 30°C overnight in 100 ul culture wells in microtiter plates. To amplify insert
DNA 2 ul of culture were placed into 25 ul Qiagen Hot Start PCR mix. PCR reactions were in 96
10 well microtiter plates. For plasmid pEP5S the following primers were used in the PCR reaction:

T7L1+: GTCGGCGATATAGGCGCCAGCAACCG (SEQ ID NO: 78590)

pStrA3: ATAATCGAGCATGAGTATCATACG (SEQ ID NO: 78591)

PCR was carried out in a PE GenAmp with the following cycle times:

Step 1. 95° C 15 min

15 Step 2. 94° C 45 sec

Step 3. 54° C 45 sec

Step 4. 72° C 1 minute

Step 5. Return to step 2, 29 times

Step 6. 72° C 10 minutes

20 Step 7. 4° C hold

The PCR products were cleaned using Qiagen Qiaquick PCR plates according to the manufacturer's instructions.

The purified PCR products were then directly cycle sequenced with Qiagen Hot Start PCR
mix. The following primers were used in the sequencing reaction:

25 T7/L2: ATGCGTCCGGCGTAGAGGAT (SEQ ID NO: 78592)

PCR was carried out in a PE GenAmp with the following cycle times:

Step 1. 94° C 15 min

Step 2. 96° C 10 sec

Step 3. 50° C 5 sec

30 Step 4. 60 C 4 min

Step 5. Return to step 2, 24 times

Step 6. 4° C hold

The PCR products were cleaned using Qiagen Qiaquick PCR plates according to the manufacturer's instructions.

35 For *E. faecalis*, plasmids from transformant colonies that received a dilution plating score
of "2" or greater were isolated to obtain the genomic DNA insert responsible for growth inhibition
as follows. *E. faecalis* were grown in THB 10 µg/ml Erm at 30°C overnight in 100 ul culture wells

in microtiter plates. To amplify insert DNA 2 μ l of culture were placed into 25 μ l Qiagen Hot Start PCR mix. PCR reactions were in 96 well microtiter plates. The following primers were used in the PCR reaction:

pXylT5: CAGCAGTCTGAGTTATAAAATAG (SEQ ID NO: 78588) and the

5 pEP/pAK1 primer.

PCR was carried out in a PE GenAmp with the following cycle times:

Step 1. 95° C 15 min

Step 2. 94° C 45 sec

Step 3. 54° C 45 sec

10 Step 4. 72° C 1 minute

Step 5. Return to step 2, 29 times

Step 6. 72° C 10 minutes

Step 7. 4° C hold

The PCR products were cleaned using Qiagen Qiaquick PCR plates according to the manufacturer's

15 instructions.

The purified PCR products were then directly cycle sequenced with Qiagen Hot Start PCR mix. The following primers were used in the PCR reaction:

pXylT5: CAGCAGTCTGAGTTATAAAATAG (SEQ ID NO: 78588)

PCR was carried out in a PE GenAmp with the following cycle times:

20 Step 1. 94° C 15 min

Step 2. 96° C 10 sec

Step 3. 50° C 5 sec

Step 4. 60° C 4 min

Step 5. Return to step 2, 24 times

25 Step 6. 4° C hold

The PCR products were cleaned using Qiagen Qiaquick PCR plates according to the manufacturer's instructions.

The amplified genomic DNA inserts from each of the above procedures were subjected to automated sequencing. Sequence identification numbers (SEQ ID NOs) and clone names for the

30 identified inserts are listed in Table IA and discussed below.

TABLE IA

SeqID	Clone Name	SeqID	Clone Name	SeqID	Clone Name	SeqID	Clone Name	SeqID	Clone Name
1	E3M10000001B01	1243	P33-1.C22	2485	E1M10000260G02	3727	P1M10000105C04	4969	S1M10000025G06
2	E3M10000001A02	1244	X3S107-17	2486	E1M10000260F04	3728	P1M10000105D04	4970	S1M10000025H06
3	E3M100000001B02	1245	P35-7	2487	E1M10000260A05	3729	P1M10000105C05	4971	S1M10000025H07
4	E3M100000001C02	1246	X3S118-9	2488	E1M10000260C05	3730	P1M10000105B06	4972	S1M10000025A08
5	E3M100000001D02	1247	X3S163-1	2489	E1M10000260E05	3731	P1M10000105C08	4973	S1M10000025D08
6	E3M100000001E02	1248	X3S204-7	2490	E1M10000260C07	3732	P1M10000105H08	4974	S1M10000025F08
7	E3M100000001F02	1249	X3S177-4	2491	E1M10000260G07	3733	P1M10000105D09	4975	S1M10000025H08
8	E3M100000001G02	1250	P342-3	2492	E1M10000260B08	3734	P1M10000110E01	4976	S1M10000025A09
9	E3M100000001H02	1251	SC21.1	2493	E1M10000260D08	3735	P1M10000110F01	4977	S1M10000025B09
10	E3M100000001E03	1252	SC17.1	2494	E1M10000260E08	3736	P1M10000110G01	4978	S1M10000025C09
11	E3M100000001G03	1253	SC13.1	2495	E1M10000260E09	3737	P1M10000110B02	4979	S1M10000025D09
12	E3M100000001H03	1254	MC9.6	2496	E1M10000260C10	3738	P1M10000110B03	4980	S1M10000025E09
13	E3M100000001D04	1255	Z60-P16	2497	E1M10000260D10	3739	P1M10000110F03	4981	S1M10000025F09
14	E3M100000001E04	1256	Z86-121	2498	E1M10000260E10	3740	P1M10000110G03	4982	S1M10000025A10
15	E3M100000001F04	1257	E1M10000109A02	2499	E1M10000260G10	3741	P1M10000110D04	4983	S1M10000025C10
16	E3M100000001G04	1258	E1M10000109A11	2500	E1M10000260H10	3742	P1M10000110F04	4984	S1M10000025D10
17	E3M100000001H04	1259	E1M10000101F05	2501	E1M10000260H11	3743	P1M10000110B05	4985	S1M10000025F10
18	E3M100000001B05	1260	E1M10000101D06	2502	E1M10000260B12	3744	P1M10000110E05	4986	S1M10000025G10
19	E3M100000001D05	1261	E1M10000101A07	2503	E1M10000260D12	3745	P1M10000110B07	4987	S1M10000025H10
20	E3M100000001G05	1262	E1M10000101H07	2504	E1M10000260G12	3746	P1M10000110B08	4988	S1M10000025C11
21	E3M100000001A06	1263	E1M10000101H09	2505	E1M10000261F01	3747	P1M10000110F08	4989	S1M10000025E11
22	E3M100000001F06	1264	E1M10000101C12	2506	E1M10000261B02	3748	P1M10000110A09	4990	S1M10000025B12
23	E3M100000001B08	1265	E1M10000103B04	2507	E1M10000261H02	3749	P1M10000110E09	4991	S1M10000025F12
24	E3M100000001E08	1266	E1M10000103D11	2508	E1M10000261G04	3750	P1M10000110F09	4992	S1M10000026C01
25	E3M100000001C09	1267	E1M10000110G01	2509	E1M10000261H05	3751	P1M10000100F01	4993	S1M10000026E01
26	E3M100000001D09	1268	E1M10000110H01	2510	E1M10000261G06	3752	P1M10000098A02	4994	S1M10000026F01
27	E3M100000001E09	1269	E1M10000110E09	2511	E1M10000261H06	3753	P1M10000098B02	4995	S1M10000026G01
28	E3M100000001B10	1270	E1M10000110A12	2512	E1M10000261D08	3754	P1M10000098A03	4996	S1M10000026H01
29	E3M100000004D01	1271	E1M10000112F05	2513	E1M10000261F08	3755	P1M10000098D03	4997	S1M10000026A02
30	E3M100000004G01	1272	E1M10000113F02	2514	E1M10000261C09	3756	P1M10000098E04	4998	S1M10000026B02
31	E3M100000004D02	1273	E1M10000113A11	2515	E1M10000261H09	3757	P1M10000098G04	4999	S1M10000026H02
32	E3M100000004C03	1274	E1M10000111C03	2516	E1M10000261E10	3758	P1M10000098A05	5000	S1M10000026B03
33	E3M100000004A04	1275	E1M10000111E04	2517	E1M10000262E01	3759	P1M10000098C05	5001	S1M10000026F03

SeqID	Clone Name	SeqID	Clone Name	SeqID	Clone Name	SeqID	Clone Name	SeqID	Clone Name
34	E3M10000004F08	1276	E1M10000111F09	2518	E1M10000262C02	3760	P1M10000098G06	5002	S1M10000026G03
35	E3M10000004D10	1277	E1M10000115H01	2519	E1M10000262E02	3761	P1M10000098H06	5003	S1M10000026H03
36	E3M10000004F10	1278	E1M10000115G02	2520	E1M10000262F02	3762	P1M10000098C07	5004	S1M10000026A04
37	E3M10000004E11	1279	E1M10000115E03	2521	E1M10000262D03	3763	P1M10000098F07	5005	S1M10000026D04
38	E3M10000004H11	1280	E1M10000115G04	2522	E1M10000262G04	3764	P1M10000098A08	5006	S1M10000026F04
39	E3M10000005B01	1281	E1M10000115C06	2523	E1M10000262C05	3765	P1M10000098G08	5007	S1M10000026G04
40	E3M10000005C01	1282	E1M10000116B01	2524	E1M10000262A06	3766	P1M10000098H09	5008	S1M10000026H04
41	E3M10000005E01	1283	E1M10000106D02	2525	E1M10000262A07	3767	P1M10000098B11	5009	S1M10000026A05
42	E3M10000005E02	1284	E1M10000106G02	2526	E1M10000262E07	3768	P1M10000098C12	5010	S1M10000026B05
43	E3M10000005C03	1285	E1M10000106E04	2527	E1M10000262E08	3769	P1M10000099G03	5011	S1M10000026D05
44	E3M10000005D03	1286	E1M10000106F05	2528	E1M10000262B10	3770	P1M10000099A09	5012	S1M10000026F05
45	E3M10000005E03	1287	E1M10000106H05	2529	E1M10000262H10	3771	P1M10000099E10	5013	S1M10000026G05
46	E3M10000005C04	1288	E1M10000106H06	2530	E1M10000262G11	3772	P1M10000099A10	5014	S1M10000026H05
47	E3M10000005D04	1289	E1M10000106A08	2531	E1M10000262G12	3773	P1M10000099E10	5015	S1M10000026A06
48	E3M10000005H04	1290	E1M10000106E09	2532	E1M10000263F01	3774	P1M10000099F10	5016	S1M10000026B06
49	E3M10000005G05	1291	E1M10000106G10	2533	E1M10000263H05	3775	P1M10000106D02	5017	S1M10000026C06
50	E3M10000005A07	1292	E1M10000106D11	2534	E1M10000263C06	3776	P1M10000106F03	5018	S1M10000026D06
51	E3M10000005F07	1293	E1M10000122B03	2535	E1M10000263G06	3777	P1M10000106H03	5019	S1M10000026F06
52	E3M10000005B08	1294	E1M10000123D05	2536	E1M10000263G07	3778	P1M10000106F04	5020	S1M10000026G06
53	E3M10000005E08	1295	E1M10000123C09	2537	E1M10000263B07	3779	P1M10000106F05	5021	S1M10000026A07
54	E3M10000005D10	1296	E1M10000123E09	2538	E1M10000263F08	3780	P1M10000106D05	5022	S1M10000026B07
55	E3M10000005F10	1297	E1M10000123H10	2539	E1M10000263A10	3781	P1M10000106E07	5023	S1M10000026C07
56	E3M10000006C01	1298	E1M10000123F11	2540	E1M10000263A11	3782	P1M10000107E02	5024	S1M10000026D07
57	E3M10000006G02	1299	E1M10000107B02	2541	E1M10000263H11	3783	P1M10000107H02	5025	S1M10000026F07
58	E3M10000006B03	1300	E1M10000107E02	2542	E1M10000263C12	3784	P1M10000107C03	5026	S1M10000026G07
59	E3M10000006D03	1301	E1M10000107G02	2543	E1M10000263D12	3785	P1M10000107A04	5027	S1M10000026H07
60	E3M10000006F04	1302	E1M10000107B03	2544	E1M10000264B02	3786	P1M10000107C04	5028	S1M10000026A08
61	E3M10000006G04	1303	E1M10000107C03	2545	E1M10000264C02	3787	P1M10000107C09	5029	S1M10000026C08
62	E3M10000006H09	1304	E1M10000107H04	2546	E1M10000264F02	3788	P1M10000107C10	5030	S1M10000026D08
63	E3M10000006E11	1305	E1M10000107G08	2547	E1M10000264D03	3789	P1M10000107D10	5031	S1M10000026F08
64	E3M10000006C12	1306	E1M10000107F09	2548	E1M10000264F03	3790	P1M10000107H10	5032	S1M10000026G08
65	E3M10000006G12	1307	E1M10000107H09	2549	E1M10000264A04	3791	P1M10000108C01	5033	S1M10000026A09
66	E3M10000007F01	1308	E1M10000117C12	2550	E1M10000264B04	3792	P1M10000108A02	5034	S1M10000026E09
67	E3M10000007G01	1309	E1M10000118C04	2551	E1M10000264C04	3793	P1M10000108B02	5035	S1M10000026G09
68	E3M10000007A02	1310	E1M10000118B05	2552	E1M10000264E04	3794	P1M10000108A03	5036	S1M10000026H09
69	E3M10000007B02	1311	E1M10000118C05	2553	E1M10000264F04	3795	P1M10000108D04	5037	S1M10000026A10

SeqID	Clone Name	SeqID	Clone Name	SeqID	Clone Name	SeqID	Clone Name	SeqID	Clone Name
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71	E3M10000007C03	1313	E1M10000119D02	2555	E1M10000264B06	3797	P1M10000108E05	5039	S1M10000026D10
72	E3M10000007D03	1314	E1M10000119D03	2556	E1M10000264G09	3798	P1M10000108F05	5040	S1M10000026E10
73	E3M10000007H03	1315	E1M10000119A04	2557	E1M10000264D11	3799	P1M10000108F06	5041	S1M10000026F10
74	E3M10000007C04	1316	E1M10000131H01	2558	E1M10000264F11	3800	P1M10000108G06	5042	S1M10000026G10
75	E3M10000007E05	1317	E1M10000131F04	2559	E1M10000264H11	3801	P1M10000109A02	5043	S1M10000026H10
76	E3M10000007F06	1318	E1M10000131C06	2560	E1M10000264B12	3802	P1M10000109C03	5044	S1M10000026A11
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81	E3M10000008C08	1323	E1M10000135B02	2565	E1M10000265D04	3807	P1M10000109H09	5049	S1M10000026C12
82	E3M10000008D08	1324	E1M10000132C01	2566	E1M10000265F04	3808	P1M10000109E10	5050	S1M10000026D12
83	E3M10000008C09	1325	E1M10000132F02	2567	E1M10000265E05	3809	P1M10000109F10	5051	S1M10000026E12
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86	E3M10000009E02	1328	E1M10000133A06	2570	E1M10000265E09	3812	S4M10000001C01	5054	S1M10000027G01
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104	E3M10000011A09	1346	E1M10000124G04	2588	E1M10000267H07	3830	S4M10000010D08	5072	S1M10000027G05
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114	E3M10000012G07	1356	E1M10000120A06	2598	E1M10000268F03	3840	S4M10000011F10	5082	S1M10000027D07
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118	E3M10000013D02	1360	E1M10000136C01	2602	E1M10000268E07	3844	S4M10000012B12	5086	S1M10000027A08
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131	E3M10000014B12	1373	E1M10000126E08	2615	E1M10000269D01	3857	S4M10000022B05	5099	S1M10000027G09
132	E3M10000014E12	1374	E1M10000126F12	2616	E1M10000269B02	3858	S4M10000022G07	5100	S1M10000027H09
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138	E3M10000016A04	1380	E1M10000137E07	2622	E1M10000269H05	3864	S4M10000024F08	5106	S1M10000027E11
139	E3M10000016G05	1381	E1M10000137B08	2623	E1M10000269A06	3865	S4M10000024G09	5107	S1M10000027G11
140	E3M10000016H05	1382	E1M10000137G09	2624	E1M10000269E07	3866	S4M10000024C11	5108	S1M10000027H11
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176	E3M10000022C06	1418	E1M10000153H03	2660	E1M10000273E01	3902	S4M10000037A08	5144	S1M10000028H07
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212	E3M10000025B01	1454	E1M10000163H01	2696	E1M10000275E05	3938	S1M10000002F02	5180	S1M100000029C07
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216	E3M10000025C04	1458	E1M10000163B12	2700	E1M10000275A08	3942	S1M10000002B04	5184	S1M10000029H08
217	E3M10000025F04	1459	E1M10000164A02	2701	E1M10000275D08	3943	S1M10000002B05	5185	S1M10000029A09
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227	E3M10000025F08	1469	E1M10000159F03	2711	E1M10000276B03	3953	S1M10000002G08	5195	S1M10000029F10
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292	E3M10000028A08	1534	E1M10000189H05	2776	E1M10000315G01	4018	S1M100000004E04	5260	S1M100000031F02
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363	E3M10000030B04	1605	E1M10000195G03	2847	E1M10000280C05	4089	S1M10000006A03	5331	S1M10000032D07
364	E3M10000030C04	1606	E1M10000195A04	2848	E1M10000280E05	4090	S1M10000006B03	5332	S1M10000032F07
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367	E3M10000030H04	1609	E1M10000195E07	2851	E1M10000280H06	4093	S1M10000006F03	5335	S1M10000032B08
368	E3M10000030A05	1610	E1M10000195A08	2852	E1M10000280A07	4094	S1M10000006G03	5336	S1M10000032D08
369	E3M10000030B05	1611	E1M10000195E09	2853	E1M10000280C07	4095	S1M10000006A04	5337	S1M10000032E08
370	E3M10000030D05	1612	E1M10000195D10	2854	E1M10000280G07	4096	S1M10000006B04	5338	S1M10000032G08
371	E3M10000030E05	1613	E1M10000195E10	2855	E1M10000280E08	4097	S1M10000006C04	5339	S1M10000032B09
372	E3M10000030B06	1614	E1M10000195D11	2856	E1M10000280F08	4098	S1M10000006E04	5340	S1M10000032C09
373	E3M10000030D06	1615	E1M10000195F11	2857	E1M10000280C09	4099	S1M10000006F04	5341	S1M10000032D09
374	E3M10000030F06	1616	E1M10000196B02	2858	E1M10000280H09	4100	S1M10000006G04	5342	S1M10000032E09
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376	E3M10000030H06	1618	E1M10000196E02	2860	E1M10000280C11	4102	S1M10000006D05	5344	S1M10000032A10
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387	E3M10000030D09	1629	E1M10000196H07	2871	E1M10000281B10	4113	S1M10000006G07	5355	S1M10000032H11
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389	E3M10000030G09	1631	E1M10000196A10	2873	E1M10000281G11	4115	S1M10000006E08	5357	S1M10000032C12
390	E3M10000030B10	1632	E1M10000196B10	2874	E1M10000281D12	4116	S1M10000006A10	5358	S1M10000032E12
391	E3M10000030D10	1633	E1M10000196D11	2875	E1M10000281F12	4117	S1M10000006B10	5359	S1M10000032F12
392	E3M10000030E10	1634	E1M10000196D12	2876	E1M10000282D01	4118	S1M10000006C10	5360	S1M10000032G12
393	E3M10000030F10	1635	E1M10000197E02	2877	E1M10000282F01	4119	S1M10000006G10	5361	S1M10000033H01

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396	E3M10000030B11	1638	E1M10000197D04	2880	E1M10000282F03	4122	S1M10000006A12	5364	S1M10000033D02
397	E3M10000030H11	1639	E1M10000197B05	2881	E1M10000282C04	4123	S1M10000006B12	5365	S1M10000033F02
398	E3M10000030B12	1640	E1M10000197E07	2882	E1M10000282E04	4124	S1M10000007F01	5366	S1M10000033H02
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405	E3M10000031B02	1647	E1M10000197G10	2889	E1M10000282B08	4131	S1M10000007C04	5373	S1M10000033D05
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407	E3M10000031B03	1649	E1M10000197A11	2891	E1M10000282E08	4133	S1M10000007F04	5375	S1M10000033D06
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409	E3M10000031E03	1651	E1M10000197B12	2893	E1M10000282G08	4135	S1M10000007G05	5377	S1M10000033A07
410	E3M10000031G03	1652	E1M10000198C02	2894	E1M10000282H08	4136	S1M10000007C06	5378	S1M10000033B07
411	E3M10000031B04	1653	E1M10000198B03	2895	E1M10000282A09	4137	S1M10000007D06	5379	S1M10000033F07
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413	E3M10000031D04	1655	E1M10000198F04	2897	E1M10000282C11	4139	S1M10000007C07	5381	S1M10000033H07
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432	E3M10000031B09	1674	E1M10000199G09	2916	E1M10000283F08	4158	S1M10000008B04	5400	S1M10000033G12
433	E3M10000031E09	1675	E1M10000199H09	2917	E1M10000283B10	4159	S1M10000008D05	5401	S1M10000034B01
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436	E3M10000031C10	1678	E1M10000199F10	2920	E1M10000283E12	4162	S1M10000008B06	5404	S1M10000034F01
437	E3M10000031H10	1679	E1M10000199D11	2921	E1M10000302F01	4163	S1M10000008F06	5405	S1M10000034H01
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462	E3M100000332B05	1704	E1M10000201D06	2946	E1M10000304H02	4188	S1M10000009E02	5430	S1M10000034H06
463	E3M100000332E05	1705	E1M10000201G06	2947	E1M10000304A03	4189	S1M10000009F02	5431	S1M10000034B07
464	E3M100000332F05	1706	E1M10000201H07	2948	E1M10000304C03	4190	S1M10000009G02	5432	S1M10000034C07
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500	E3M10000033B02	1742	E1M10000205D08	2984	E1M10000307E05	4226	S1M10000009G09	5468	S1M10000035D01
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795	E3M10000038G11	2037	E1M10000226D09	3279	E1M10000300G09	4521	S1M10000016E05	5763	S1M10000040H08
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799	E3M10000039B01	2041	E1M10000226G11	3283	E1M10000301C06	4525	S1M10000016B06	5767	S1M10000040C10
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864	E3M10000040C05	2106	E1M10000235H09	3348	E1M10000284A03	4590	S1M10000017A11	5832	S1M10000042C06
865	E3M10000040G05	2107	E1M10000235B10	3349	E1M10000284B03	4591	S1M10000017B11	5833	S1M10000042E06
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869	E3M10000040A07	2111	E1M10000236A02	3353	E1M10000284D06	4595	S1M10000017A12	5837	S1M10000042D07
870	E3M10000040C07	2112	E1M10000236E02	3354	E1M10000284H06	4596	S1M10000017B12	5838	S1M10000042H07
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1004	E3M10000043A02	2246	E1M10000245B04	3488	P1M10000040E10	4730	S1M10000020B06	5972	S1M10000045E04
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1081	E3M10000050H07	2323	E1M10000249E10	3565	P1M10000066A10	4807	S1M10000021F11	6049	S1M10000046A09
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1084	E3M10000050F08	2326	E1M10000250F02	3568	P1M10000067E01	4810	S1M10000021E12	6052	S1M10000046F09
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1088	E3M10000050G09	2330	E1M10000250A04	3572	P1M10000067F05	4814	S1M10000022B02	6056	S1M10000046F10
1089	E3M10000050H09	2331	E1M10000250E04	3573	P1M10000067G05	4815	S1M10000022C02	6057	S1M10000046G10
1090	E3M10000050B10	2332	E1M10000250H04	3574	P1M10000067A06	4816	S1M10000022A03	6058	S1M10000046H10
1091	E3M10000051C01	2333	E1M10000250A05	3575	P1M10000067C06	4817	S1M10000022B03	6059	S1M10000046A11
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1095	E3M10000051H03	2337	E1M10000250G09	3579	P1M10000068F04	4821	S1M10000022G03	6063	S1M10000046A12
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1097	E3M10000051B04	2339	E1M10000250E10	3581	P1M10000068F08	4823	S1M10000022C04	6065	S1M10000046C12
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1108	E3M10000051F07	2350	E1M10000251B08	3592	P1M10000070D08	4834	S1M10000022F06	6076	S1M10000047F02
1109	E3M10000051A08	2351	E1M10000251H08	3593	P1M10000070B10	4835	S1M10000022H06	6077	S1M10000047G02
1110	E3M10000051B08	2352	E1M10000251H09	3594	P1M10000070G12	4836	S1M10000022B07	6078	S1M10000047A03
1111	E3M10000051D08	2353	E1M10000251C10	3595	P1M10000071B01	4837	S1M10000022C07	6079	S1M10000047C03
1112	E3M10000051H08	2354	E1M10000251F11	3596	P1M10000071C01	4838	S1M10000022D07	6080	S1M10000047D03
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1116	E3M10000051E09	2358	E1M10000251F12	3600	P1M10000073G03	4842	S1M10000022A08	6084	S1M10000047H03
1117	E3M10000051G09	2359	E1M10000252D01	3601	P1M10000073D04	4843	S1M10000022B08	6085	S1M10000047A04
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1119	E3M10000051A10	2361	E1M10000252C03	3603	P1M10000073D09	4845	S1M10000022D08	6087	S1M10000047C04
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1121	E3M10000051D10	2363	E1M10000252B04	3605	P1M10000074B01	4847	S1M10000022G08	6089	S1M10000047E04
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1126	E3M10000051D11	2368	E1M10000252D06	3610	P1M10000074G12	4852	S1M10000022B11	6094	S1M10000047B05
1127	E3M10000051E11	2369	E1M10000252A07	3611	P1M10000075F02	4853	S1M10000022C11	6095	S1M10000047C05
1128	E3M10000051F11	2370	E1M10000252H07	3612	P1M10000075B03	4854	S1M10000022D11	6096	S1M10000047D05
1129	E3M10000051G11	2371	E1M10000252A09	3613	P1M10000075A04	4855	S1M10000022F11	6097	S1M10000047E05
1130	E3M10000051F12	2372	E1M10000252E09	3614	P1M10000075C04	4856	S1M10000022H11	6098	S1M10000047F05
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1132	E3M10000050G01	2374	E1M10000252D10	3616	P1M10000075G05	4858	S1M10000022B12	6100	S1M10000047H05
1133	E3M10000050B03	2375	E1M10000252E10	3617	P1M10000076D05	4859	S1M10000022G12	6101	S1M10000047A06
1134	E3M10000050C03	2376	E1M10000252E11	3618	P1M10000076C08	4860	S1M10000023B01	6102	S1M10000047B06
1135	E3M10000050D03	2377	E1M10000252E12	3619	P1M10000076D10	4861	S1M10000023D01	6103	S1M10000047C06
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1139	E3M10000050H08	2381	E1M10000253D04	3623	P1M10000077C08	4865	S1M10000023G02	6107	S1M10000047A07
1140	E3M10000052C01	2382	E1M10000253F04	3624	P1M10000096F01	4866	S1M10000023H02	6108	S1M10000047C07
1141	E3M10000052F01	2383	E1M10000253H05	3625	P1M10000096E04	4867	S1M10000023B03	6109	S1M10000047D07
1142	E3M10000052C02	2384	E1M10000253D08	3626	P1M10000096E12	4868	S1M10000023D03	6110	S1M10000047F07
1143	E3M10000052D02	2385	E1M10000253E08	3627	P1M10000097G05	4869	S1M10000023G03	6111	S1M10000047G07
1144	E3M10000052G02	2386	E1M10000253A09	3628	P1M10000059B04	4870	S1M10000023D04	6112	S1M10000047H07
1145	E3M10000052B03	2387	E1M10000253D09	3629	P1M10000059H08	4871	S1M10000023E04	6113	S1M10000047A08
1146	E3M10000052E03	2388	E1M10000253E09	3630	P1M10000059H09	4872	S1M10000023F04	6114	S1M10000047B08
1147	E3M10000052G03	2389	E1M10000253F09	3631	P1M10000059B10	4873	S1M10000023A05	6115	S1M10000047C08
1148	E3M10000052B04	2390	E1M10000253G09	3632	P1M10000059B11	4874	S1M10000023D05	6116	S1M10000047E08
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1152	E3M10000052D05	2394	E1M10000253B11	3636	P1M10000060H04	4878	S1M10000023B07	6120	S1M10000047A09
1153	E3M10000052F05	2395	E1M10000253F11	3637	P1M10000079D01	4879	S1M10000023D07	6121	S1M10000047B09
1154	E3M10000052G05	2396	E1M10000253D12	3638	P1M10000079F06	4880	S1M10000023E07	6122	S1M10000047C09
1155	E3M10000052G06	2397	E1M10000253G12	3639	P1M10000079A10	4881	S1M10000023F07	6123	S1M10000047D09
1156	E3M10000052H06	2398	E1M10000254A03	3640	P1M10000079B10	4882	S1M10000023G07	6124	S1M10000047E09
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1163	E3M10000052D12	2405	E1M10000254B06	3647	P1M10000080C06	4889	S1M10000023B09	6131	S1M10000047E10
1164	1008-H20	2406	E1M10000254A07	3648	P1M10000081G05	4890	S1M10000023D09	6132	S1M10000047F10
1165	1011-P20	2407	E1M10000254E07	3649	P1M10000081H05	4891	S1M10000023G09	6133	S1M10000047G10
1166	1053-37	2408	E1M10000254G07	3650	P1M10000081A06	4892	S1M10000023H09	6134	S1M10000047H10
1167	1010-C11	2409	E1M10000254A08	3651	P1M10000081D12	4893	S1M10000023B10	6135	S1M10000047A11
1168	1017-H1	2410	E1M10000254B09	3652	P1M10000082A02	4894	S1M10000023C10	6136	S1M10000047B11
1169	1067-16	2411	E1M10000254F10	3653	P1M10000082B04	4895	S1M10000023D10	6137	S1M10000047C11
1170	1083-27	2412	E1M10000254A11	3654	P1M10000082A05	4896	S1M10000023E10	6138	S1M10000047E11
1171	1065-12	2413	E1M10000254C11	3655	P1M10000082C05	4897	S1M10000023F10	6139	S1M10000047F11
1172	221-41	2414	E1M10000254E12	3656	P1M10000082D05	4898	S1M10000023H10	6140	S1M10000047H11
1173	B17-6.O10	2415	E1M10000255C01	3657	P1M10000082E05	4899	S1M10000023A11	6141	S1M10000047A12
1174	910-B20	2416	E1M10000255G02	3658	P1M10000083B01	4900	S1M10000023B11	6142	S1M10000047B12
1175	B18-2.N21	2417	E1M10000255H02	3659	P1M10000083A11	4901	S1M10000023C11	6143	S1M10000047C12
1176	971-B20	2418	E1M10000255A04	3660	P1M10000083B12	4902	S1M10000023E11	6144	S1M10000047D12
1177	D1-1.A15	2419	E1M10000255D05	3661	P1M10000083C12	4903	S1M10000023F11	6145	S1M10000047E12
1178	4-28.1	2420	E1M10000255F06	3662	P1M10000084D03	4904	S1M10000023G11	6146	S1M10000047F12
1179	D1-2.B13	2421	E1M10000255G06	3663	P1M10000084A04	4905	S1M10000023A12	6147	S1M10000048C01
1180	D1-2.P21	2422	E1M10000255B08	3664	P1M10000084E04	4906	S1M10000023B12	6148	S1M10000048D01
1181	Z56-D2	2423	E1M10000255D09	3665	P1M10000084F08	4907	S1M10000023C12	6149	S1M10000048G01
1182	PJMF55	2424	E1M10000255F09	3666	P1M10000084E11	4908	S1M10000023D12	6150	S1M10000048H01
1183	R1-15.A13	2425	E1M10000255B10	3667	P1M10000085D06	4909	S1M10000023F12	6151	S1M10000048A02
1184	R1-19.H1	2426	E1M10000256F01	3668	P1M10000086B01	4910	S1M10000024D01	6152	S1M10000048B02
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1188	E1M10000007B04	2430	E1M10000256C05	3672	P1M10000086E05	4914	S1M10000024F02	6156	S1M10000048F02
1189	227-10	2431	E1M10000256E07	3673	P1M10000087E04	4915	S1M10000024H02	6157	S1M10000048G02
1190	709-F23	2432	E1M10000256E09	3674	P1M10000087F04	4916	S1M10000024D03	6158	S1M10000048H02
1191	801-C15	2433	E1M10000256A10	3675	P1M10000087C09	4917	S1M10000024E03	6159	S1M10000048A03
1192	801-H19	2434	E1M10000256F10	3676	P1M10000087F09	4918	S1M10000024F03	6160	S1M10000048B03
1193	804-P6	2435	E1M10000256C12	3677	P1M10000087A11	4919	S1M10000024A04	6161	S1M10000048C03
1194	807-D20	2436	E1M10000257C01	3678	P1M10000088C04	4920	S1M10000024C04	6162	S1M10000048E03
1195	B13-17.G8	2437	E1M10000257G01	3679	P1M10000088A07	4921	S1M10000024D04	6163	S1M10000048F03
1196	B5-6.C8	2438	E1M10000257A02	3680	P1M10000089G08	4922	S1M10000024H04	6164	S1M10000048G03
1197	B8-2.D9	2439	E1M10000257D02	3681	P1M10000089D11	4923	S1M10000024B05	6165	S1M10000048H03
1198	B15-8.P13	2440	E1M10000257H02	3682	P1M10000090E01	4924	S1M10000024E05	6166	S1M10000048E04
1199	T13-5.A2	2441	E1M10000257C03	3683	P1M10000090F06	4925	S1M10000024F05	6167	S1M10000048G04
1200	T12-3.I11	2442	E1M10000257F04	3684	P1M10000090F08	4926	S1M10000024G05	6168	S1M10000048H04
1201	T20-15.D4	2443	E1M10000257G04	3685	P1M10000090B11	4927	S1M10000024B06	6169	S1M10000048A05
1202	T24-15.G6	2444	E1M10000257B05	3686	P1M10000091A09	4928	S1M10000024E06	6170	S1M10000048B05
1203	T24-17.C6	2445	E1M10000257D05	3687	P1M10000091E09	4929	S1M10000024G06	6171	S1M10000048C05
1204	244.B12	2446	E1M10000257F06	3688	P1M10000091G10	4930	S1M10000024H06	6172	S1M10000048F05
1205	1042-J1	2447	E1M10000257G07	3689	P1M10000092B02	4931	S1M10000024A07	6173	S1M10000048G05
1206	195.F5	2448	E1M10000257H07	3690	P1M10000092E02	4932	S1M10000024C07	6174	S1M10000048H05
1207	25.D5	2449	E1M10000257H08	3691	P1M10000092B04	4933	S1M10000024E07	6175	S1M10000048A06
1208	25.D6	2450	E1M10000257A09	3692	P1M10000092F05	4934	S1M10000024G07	6176	S1M10000048B06
1209	177.F3	2451	E1M10000257D09	3693	P1M10000092F06	4935	S1M10000024H07	6177	S1M10000048C06
1210	525.H11	2452	E1M10000257G10	3694	P1M10000092D09	4936	S1M10000024A08	6178	S1M10000048E06
1211	632.N2	2453	E1M10000257H10	3695	P1M10000092B10	4937	S1M10000024B08	6179	S1M10000048A07
1212	633.B7	2454	E1M10000257A11	3696	P1M10000092B12	4938	S1M10000024E08	6180	S1M10000048C07
1213	671.I20	2455	E1M10000257C11	3697	P1M10000093A03	4939	S1M10000024F08	6181	S1M10000048E07
1214	676.B12	2456	E1M10000257F11	3698	P1M10000093B03	4940	S1M10000024G08	6182	S1M10000048F07
1215	643.B19	2457	E1M10000257B12	3699	P1M10000093F03	4941	S1M10000024H08	6183	S1M10000048G07
1216	720.O16	2458	E1M10000257F12	3700	P1M10000093H07	4942	S1M10000024B09	6184	S1M10000048H07
1217	666.H12	2459	E1M10000258C01	3701	P1M10000093C08	4943	S1M10000024B10	6185	S1M10000048B08
1218	98.D4	2460	E1M10000258H02	3702	P1M10000093B09	4944	S1M10000024D10	6186	S1M10000048C08
1219	844.B21	2461	E1M10000258G03	3703	P1M10000093E09	4945	S1M10000024F10	6187	S1M10000048D08
1220	P31-25.F3	2462	E1M10000258A04	3704	P1M10000094H03	4946	S1M10000024G10	6188	S1M10000048E08
1221	P335-8.H8	2463	E1M10000258C04	3705	P1M10000094F04	4947	S1M10000024A11	6189	S1M10000048F08

SeqID	Clone Name	SeqID	Clone Name	SeqID	Clone Name	SeqID	Clone Name	SeqID	Clone Name
1222	P347.2	2464	E1M10000258G04	3706	P1M10000094H04	4948	S1M10000024D11	6190	S1M10000048H08
1223	P31-11-J20	2465	E1M10000258C05	3707	P1M10000094A10	4949	S1M10000024G12	6191	S1M10000048A09
1224	P336-14.F20	2466	E1M10000258D05	3708	P1M10000095C01	4950	S1M10000025B01	6192	S1M10000048C09
1225	P31-27-M1	2467	E1M10000258F05	3709	P1M10000095E04	4951	S1M10000025C01	6193	S1M10000048D09
1226	P338-4.M21	2468	E1M10000258G05	3710	P1M10000095G04	4952	S1M10000025D01	6194	S1M10000048E09
1227	P334-8.L7	2469	E1M10000258A06	3711	P1M10000095C09	4953	S1M10000025E01	6195	S1M10000048F09
1228	P31-2-E16	2470	E1M10000258D06	3712	P1M10000102E05	4954	S1M10000025B02	6196	S1M10000048H09
1229	P335-3.J14	2471	E1M10000258B07	3713	P1M10000102B07	4955	S1M10000025A03	6197	S1M10000048A10
1230	P334-5.H2	2472	E1M10000258G07	3714	P1M10000103B05	4956	S1M10000025B03	6198	S1M10000048B10
1231	P31-33-N2	2473	E1M10000258G08	3715	P1M10000103D06	4957	S1M10000025C03	6199	S1M10000048C10
1232	P332-11.C20	2474	E1M10000258B09	3716	P1M10000103E08	4958	S1M10000025D03	6200	S1M10000048D10
1233	869.A23	2475	E1M10000258D09	3717	P1M10000104A02	4959	S1M10000025F03	6201	S1M10000048E10
1234	P317-2.A3	2476	E1M10000258F10	3718	P1M10000104H02	4960	S1M10000025D04	6202	S1M10000048G10
1235	P326-9.K2	2477	E1M10000258C11	3719	P1M10000104A03	4961	S1M10000025E04	6203	S1M10000048H10
1236	P323-8.P1	2478	E1M10000258F11	3720	P1M10000104E03	4962	S1M10000025G04	6204	S1M10000048A11
1237	P35-8	2479	E1M10000259C03	3721	P1M10000104F07	4963	S1M10000025B05	6205	S1M10000048C11
1238	P36-13.E2	2480	E1M10000259B04	3722	P1M10000104D11	4964	S1M10000025C05	6206	S1M10000048D11
1239	P38-1.G20	2481	E1M10000259E04	3723	P1M10000105D01	4965	S1M10000025F05	6207	S1M10000048F11
1240	P327-50.M10	2482	E1M10000259E05	3724	P1M10000105E02	4966	S1M10000025H05	6208	S1M10000048G11
1241	P328-8.D21	2483	E1M10000259B12	3725	P1M10000105C03	4967	S1M10000025B06	6209	S1M10000048H11
1242	P328-20.P20	2484	E1M10000260E02	3726	P1M10000105G03	4968	S1M10000025D06	6210	S1M10000048A12

EXAMPLE 3

Comparison Of Isolated Nucleic Acids to Known Sequences

The nucleotide sequences of the subcloned fragments from *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* and *Salmonella typhimurium* obtained from the expression vectors discussed above were compared to known sequences from *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Salmonella typhimurium* and other microorganisms as follows. First, to confirm that each clone originated from one location on the chromosome and was not chimeric, the nucleotide sequences of the selected clones were compared against the *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* or *Salmonella typhimurium* genomic sequences to align the clone to the correct position on the chromosome. The NCBI BLASTN v 2.0.9 program was used for this comparison, and the incomplete *Staphylococcus aureus* genomic sequences licensed from TIGR, as well as the NCBI nonredundant GenBank database were used as the source of genomic data. *Salmonella typhimurium* sequences were compared to sequences available from the Genome Sequencing Center (<http://genome.wustl.edu/gsc/salmonella.shtml>), and the Sanger Centre (http://www.sanger.ac.uk/projects/S__typhi). *Pseudomonas aeruginosa* sequences were compared to a proprietary database and the NCBI GenBank database. The *E. faecalis* sequences were compared to a proprietary database.

The BLASTN analysis was performed using the default parameters except that the filtering was turned off. No further analysis was performed on inserts which resulted from the ligation of multiple fragments.

In general, antisense molecules and their complementary genes are identified as follows. First, all possible full length open reading frames (ORFs) are extracted from available genomic databases. Such databases include the GenBank nonredundant (nr) database, the unfinished genome database available from TIGR and the PathoSeq database developed by Incyte Genomics. The latter database comprises over 40 annotated bacterial genomes including complete ORF analysis. If databases are incomplete with regard to the bacterial genome of interest, it is not necessary to extract all ORFs in the genome but only to extract the ORFs within the portions of the available genomic sequences which are complementary to the clones of interest. Computer algorithms for identifying ORFs, such as GeneMark, are available and well known to those in the art. Comparison of the clone DNA to the complementary ORF(s) allows determination of whether the clone is a sense or antisense clone. Furthermore, each ORF extracted from the database can be compared to sequences in well annotated databases including the GenBank (nr) protein database, SWISSPROT and the like. A description of the gene or of a closely related gene in a closely related microorganism is often available in these databases. Similar methods are used to identify antisense clones corresponding to genes encoding non-translated RNAs.

In order to generate the gene identification data compiled in Table IB, each of the cloned nucleic acid sequences discussed above corresponding to SEQ ID NO.s 1-6213 was used to identify the corresponding *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* or *Salmonella typhimurium* ORFs in the PathoSeq v.4.1 (March 2000 release) database of microbial genomic sequences. For this purpose, the NCBI BLASTN 2.0.9 computer algorithm was used. The default parameters were used except that filtering was turned off. The default parameters for the BLASTN and BLASTX analyses were:

Expectation value (e)=10
 Alignment view options: pairwise
 Filter query sequence (DUST with BLASTN, SEG with others)=T
 Cost to open a gap (zero invokes behavior)=0
 Cost to extend a gap (zero invokes behavior)=0
 X dropoff value for gapped alignment (in bits) (zero invokes behavior)=0
 Show GI's in defines=F
 Penalty for a nucleotide mismatch (BLASTN only)=!3
 Reward for a nucleotide match (BLASTN only)=1
 Number of one-line descriptions (V)=500
 Number of alignments to show (B)=250
 Threshold for extending hits=default
 Perform gapped alignment (not available with BLASTX)=T
 Query Genetic code to use=1
 DB Genetic code (for TBLAST[nx] only)=1
 Number of processors to use=1
 SeqAlign file
 Believe the query define=F
 Matrix=BLOSUM62
 Word Size= default
 Effective length of the database (use zero for the real size)=0
 Number of best hits from a region to keep=100
 Length of region used to judge hits=20
 Effective length of the search space (use zero for the real size)=0
 Query strands to search against database (for BLAST[nx] and TBLASTX), 3 is both, 1 is top, 2 is bottom=3
 Produce HTML output=F

Alternatively, ORFs were identified and refined by conducting a survey of the public and private data sources. Full-length gene protein and nucleotide sequences for these organisms were assembled from various sources. For *Pseudomonas aeruginosa*, gene sequences were adopted from the *Pseudomonas* genome sequencing project (downloaded from <http://www.pseudomonas.com>). For *Klebsiella pneumoniae*, *Staphylococcus aureus*, *Streptococcus pneumoniae* and *Salmonella typhi*, genomic sequences from PathoSeq v 4.1 (Mar 2000 release) was reanalyzed for ORFs using the gene finding software GeneMark v 2.4a, which was purchased from GenePro Inc. 451 Bishop St., N.W., Suite B, Atlanta, GA, 30318, USA.

Antisense clones were identified as those clones for which transcription from the inducible promoter would result in the expression of an RNA antisense to a complementary ORF, intergenic

or intragenic sequence. Those clones containing single inserts and that caused growth sensitivity upon induction are listed in Table IA.

The gene descriptions in the PathoSeq database derive from annotations available in the public sequence databases described above. Where a clone was found to share significant sequence identity to two or more adjacent ORFs, it was listed once for each ORF and the PathoSeq information for each ORF was compiled in Table IB.

Table IA lists the SEQ ID NOs. and clone names of the inserts which inhibited proliferation. This information was used to identify the ORFs (SEQ ID NOs.: 6214-42397) whose gene products (SEQ ID NOs. 42398-78581) were inhibited by the nucleic acids comprising the nucleotide sequences of SEQ ID NOs. 1-6213. Table IB lists the clone name and the PathoSeq Locus containing the clone.

TABLE IB

Clone Name	Gene LocusID	Clone Name	Gene LocusID	Clone Name	Gene LocusID
E3M10000001B01	EFA205257	E1M10000233C05	ECO103161	S1M10000005E05	SAU802496
E3M10000001B01	EFA205258	E1M10000233H05	ECO103224	S1M10000005C06	SAU802121
E3M10000001A02	EFA205257	E1M10000233H05	ECO103225	S1M10000005D06	SAU801183
E3M10000001A02	EFA205258	E1M10000233D08	ECO103185	S1M10000005D06	SAU801184
E3M10000001B02	EFA205225	E1M10000233F08	ECO103265	S1M10000005A07	SAU800967
E3M10000001B02	EFA201977	E1M10000233F08	ECO103266	S1M10000005B07	SAU802496
E3M10000001B02	EFA203137	E1M10000233A09	ECO104092	S1M10000005D07	SAU801264
E3M10000001C02	EFA200840	E1M10000233A09	ECO104093	S1M10000005A08	SAU802496
E3M10000001D02	EFA202003	E1M10000233E09	ECO103238	S1M10000005B08	SAU800548
E3M10000001E02	EFA200840	E1M10000233E09	ECO103239	S1M10000005D08	SAU800607
E3M10000001F02	EFA200807	E1M10000233F09	ECO103886	S1M10000005E08	SAU802496
E3M10000001G02	EFA205257	E1M10000233D10	ECO103242	S1M10000005B09	SAU800122
E3M10000001G02	EFA205258	E1M10000233D10	ECO103243	S1M10000005C09	SAU801481
E3M10000001H02	EFA200811	E1M10000233H10	ECO100094	S1M10000005D09	SAU800542
E3M10000001E03	EFA201987	E1M10000234E01	ECO103884	S1M10000005A10	SAU801723
E3M10000001E03	EFA205258	E1M10000234B02	ECO103886	S1M10000005A10	SAU801722
E3M10000001G03	EFA201987	E1M10000234G02	ECO103233	S1M10000005A11	SAU801644
E3M10000001G03	EFA205258	E1M10000234G02	ECO103234	S1M10000005C11	SAU801113
E3M10000001H03	EFA201987	E1M10000234C05	ECO103181	S1M10000005D11	SAU800547
E3M10000001H03	EFA205258	E1M10000234C07	ECO103844	S1M10000005E11	SAU800155
E3M10000001D04	EFA201980	E1M10000234C08	ECO103878	S1M10000005B12	SAU802160
E3M10000001D04	EFA201981	E1M10000234C08	ECO204942	S1M10000005B12	SAU603460
E3M10000001D04	EFA205229	E1M10000234F08	ECO103461	S1M10000005D12	SAU801644
E3M10000001E04	EFA201028	E1M10000234H08	ECO103226	S1M10000006F01	SAU801264
E3M10000001F04	EFA200811	E1M10000234F09	ECO103055	S1M10000006B02	SAU800381
E3M10000001G04	EFA201993	E1M10000234D10	ECO100876	S1M10000006E02	SAU802496
E3M10000001H04	EFA201980	E1M10000234G10	ECO100886	S1M10000006F02	SAU802160
E3M10000001H04	EFA201981	E1M10000234B12	ECO104010	S1M10000006G02	SAU802125
E3M10000001H04	EFA205229	E1M10000235D01	ECO102233	S1M10000006A03	SAU802496
E3M10000001B05	EFA201993	E1M10000235A03	ECO100798	S1M10000006B03	SAU802655
E3M10000001D05	EFA201974	E1M10000235H03	ECO103886	S1M10000006D03	SAU801740
E3M10000001D05	EFA201975	E1M10000235E04	ECO103236	S1M10000006E03	SAU801256
E3M10000001G05	EFA202001	E1M10000235B06	ECO103886	S1M10000006F03	SAU801434
E3M10000001G05	EFA202003	E1M10000235F06	ECO103481	S1M10000006G03	SAU801275
E3M10000001A06	EFA201028	E1M10000235B08	ECO103885	S1M10000006A04	SAU801139
E3M10000001F06	EFA201028	E1M10000235E08	ECO103161	S1M10000006B04	SAU802496
E3M10000001B08	EFA201028	E1M10000235B09	ECO101848	S1M10000006C04	SAU802158
E3M10000001E08	EFA200807	E1M10000235H09	ECO103481	S1M10000006E04	SAU801089
E3M10000001C09	EFA200839	E1M10000235H09	ECO103482	S1M10000006F04	SAU801644
E3M10000001D09	EFA201987	E1M10000235B10	ECO100886	S1M10000006G04	SAU801740
E3M10000001D09	EFA205258	E1M10000235A11	ECO102299	S1M10000006A05	SAU802224
E3M10000001E09	EFA201987	E1M10000235F12	ECO103233	S1M10000006A05	SAU802223
E3M10000001E09	EFA205258	E1M10000235F12	ECO103234	S1M10000006D05	SAU802496
E3M10000001B10	EFA205257	E1M10000236E01	ECO100095	S1M10000006G05	SAU801256
E3M10000001B10	EFA205258	E1M10000236A02	ECO102340	S1M10000006C06	SAU800331
E3M10000004D01	EFA201985	E1M10000236E02	ECO103878	S1M10000006C06	SAU800332
E3M10000004D01	EFA201984	E1M10000236E02	ECO204942	S1M10000006D06	SAU802496
E3M10000004D01	EFA202953	E1M10000236A03	ECO103287	S1M10000006F06	SAU800548
E3M10000004G01	EFA200839	E1M10000236D03	ECO102556	S1M10000006G06	SAU800006
E3M10000004D02	EFA202022	E1M10000236G03	ECO102655	S1M10000006A07	SAU800967
E3M10000004D02	EFA202028	E1M10000236A04	ECO103186	S1M10000006B07	SAU801760

Clone Name	Gene LocusID	Clone Name	Gene LocusID	Clone Name	Gene LocusID
E3M10000004D02	EFA202536	E1M10000236D04	ECO103481	S1M10000006C07	SAU800546
E3M10000004C03	EFA200412	E1M10000236G04	ECO103510	S1M10000006D07	SAU801105
E3M10000004A04	EFA201981	E1M10000236A05	ECO102847	S1M10000006E07	SAU802496
E3M10000004A04	EFA205229	E1M10000236F05	ECO103181	S1M10000006G07	SAU801731
E3M10000004F08	EFA201977	E1M10000236F05	ECO103182	S1M10000006A08	SAU802496
E3M10000004F08	EFA203137	E1M10000236H06	ECO103242	S1M10000006E08	SAU802238
E3M10000004D10	EFA201999	E1M10000236H06	ECO103243	S1M10000006A10	SAU802496
E3M10000004D10	EFA201997	E1M10000236D08	ECO103669	S1M10000006B10	SAU802240
E3M10000004F10	EFA200624	E1M10000236F09	ECO103228	S1M10000006C10	SAU802496
E3M10000004E11	EFA200624	E1M10000236C10	ECO102227	S1M10000006G10	SAU802247
E3M10000004H11	EFA205225	E1M10000236A11	ECO102986	S1M10000006G10	SAU802248
E3M10000004H11	EFA201977	E1M10000236C11	ECO101088	S1M10000006B11	SAU801618
E3M10000004H11	EFA203137	E1M10000236F12	ECO101355	S1M10000006G11	SAU802119
E3M10000005B01	EFA201984	E1M10000237A02	ECO103161	S1M10000006G11	SAU802118
E3M10000005B01	EFA201983	E1M10000237B02	ECO101830	S1M10000006A12	SAU800548
E3M10000005C01	EFA200839	E1M10000237E04	ECO103217	S1M10000006B12	SAU802558
E3M10000005E01	EFA201977	E1M10000237E04	ECO103218	S1M10000007F01	SAU801256
E3M10000005E01	EFA203137	E1M10000237H04	ECO103624	S1M10000007B02	SAU800591
E3M10000005E02	EFA201977	E1M10000237H04	ECO103625	S1M10000007B02	SAU800592
E3M10000005E02	EFA203137	E1M10000237G06	ECO103232	S1M10000007F02	SAU801366
E3M10000005C03	EFA200811	E1M10000237G06	ECO103233	S1M10000007G02	SAU801138
E3M10000005C03	EFA200812	E1M10000237C07	ECO103886	S1M10000007A03	SAU801899
E3M10000005D03	EFA200811	E1M10000237G07	ECO103263	S1M10000007D03	SAU802496
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E3M10000005E03	EFA200812	E1M10000237A08	ECO103216	S1M10000007E04	SAU802496
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E3M10000005C04	EFA200661	E1M10000237B08	ECO101186	S1M10000007C05	SAU800547
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E3M10000005A07	EFA200812	E1M10000237B09	ECO101844	S1M10000007E07	SAU801618
E3M10000005F07	EFA200839	E1M10000237D10	ECO102060	S1M10000007G07	SAU802638
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E3M10000005B08	EFA203137	E1M10000237E11	ECO100169	S1M10000007E08	SAU800700
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E3M10000005D10	EFA201977	E1M10000238A02	ECO103514	S1M10000007F09	SAU800210
E3M10000005D10	EFA203137	E1M10000238F03	ECO101939	S1M10000007D10	SAU800537
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E3M10000006G02	EFA202214	E1M10000238F04	ECO103224	S1M10000008F01	SAU802160
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E3M10000006B03	EFA201997	E1M10000238F05	ECO100194	S1M10000008G02	SAU802643
E3M10000006D03	EFA201982	E1M10000238F05	ECO100195	S1M10000008A03	SAU802177
E3M10000006D03	EFA201981	E1M10000238D06	ECO101185	S1M10000008A03	SAU802176
E3M10000006F04	EFA200811	E1M10000238D06	ECO101186	S1M10000008B03	SAU800023
E3M10000006F04	EFA200812	E1M10000238F06	ECO103229	S1M10000008F03	SAU800753
E3M10000006G04	EFA201999	E1M10000238F06	ECO103230	S1M10000008G03	SAU802369

Clone Name	Gene LocusID	Clone Name	Gene LocusID	Clone Name	Gene LocusID
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E3M1000006H09	EFA201028	E1M10000238A07	ECO103237	S1M10000008B04	SAU802496
E3M1000006E11	EFA200811	E1M10000238A08	ECO101628	S1M10000008D05	SAU800517
E3M1000006E11	EFA200812	E1M10000238E08	ECO103237	S1M10000008D05	SAU202623
E3M1000006C12	EFA205225	E1M10000238E08	ECO103238	S1M10000008E05	SAU801183
E3M1000006C12	EFA201977	E1M10000238B09	ECO102213	S1M10000008G05	SAU800305
E3M1000006C12	EFA203137	E1M10000238G09	ECO103242	S1M10000008B06	SAU802225
E3M1000006G12	EFA201999	E1M10000238H09	ECO101324	S1M10000008F06	SAU800381
E3M1000006G12	EFA201997	E1M10000238F12	ECO100179	S1M10000008A08	SAU800195
E3M10000007F01	EFA201999	E1M10000238F12	ECO100180	S1M10000008B08	SAU801900
E3M10000007F01	EFA201997	E1M10000239B01	ECO104091	S1M10000008C08	SAU800006
E3M10000007G01	EFA201999	E1M10000239B01	ECO104092	S1M10000008E08	SAU800548
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E3M10000007A02	EFA201999	E1M10000239D02	ECO103885	S1M10000008A09	SAU800381
E3M10000007A02	EFA201997	E1M10000239C03	ECO103222	S1M10000008B09	SAU801193
E3M10000007B02	EFA201999	E1M10000239C03	ECO103223	S1M10000008C09	SAU802238
E3M10000007B02	EFA201997	E1M10000239E04	ECO104090	S1M10000008E09	SAU801698
E3M10000007B03	EFA201999	E1M10000239F04	ECO104243	S1M10000008F09	SAU802496
E3M10000007B03	EFA201997	E1M10000239F04	ECO104242	S1M10000008B10	SAU801740
E3M10000007C03	EFA201982	E1M10000239C05	ECO102827	S1M10000008E10	SAU801621
E3M10000007C03	EFA201981	E1M10000239C05	ECO102828	S1M10000008F10	SAU800537
E3M10000007D03	EFA201999	E1M10000239H05	ECO103697	S1M10000008F11	SAU802502
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E3M10000051D10	EFA202006	E1M10000290G01	ECO103886	S1M10000029C03	SAU600582
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E3M10000050E04	EFA201999	E1M10000291B02	ECO103878	S1M10000029D09	SAU801113
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E3M10000052C02	EFA200805	E1M10000291A03	ECO103238	S1M10000029A10	SAU202623
E3M10000052D02	EFA202170	E1M10000291B04	ECO103237	S1M10000029B10	SAU801790
E3M10000052G02	EFA200457	E1M10000291B04	ECO103238	S1M10000029C10	SAU800529
E3M10000052B03	EFA200239	E1M10000291E04	ECO100967	S1M10000029D10	SAU801790
E3M10000052E03	EFA202378	E1M10000291E05	ECO103223	S1M10000029E10	SAU801139
E3M10000052G03	EFA200326	E1M10000291G05	ECO102555	S1M10000029F10	SAU800266
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1008-H20	ECO100023	E1M10000291B12	ECO103882	S1M10000030H02	SAU802452
1011-P20	ECO100702	E1M10000291F12	ECO103243	S1M10000030B03	SAU802654
1053-37	ECO101256	E1M10000293B01	ECO103885	S1M10000030C03	SAU800275
1053-37	ECO202228	E1M10000293B02	ECO104093	S1M10000030D03	SAU801473
1010-C11	ECO101324	E1M10000293G02	ECO103886	S1M10000030G03	SAU800542
1017-H1	ECO304472	E1M10000293A04	ECO100402	S1M10000030H03	SAU800232
1067-16	ECO102309	E1M10000293B04	ECO103886	S1M10000030C04	SAU800526
1083-27	ECO102636	E1M10000293A05	ECO100095	S1M10000030A05	SAU800478
1065-12	ECO102557	E1M10000293E05	ECO103223	S1M10000030B05	SAU801256
221-41	ECO103884	E1M10000293E05	ECO103224	S1M10000030C05	SAU800526
B17-6.O10	ECO103884	E1M10000293G05	ECO103243	S1M10000030D05	SAU800759
910-B20	ECO103884	E1M10000293A06	ECO101175	S1M10000030D05	SAU302793
B18-2.N21	ECO100148	E1M10000293H06	ECO102654	S1M10000030G05	SAU800776
971-B20	ECO103240	E1M10000293F07	ECO101095	S1M10000030G05	SAU800777
971-B20	ECO103241	E1M10000293C08	ECO101844	S1M10000030H05	SAU800179
D1-1.A15	ECO103394	E1M10000293E08	ECO101939	S1M10000030D06	SAU800189
4-28.1	ECO101485	E1M10000293G08	ECO103101	S1M10000030E06	SAU801257
D1-2.B13	ECO102255	E1M10000293B09	ECO103181	S1M10000030B07	SAU802627
D1-2.P21	ECO102144	E1M10000293G09	ECO102144	S1M10000030D07	SAU800189
Z56-D2	ECO103911	E1M10000293H09	ECO100094	S1M10000030G07	SAU802247
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R1-15.A13	ECO101995	E1M10000293E11	ECO103242	S1M10000030F08	SAU802231
R1-19.H1	ECO101104	E1M10000293F11	ECO104091	S1M10000030F08	SAU802230
R1-55.M2	ECO103884	E1M10000293F11	ECO104092	S1M10000030G08	SAU802250
Z45-F11	ECO103263	E1M10000293C12	ECO100170	S1M10000030A09	SAU801719
Z8-B9	ECO102033	E1M10000293D12	ECO103221	S1M10000030B09	SAU802654
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227-10	ECO102562	E1M10000295D01	ECO103229	S1M10000030D09	SAU801139
709-F23	ECO101506	E1M10000295G01	ECO103532	S1M10000030F09	SAU801904
801-C15	ECO100488	E1M10000295G01	ECO103533	S1M10000030G09	SAU800542
801-C15	ECO100490	E1M10000295B02	ECO101635	S1M10000030H09	SAU801644
801-C15	ECO100491	E1M10000295E02	ECO103217	S1M10000030A10	SAU802309
801-H19	ECO100488	E1M10000295E02	ECO103218	S1M10000030A10	SAU802308
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807-D20	ECO100366	E1M10000295B07	ECO100179	S1M10000030G10	SAU800019
807-D20	ECO100367	E1M10000295B07	ECO100180	S1M10000030H10	SAU802654
B13-17.G8	ECO101111	E1M10000295C07	ECO103224	S1M10000030A11	SAU800517
B5-6.C8	ECO101475	E1M10000295C07	ECO103225	S1M10000030A11	SAU202623
B5-6.C8	ECO101476	E1M10000295C07	ECO103226	S1M10000030D11	SAU800517
B5-6.C8	ECO201962	E1M10000295D08	ECO103225	S1M10000030D11	SAU202623
B8-2.D9	ECO103461	E1M10000295D08	ECO103226	S1M10000030E11	SAU802241
B15-8.P13	ECO101328	E1M10000295F08	ECO103160	S1M10000030G11	SAU800811
B15-8.P13	ECO101329	E1M10000295G08	ECO103217	S1M10000030C12	SAU801647
T13-5.A2	ECO103059	E1M10000295G08	ECO103218	S1M10000030C12	SAU801646
T12-3.I11	ECO102857	E1M10000295B09	ECO103236	S1M10000030E12	SAU800537
T20-15.D4	ECO101475	E1M10000295F09	ECO103881	S1M10000030G12	SAU801526
T20-15.D4	ECO101476	E1M10000295F09	ECO103882	S1M10000031B01	SAU802240
T20-15.D4	ECO201962	E1M10000295G09	ECO103263	S1M10000031H01	SAU800023
T24-15.G6	ECO103059	E1M10000295D10	ECO103101	S1M10000031B02	SAU802247
T24-17.C6	ECO102857	E1M10000295H10	ECO103263	S1M10000031E02	SAU801912
244.B12	ECO101763	E1M10000295B11	ECO103229	S1M10000031F02	SAU802231
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1042-J1	ECO100702	E1M10000312D11	ECO104091	S1M10000031G02	SAU802234
1042-J1	ECO100703	E1M10000312D11	ECO104092	S1M10000031H02	SAU801355
195.F5	ECO102842	E1M10000296B01	ECO102304	S1M10000031A03	SAU802250
25.D5	ECO103059	E1M10000296C02	ECO102466	S1M10000031E03	SAU801134
25.D6	ECO103059	E1M10000296C02	ECO102467	S1M10000031E03	SAU801135
177.F3	ECO102309	E1M10000296D02	ECO103235	S1M10000031F03	SAU802240
525.H11	ECO102857	E1M10000296D02	ECO103236	S1M10000031G03	SAU801505
632.N2	ECO104277	E1M10000296D02	ECO103237	S1M10000031A04	SAU801434
633.B7	ECO103479	E1M10000296H02	ECO102556	S1M10000031A04	SAU302892
671.I20	ECO103478	E1M10000296C03	ECO100150	S1M10000031B04	SAU800543
676.B12	ECO103479	E1M10000296C03	ECO100151	S1M10000031C04	SAU800738
643.B19	ECO100702	E1M10000296E03	ECO101086	S1M10000031C04	SAU800737
720.O16	ECO103884	E1M10000296H03	ECO103227	S1M10000031E04	SAU800542
666.H12	ECO103478	E1M10000296H03	ECO103228	S1M10000031F04	SAU801517
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98.D4	ECO103263	E1M10000296G04	ECO102144	S1M10000031G04	SAU302611
844.B21	ECO102144	E1M10000296F05	ECO103886	S1M10000031G04	SAU302882
P31-25-F3	ECO101686	E1M10000296G05	ECO101467	S1M10000031F05	SAU800548
P335-8.H8	ECO101041	E1M10000296H05	ECO103094	S1M10000031D06	SAU801526
P347.2	ECO101086	E1M10000296A06	ECO100194	S1M10000031G06	SAU800548
P31-11-J20	ECO103228	E1M10000296A06	ECO100195	S1M10000031H06	SAU600582
P336-14.F20	ECO101370	E1M10000296G07	ECO102827	S1M10000031C07	SAU801760
P31-27-M1	ECO103423	E1M10000296G07	ECO102828	S1M10000031D07	SAU801181
P338-4.M21	ECO100139	E1M10000296H07	ECO103220	S1M10000031E07	SAU800016
P334-8.L7	ECO101256	E1M10000296H07	ECO103221	S1M10000031A08	SAU802365
P31-2-E16	ECO101686	E1M10000296E08	ECO100886	S1M10000031D08	SAU801790
P335-3.J14	ECO100523	E1M10000296F08	ECO103218	S1M10000031E08	SAU800547
P334-5.H2	ECO100139	E1M10000296G08	ECO103734	S1M10000031F08	SAU801264
P31-33-N2	ECO103241	E1M10000296H08	ECO100809	S1M10000031C09	SAU801193
P332-11.C20	ECO102827	E1M10000296H08	ECO100810	S1M10000031D09	SAU800019
P332-11.C20	ECO102828	E1M10000296A09	ECO100194	S1M10000031G09	SAU800006
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P326-9.K2	ECO103293	E1M10000296F12	ECO101684	S1M10000031E10	SAU800001
P323-8.P1	ECO101685	E1M10000296G12	ECO100095	S1M10000031F10	SAU800244
P35-8	ECO103692	E1M10000298C01	ECO101438	S1M10000031G10	SAU800962
P36-13.E2	ECO103059	E1M10000298G01	ECO104148	S1M10000031A11	SAU801741
P38-1.G20	ECO102227	E1M10000298G01	ECO104149	S1M10000031B11	SAU801908
P327-50.M10	ECO103242	E1M10000298G02	ECO102636	S1M10000031C11	SAU802152
P327-50.M10	ECO103243	E1M10000298C03	ECO103238	S1M10000031F11	SAU800312
P328-8.D21	ECO103240	E1M10000298C03	ECO103239	S1M10000031G11	SAU801234
P328-8.D21	ECO103241	E1M10000298D03	ECO103886	S1M10000031H11	SAU800962
P328-20.P20	ECO100541	E1M10000298H03	ECO103262	S1M10000031B12	SAU801621
P33-1.C22	ECO103227	E1M10000298H03	ECO103878	S1M10000031C12	SAU801741
X3S107-17	ECO101475	E1M10000298H03	ECO204942	S1M10000031E12	SAU801275
X3S107-17	ECO101476	E1M10000298E04	ECO100430	S1M10000031F12	SAU800244
X3S107-17	ECO201962	E1M10000298E04	ECO100431	S1M10000032B01	SAU802654
P35-7	ECO103928	E1M10000298H04	ECO100809	S1M10000032C01	SAU800548
X3S118-9	ECO103263	E1M10000298H04	ECO100808	S1M10000032F01	SAU800525
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SC13.1	ECO101348	E1M10000298G06	ECO100096	S1M10000032C03	SAU800771
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E1M10000225H09	ECO101989	S1M10000004G01	SAU802496	S1M10000048D02	SAU802548
E1M10000225F10	ECO101684	S1M10000004C02	SAU802496	S1M10000048D02	SAU104011
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E1M10000226A08	ECO104132	S1M10000004E06	SAU802240	S1M10000048G04	SAU802247
E1M10000226D08	ECO101753	S1M10000004F06	SAU800152	S1M10000048H04	SAU802586
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E1M10000226D10	ECO101623	S1M10000004E07	SAU802176	S1M10000048C05	SAU801891
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E1M10000226B12	ECO101916	S1M10000004G07	SAU801643	S1M10000048H05	SAU800546
E1M10000226F12	ECO100240	S1M10000004B08	SAU801346	S1M10000048A06	SAU800546
E1M10000227E03	ECO100975	S1M10000004B08	SAU200535	S1M10000048B06	SAU801184
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E1M10000227E11	ECO103724	S1M10000004C12	SAU800519	S1M10000048C09	SAU800548
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E1M10000227C12	ECO100395	S1M10000004D12	SAU801184	S1M10000048E09	SAU802090
E1M10000227D12	ECO104144	S1M10000004E12	SAU800528	S1M10000048F09	SAU802238
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E1M10000232B03	ECO101324	S1M10000005C01	SAU802496	S1M10000048C10	SAU800367
E1M10000232H03	ECO103097	S1M10000005E01	SAU800996	S1M10000048D10	SAU802590
E1M10000232C07	ECO100170	S1M10000005B02	SAU802243	S1M10000048E10	SAU802590
E1M10000232F07	ECO103797	S1M10000005D02	SAU800519	S1M10000048G10	SAU802238
E1M10000232F07	ECO103798	S1M10000005E02	SAU802655	S1M10000048H10	SAU802240
E1M10000232G07	ECO104010	S1M10000005F02	SAU801644	S1M10000048A11	SAU802224
E1M10000232A08	ECO100850	S1M10000005F02	SAU801643	S1M10000048C11	SAU802217
E1M10000232G08	ECO100875	S1M10000005A03	SAU802310	S1M10000048D11	SAU802090
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E1M10000233C01	ECO103886	S1M10000005F03	SAU802262	S1M10000048G11	SAU801186
E1M10000233A03	ECO100784	S1M10000005B04	SAU801183	S1M10000048H11	SAU801139
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E1M10000233D03	ECO100118	S1M10000005D04	SAU801184	S1M10000048B12	SAU802502
E1M10000233H03	ECO103238	S1M10000005F04	SAU800363	S1M10000048D12	SAU800250
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E1M10000233G04	ECO101185	S1M10000005C05	SAU801264		
E1M10000233A05	ECO102553	S1M10000005D05	SAU801644		

Table IC provides a cross reference between PathoSeq Gene Loci listed in Table IB and the SEQ ID NOs. of the corresponding PathoSeq polypeptides and the SEQ ID NOs. of the nucleic acids which encode them. The Gene Locus IDs provided in Table IC each comprise a nine digit alpha-numeric identifier that can be used to determine the organism from which each Gene Locus and corresponding SEQ ID NOs. were identified. Specifically, the first letter of the Gene Locus ID corresponds to the first letter of the genus name of the organism described herein from which the Gene Locus was identified and the second and third letters of the Gene Locus ID correspond to the first two letters of the species name of this organism. For example, the identifier EFA205257 describes a gene locus identified from *Enterococcus faecalis*. In those instances where the three letter identifier is the same for different organisms, the exact identity of the organism which corresponds to the Gene Locus ID can be determined by referring to the organism designation in the sequence listing for the coding nucleic acid or polypeptide SEQ ID NO. that corresponds to the particular Gene Locus ID.

TABLE IC

DNA SeqID	Protein SeqID	Gene LocusID	DNA SeqID	Protein SeqID	Gene LocusID	DNA SeqID	Protein SeqID	Gene LocusID
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6216	42400	EFA205225	18278	54462	CJU100855	30339	66523	PAE203656
6217	42401	EFA201977	18279	54463	CJU100856	30340	66524	PAE203658
6218	42402	EFA203137	18280	54464	CJU100859	30341	66525	PAE203668
6219	42403	EFA200840	18281	54465	CJU100860	30342	66526	PAE203670
6220	42404	EFA202003	18282	54466	CJU100861	30343	66527	PAE203672
6221	42405	EFA200807	18283	54467	CJU100862	30344	66528	PAE203677
6222	42406	EFA200811	18284	54468	CJU100863	30345	66529	PAE203684
6223	42407	EFA201987	18285	54469	CJU100866	30346	66530	PAE203691
6224	42408	EFA201980	18286	54470	CJU100870	30347	66531	PAE203698
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6226	42410	EFA205229	18288	54472	CJU100872	30349	66533	PAE203732
6227	42411	EFA201028	18289	54473	CJU100885	30350	66534	PAE203735
6228	42412	EFA201993	18290	54474	CJU100886	30351	66535	PAE203739
6229	42413	EFA201974	18291	54475	CJU100888	30352	66536	PAE203740
6230	42414	EFA201975	18292	54476	CJU100890	30353	66537	PAE203741
6231	42415	EFA202001	18293	54477	CJU100891	30354	66538	PAE203742
6232	42416	EFA200839	18294	54478	CJU100896	30355	66539	PAE203743
6233	42417	EFA201985	18295	54479	CJU100903	30356	66540	PAE203744
6234	42418	EFA201984	18296	54480	CJU100923	30357	66541	PAE203751
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6238	42422	EFA202536	18300	54484	CJU100944	30361	66545	PAE203758
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6240	42424	EFA201999	18302	54486	CJU100955	30363	66547	PAE203766
6241	42425	EFA201997	18303	54487	CJU100961	30364	66548	PAE203774
6242	42426	EFA200624	18304	54488	CJU100965	30365	66549	PAE203796
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6244	42428	EFA200812	18306	54490	CJU100967	30367	66551	PAE203799
6245	42429	EFA200660	18307	54491	CJU100970	30368	66552	PAE203800
6246	42430	EFA200661	18308	54492	CJU100980	30369	66553	PAE203801
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6252	42436	EFA200766	18314	54498	CJU100996	30375	66559	PAE203828
6253	42437	EFA200805	18315	54499	CJU100997	30376	66560	PAE203829
6254	42438	EFA201637	18316	54500	CJU100998	30377	66561	PAE203831
6255	42439	EFA201986	18317	54501	CJU100999	30378	66562	PAE203850
6256	42440	EFA205255	18318	54502	CJU101006	30379	66563	PAE203869
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6258	42442	EFA104836	18320	54504	CJU101011	30381	66565	PAE203872
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6262	42446	EFA202007	18324	54508	CJU101027	30385	66569	PAE203897
6263	42447	EFA200307	18325	54509	CJU101028	30386	66570	PAE203898
6264	42448	EFA201888	18326	54510	CJU101029	30387	66571	PAE203900
6265	42449	EFA205285	18327	54511	CJU101031	30388	66572	PAE203911

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6268	42452	EFA201611	18330	54514	CJU101046	30391	66575	PAE203920
6269	42453	EFA201946	18331	54515	CJU101050	30392	66576	PAE203943
6270	42454	EFA201512	18332	54516	CJU101054	30393	66577	PAE203958
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6272	42456	EFA203140	18334	54518	CJU101065	30395	66579	PAE203973
6273	42457	EFA200544	18335	54519	CJU101068	30396	66580	PAE203980
6274	42458	EFA203904	18336	54520	CJU101072	30397	66581	PAE203984
6275	42459	EFA202006	18337	54521	CJU101074	30398	66582	PAE203993
6276	42460	EFA202298	18338	54522	CJU101075	30399	66583	PAE204001
6277	42461	EFA200326	18339	54523	CJU101080	30400	66584	PAE204004
6278	42462	EFA200662	18340	54524	CJU101081	30401	66585	PAE204008
6279	42463	EFA202217	18341	54525	CJU101082	30402	66586	PAE204019
6280	42464	EFA201869	18342	54526	CJU101094	30403	66587	PAE204027
6281	42465	EFA203598	18343	54527	CJU101100	30404	66588	PAE204031
6282	42466	EFA200894	18344	54528	CJU101103	30405	66589	PAE204040
6283	42467	EFA200613	18345	54529	CJU101106	30406	66590	PAE204042
6284	42468	EFA202166	18346	54530	CJU101107	30407	66591	PAE204048
6285	42469	EFA202168	18347	54531	CJU101113	30408	66592	PAE204049
6286	42470	EFA201087	18348	54532	CJU101117	30409	66593	PAE204050
6287	42471	EFA201084	18349	54533	CJU101119	30410	66594	PAE204051
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6289	42473	EFA201905	18351	54535	CJU101121	30412	66596	PAE204053
6290	42474	EFA202015	18352	54536	CJU101122	30413	66597	PAE204077
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7186	43370	ECO103399	19248	55432	EBC100570	31309	67493	PPU100250			
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7190	43374	ECO104241	19252	55436	EBC100624	31313	67497	PPU100404			
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7196	43380	ECO103284	19258	55442	EBC100654	31319	67503	PPU100478			
7197	43381	ECO102066	19259	55443	EBC100655	31320	67504	PPU100484			
7198	43382	ECO102355	19260	55444	EBC100656	31321	67505	PPU100534			
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7204	43388	ECO102351	19266	55450	EBC100689	31327	67511	PPU100621
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7208	43392	ECO101499	19270	55454	EBC100704	31331	67515	PPU100641
7209	43393	ECO101671	19271	55455	EBC100706	31332	67516	PPU100647
7210	43394	ECO100867	19272	55456	EBC100717	31333	67517	PPU100648
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7221	43405	KPN201990	19283	55467	EBC100805	31344	67528	PPU100881
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7230	43414	KPN203534	19292	55476	EBC100833	31353	67537	PPU101006
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7240	43424	PAE202422	19302	55486	EBC100895	31363	67547	PPU101071
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7246	43430	PAE204064	19308	55492	EBC100919	31369	67553	PPU101132
7247	43431	PAE204269	19309	55493	EBC100920	31370	67554	PPU101135
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7254	43438	PAE203158	19316	55500	EBC100965	31377	67561	PPU101164
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7258	43442	PAE203152	19320	55504	EBC100976	31381	67565	PPU101173			
7259	43443	PAE203011	19321	55505	EBC100985	31382	67566	PPU101175			
7260	43444	PAE202220	19322	55506	EBC100989	31383	67567	PPU101184			
7261	43445	PAE200714	19323	55507	EBC101014	31384	67568	PPU101189			
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7268	43452	PAE200787	19330	55514	EBC101041	31391	67575	PPU101373			
7269	43453	PAE201300	19331	55515	EBC101043	31392	67576	PPU101392			
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7274	43458	PAE203981	19336	55520	EBC101089	31397	67581	PPU101429			
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7315	43499	PAE201397	19377	55561	EBC101263	31438	67622	PPU101878			
7316	43500	PAE201269	19378	55562	EBC101268	31439	67623	PPU101891			
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7322	43506	PAE201359	19384	55568	EBC101285	31445	67629	PPU101976			
7323	43507	PAE202724	19385	55569	EBC101287	31446	67630	PPU101981			
7324	43508	PAE204241	19386	55570	EBC101290	31447	67631	PPU101984			
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7329	43513	PAE204244	19391	55575	EBC101305	31452	67636	PPU102022			
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7332	43516	PAE204596	19394	55578	EBC101311	31455	67639	PPU102034			
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7334	43518	PAE204260	19396	55580	EBC101321	31457	67641	PPU102041			
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7337	43521	PAE205025	19399	55583	EBC101339	31460	67644	PPU102065			
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7339	43523	PAE204510	19401	55585	EBC101345	31462	67646	PPU102082			
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7387	43571	PAE202494	19449	55633	EBC101544	31510	67694	PPU102683			
7388	43572	PAE201635	19450	55634	EBC101545	31511	67695	PPU102698			
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7393	43577	PAE200933	19455	55639	EBC101577	31516	67700	PPU102796			
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7976	44160	SAU802181	20038	56222	EBC103996	32099	68283	PPU111291
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7981	44165	SAU802473	20043	56227	EBC104008	32104	68288	PPU111323
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8063	44247	SAU801905	20125	56309	EBC104475	32186	68370	PRT100032
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8139	44323	SAU802308	20201	56385	EBC107179	32262	68446	PRT100555
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8304	44488	SAU801919	20366	56550	ECO101469	32427	68611	PRT101434
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8307	44491	ABA100013	20369	56553	ECO101491	32430	68614	PRT101464
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8315	44499	ABA100056	20377	56561	ECO101619	32438	68622	PRT101499
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8354	44538	ABA100136	20416	56600	ECO102073	32477	68661	PRT101762
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8417	44601	ABA100413	20479	56663	ECO102724	32540	68724	PRT102211
8418	44602	ABA100417	20480	56664	ECO102754	32541	68725	PRT102221
8419	44603	ABA100431	20481	56665	ECO102756	32542	68726	PRT102223
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8520	44704	ABA100892	20582	56766	ECO103758	32643	68827	PRT102737

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8525	44709	ABA100914	20587	56771	ECO103822	32648	68832	PRT102791
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8528	44712	ABA100922	20590	56774	ECO103868	32651	68835	PRT102814
8529	44713	ABA100924	20591	56775	ECO103874	32652	68836	PRT102819
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8532	44716	ABA100933	20594	56778	ECO103891	32655	68839	PRT102825
8533	44717	ABA100939	20595	56779	ECO103909	32656	68840	PRT102826
8534	44718	ABA100945	20596	56780	ECO103913	32657	68841	PRT102830
8535	44719	ABA100967	20597	56781	ECO103916	32658	68842	PRT102833
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8574	44758	ABA101266	20636	56820	ECO201335	32697	68881	PRT103094
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8579	44763	ABA101290	20641	56825	ECO201402	32702	68886	PRT103159
8580	44764	ABA101297	20642	56826	ECO201939	32703	68887	PRT103160
8581	44765	ABA101300	20643	56827	ECO202018	32704	68888	PRT103179
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8596	44780	ABA101377	20658	56842	ECO204773	32719	68903	PRT103332
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8629	44813	ABA101593	20691	56875	EFA200150	32752	68936	PRT103773
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8635	44819	ABA101674	20697	56881	EFA200173	32758	68942	PRT103877
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8637	44821	ABA101702	20699	56883	EFA200190	32760	68944	PRT103897
8638	44822	ABA101710	20700	56884	EFA200191	32761	68945	PRT103903
8639	44823	ABA101740	20701	56885	EFA200193	32762	68946	PRT103927
8640	44824	ABA101766	20702	56886	EFA200201	32763	68947	PRT103939
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8646	44830	ABA101828	20708	56892	EFA200232	32769	68953	PRT104002
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8690	44874	ABA102358	20752	56936	EFA200401	32813	68997	PRT104542
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8744	44928	ABA103247	20806	56990	EFA200701	32867	69051	PRT104914
8745	44929	ABA103339	20807	56991	EFA200703	32868	69052	PRT104931
8746	44930	ABA103347	20808	56992	EFA200704	32869	69053	PRT104944
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8794	44978	ABA103859	20856	57040	EFA200870	32917	69101	PRT105280
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8801	44985	ABA103947	20863	57047	EFA200904	32924	69108	PRT105340
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8856	45040	ABA104393	20918	57102	EFA201241	32979	69163	PRT105730
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8911	45095	ABA104828	20973	57157	EFA201508	33034	69218	PRT106151
8912	45096	ABA104830	20974	57158	EFA201509	33035	69219	PRT106157
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8916	45100	ABA104905	20978	57162	EFA201530	33039	69223	PRT106179
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8959	45143	ABA105158	21021	57205	EFA201740	33082	69266	PSY100579
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8968	45152	ABA105195	21030	57214	EFA201808	33091	69275	PSY100727
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8970	45154	ABA105208	21032	57216	EFA201812	33093	69277	PSY100759
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8988	45172	ABA105410	21050	57234	EFA201894	33111	69295	PSY100971
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8993	45177	ABA105449	21055	57239	EFA201924	33116	69300	PSY101023
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9003	45187	ABA105518	21065	57249	EFA201972	33126	69310	PSY101054
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9013	45197	ABA105571	21075	57259	EFA202033	33136	69320	PSY101139
9014	45198	ABA105572	21076	57260	EFA202035	33137	69321	PSY101154
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9069	45253	ABA105994	21131	57315	EFA202344	33192	69376	PSY101677
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9074	45258	ABA106040	21136	57320	EFA202357	33197	69381	PSY101698
9075	45259	ABA106047	21137	57321	EFA202358	33198	69382	PSY101701
9076	45260	ABA106057	21138	57322	EFA202359	33199	69383	PSY101711
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9129	45313	BAN100279	21191	57375	EFA203174	33252	69436	PSY102222
9130	45314	BAN100298	21192	57376	EFA203222	33253	69437	PSY102225
9131	45315	BAN100304	21193	57377	EFA203228	33254	69438	PSY102229
9132	45316	BAN100305	21194	57378	EFA203247	33255	69439	PSY102269
9133	45317	BAN100313	21195	57379	EFA203403	33256	69440	PSY102309
9134	45318	BAN100334	21196	57380	EFA203405	33257	69441	PSY102320
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9144	45328	BAN100388	21206	57390	EFA204183	33267	69451	PSY102383
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9149	45333	BAN100418	21211	57395	EFA204507	33272	69456	PSY102424
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9184	45368	BAN100648	21246	57430	EFM100483	33307	69491	PSY102683
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10991	47175	BBU100507	23053	59237	KPN300322	35114	71298	SHA100142
10992	47176	BBU100512	23054	59238	KPN300323	35115	71299	SHA100143
10993	47177	BBU100513	23055	59239	KPN300325	35116	71300	SHA100146
10994	47178	BBU100517	23056	59240	KPN300326	35117	71301	SHA100148
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10998	47182	BBU100541	23060	59244	KPN300345	35121	71305	SHA100169			
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11000	47184	BBU100545	23062	59246	KPN300357	35123	71307	SHA100171			
11001	47185	BBU100547	23063	59247	KPN300374	35124	71308	SHA100172			
11002	47186	BBU100551	23064	59248	KPN300375	35125	71309	SHA100177			
11003	47187	BBU100556	23065	59249	KPN300377	35126	71310	SHA100178			
11004	47188	BBU100557	23066	59250	KPN300384	35127	71311	SHA100179			
11005	47189	BBU100559	23067	59251	KPN300389	35128	71312	SHA100180			
11006	47190	BBU100560	23068	59252	KPN300399	35129	71313	SHA100193			
11007	47191	BBU100564	23069	59253	KPN300407	35130	71314	SHA100217			
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11009	47193	BBU100571	23071	59255	KPN300418	35132	71316	SHA100223			
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11070	47254	BBU100736	23132	59316	KPN300640	35193	71377	SHA100443
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11078	47262	BBU100777	23140	59324	KPN300695	35201	71385	SHA100469
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11104	47288	BBU100834	23166	59350	KPN300814	35227	71411	SHA100553
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11114	47298	BCE100122	23176	59360	KPN300870	35237	71421	SHA100589			
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11116	47300	BCE100189	23178	59362	KPN300872	35239	71423	SHA100595			
11117	47301	BCE100228	23179	59363	KPN300875	35240	71424	SHA100600			
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11123	47307	BCE100299	23185	59369	KPN300885	35246	71430	SHA100631			
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11133	47317	BCE100467	23195	59379	KPN300966	35256	71440	SHA100649			
11134	47318	BCE100474	23196	59380	KPN300967	35257	71441	SHA100651			
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11136	47320	BCE100512	23198	59382	KPN300973	35259	71443	SHA100656			
11137	47321	BCE100520	23199	59383	KPN300984	35260	71444	SHA100660			
11138	47322	BCE100539	23200	59384	KPN300994	35261	71445	SHA100662			
11139	47323	BCE100542	23201	59385	KPN300997	35262	71446	SHA100663			
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11141	47325	BCE100574	23203	59387	KPN301023	35264	71448	SHA100679			
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11145	47329	BCE100659	23207	59391	KPN301041	35268	71452	SHA100697			
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11147	47331	BCE100671	23209	59393	KPN301045	35270	71454	SHA100699			
11148	47332	BCE100683	23210	59394	KPN301047	35271	71455	SHA100701			
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11164	47348	BCE100967	23226	59410	KPN301099	35287	71471	SHA100763
11165	47349	BCE100976	23227	59411	KPN301102	35288	71472	SHA100764
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11169	47353	BCE101034	23231	59415	KPN301113	35292	71476	SHA100769
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11194	47378	BCE101317	23256	59440	KPN301209	35317	71501	SHA100833
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11202	47386	BCE101419	23264	59448	KPN301264	35325	71509	SHA100853
11203	47387	BCE101423	23265	59449	KPN301265	35326	71510	SHA100854
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11210	47394	BCE101537	23272	59456	KPN301296	35333	71517	SHA100894
11211	47395	BCE101546	23273	59457	KPN301297	35334	71518	SHA100895
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11213	47397	BCE101562	23275	59459	KPN301301	35336	71520	SHA100899
11214	47398	BCE101565	23276	59460	KPN301302	35337	71521	SHA100902
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11440	47624	BCE105408	23502	59686	KPN302255	35563	71747	SHA101604
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11470	47654	BCE105851	23532	59716	KPN302468	35593	71777	SHA101691
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11604	47788	BCE107846	23666	59850	KPN303149	35727	71911	SHA102263
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11660	47844	BCE108969	23722	59906	KPN303463	35783	71967	SHA102750
11661	47845	BCE108996	23723	59907	KPN303464	35784	71968	SHA102754
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11663	47847	BCE109015	23725	59909	KPN303475	35786	71970	SHA102778
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11668	47852	BCE109138	23730	59914	KPN303487	35791	71975	SHA102823
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14569	50753	BMA109618	26631	62815	MBV105423	38692	74876	STM100295
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14602	50786	BPT100013	26664	62848	MBV105819	38725	74909	STM100533
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14623	50807	BPT100086	26685	62869	MBV106246	38746	74930	STM100668
14624	50808	BPT100089	26686	62870	MBV106247	38747	74931	STM100673
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14648	50832	BPT100226	26710	62894	MCA100127	38771	74955	STM100987
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14658	50842	BPT100261	26720	62904	MCA100159	38781	74965	STM101036
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14685	50869	BPT100434	26747	62931	MCA100258	38808	74992	STM101284
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14743	50927	BPT100743	26805	62989	MCA100529	38866	75050	STM101689
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14758	50942	BPT100807	26820	63004	MCA100612	38881	75065	STM101862
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14785	50969	BPT100871	26847	63031	MCA100752	38908	75092	STM102069
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14794	50978	BPT100893	26856	63040	MCA100777	38917	75101	STM102148
14795	50979	BPT100894	26857	63041	MCA100778	38918	75102	STM102165
14796	50980	BPT100895	26858	63042	MCA100779	38919	75103	STM102169
14797	50981	BPT100896	26859	63043	MCA100780	38920	75104	STM102195
14798	50982	BPT100897	26860	63044	MCA100781	38921	75105	STM102200
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14800	50984	BPT100905	26862	63046	MCA100789	38923	75107	STM102228
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14803	50987	BPT100913	26865	63049	MCA100801	38926	75110	STM102232
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14808	50992	BPT100929	26870	63054	MCA100816	38931	75115	STM102273
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14820	51004	BPT100969	26882	63066	MCA100865	38943	75127	STM102408
14821	51005	BPT100971	26883	63067	MCA100866	38944	75128	STM102429
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14844	51028	BPT101104	26906	63090	MCA100972	38967	75151	STM102720
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14850	51034	BPT101112	26912	63096	MCA101000	38973	75157	STM102728
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14864	51048	BPT101147	26926	63110	MCA101062	38987	75171	STM102815
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14866	51050	BPT101152	26928	63112	MCA101080	38989	75173	STM102828
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14897	51081	BPT101374	26959	63143	MCA101187	39020	75204	STM102974
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14899	51083	BPT101379	26961	63145	MCA101196	39022	75206	STM103008
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14907	51091	BPT101402	26969	63153	MCA101238	39030	75214	STM103140
14908	51092	BPT101404	26970	63154	MCA101240	39031	75215	STM103141
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14910	51094	BPT101412	26972	63156	MCA101243	39033	75217	STM103149
14911	51095	BPT101413	26973	63157	MCA101251	39034	75218	STM103155
14912	51096	BPT101418	26974	63158	MCA101252	39035	75219	STM103167
14913	51097	BPT101420	26975	63159	MCA101253	39036	75220	STM103175
14914	51098	BPT101422	26976	63160	MCA101259	39037	75221	STM103176
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14916	51100	BPT101434	26978	63162	MCA101274	39039	75223	STM103181
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14918	51102	BPT101441	26980	63164	MCA101289	39041	75225	STM103199
14919	51103	BPT101443	26981	63165	MCA101313	39042	75226	STM103201
14920	51104	BPT101446	26982	63166	MCA101332	39043	75227	STM103203
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14975	51159	BPT101790	27037	63221	MCA101639	39098	75282	STM103593
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15005	51189	BPT101965	27067	63251	MCA101940	39128	75312	STM103821
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15014	51198	BPT102004	27076	63260	MCA101981	39137	75321	STM103926
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15016	51200	BPT102032	27078	63262	MCA101994	39139	75323	STM103969
15017	51201	BPT102034	27079	63263	MCA101998	39140	75324	STM104010
15018	51202	BPT102039	27080	63264	MCA102001	39141	75325	STM104011
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15559	51743	CAC101539	27621	63805	MLP100688	39682	75866	STY102437
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15742	51926	CAC102434	27804	63988	MLP101209	39865	76049	STY103325
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15786	51970	CAC102661	27848	64032	MLP101439	39909	76093	STY103526
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15824	52008	CAC102804	27886	64070	MPN100010	39947	76131	STY103809
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15833	52017	CAC102879	27895	64079	MPN100073	39956	76140	STY103840
15834	52018	CAC102880	27896	64080	MPN100074	39957	76141	STY103841
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15897	52081	CAC103209	27959	64143	MPN100223	40020	76204	STY104029
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15948	52132	CAC103561	28010	64194	MPN100414	40071	76255	STY104247
15949	52133	CAC103563	28011	64195	MPN100415	40072	76256	STY104257
15950	52134	CAC103566	28012	64196	MPN100416	40073	76257	STY104266
15951	52135	CAC103575	28013	64197	MPN100417	40074	76258	STY104272
15952	52136	CAC103585	28014	64198	MPN100419	40075	76259	STY104274
15953	52137	CAC103586	28015	64199	MPN100420	40076	76260	STY104276
15954	52138	CAC103600	28016	64200	MPN100421	40077	76261	STY104279
15955	52139	CAC103602	28017	64201	MPN100422	40078	76262	STY104286
15956	52140	CAC103604	28018	64202	MPN100427	40079	76263	STY104295
15957	52141	CAC103605	28019	64203	MPN100430	40080	76264	STY104298
15958	52142	CAC103617	28020	64204	MPN100432	40081	76265	STY104302
15959	52143	CAC103620	28021	64205	MPN100436	40082	76266	STY104305
15960	52144	CAC103630	28022	64206	MPN100441	40083	76267	STY104319
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15962	52146	CAC103641	28024	64208	MPN100446	40085	76269	STY104331
15963	52147	CAC103650	28025	64209	MPN100447	40086	76270	STY104333
15964	52148	CAC103652	28026	64210	MPN100448	40087	76271	STY104335
15965	52149	CAC103654	28027	64211	MPN100453	40088	76272	STY104336
15966	52150	CAC103664	28028	64212	MPN100457	40089	76273	STY104340
15967	52151	CAC103671	28029	64213	MPN100458	40090	76274	STY104341
15968	52152	CAC103674	28030	64214	MPN100459	40091	76275	STY104352
15969	52153	CAC103679	28031	64215	MPN100475	40092	76276	STY104356
15970	52154	CAC103684	28032	64216	MPN100476	40093	76277	STY104366
15971	52155	CAC103685	28033	64217	MPN100479	40094	76278	STY104382
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15973	52157	CAC103696	28035	64219	MPN100482	40096	76280	STY104391
15974	52158	CAC103704	28036	64220	MPN100483	40097	76281	STY104414
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15976	52160	CAC103721	28038	64222	MPN100486	40099	76283	STY104427
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15985	52169	CAC103767	28047	64231	MPN100504	40108	76292	STY104481
15986	52170	CAC103770	28048	64232	MPN100508	40109	76293	STY104484
15987	52171	CAC103773	28049	64233	MPN100509	40110	76294	STY104486
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15999	52183	CBO100087	28061	64245	MPN100526	40122	76306	STY104553
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16005	52189	CBO100125	28067	64251	MPN100537	40128	76312	STY104567
16006	52190	CBO100136	28068	64252	MPN100538	40129	76313	STY104568
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16013	52197	CBO100172	28075	64259	MPN100566	40136	76320	STY104584
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16015	52199	CBO100196	28077	64261	MPN100572	40138	76322	STY104592
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16061	52245	CBO100415	28123	64307	MPN100654	40184	76368	TPA100028
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16066	52250	CBO100441	28128	64312	MPN100659	40189	76373	TPA100051
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16159	52343	CBO100995	28221	64405	MTU200575	40282	76466	TPA100288
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16164	52348	CBO101009	28226	64410	MTU200637	40287	76471	TPA100303
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16170	52354	CBO101031	28232	64416	MTU200667	40293	76477	TPA100333
16171	52355	CBO101032	28233	64417	MTU200671	40294	76478	TPA100337
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16274	52458	CBO101553	28336	64520	MTU201262	40397	76581	TPA100720
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16624	52808	CBO103745	28686	64870	MTU203335	40747	76931	UUR100609
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16630	52814	CBO103765	28692	64876	MTU203377	40753	76937	VCH100007
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16640	52824	CBO103826	28702	64886	MTU203412	40763	76947	VCH100040
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16648	52832	CBO103872	28710	64894	MTU203456	40771	76955	VCH100083
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16650	52834	CBO103874	28712	64896	MTU203462	40773	76957	VCH100108
16651	52835	CBO103886	28713	64897	MTU203475	40774	76958	VCH100112
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16658	52842	CBO103931	28720	64904	MTU203540	40781	76965	VCH100138
16659	52843	CBO103935	28721	64905	MTU203543	40782	76966	VCH100146
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17539	53723	CDP100250	29601	65785	NME200684	41662	77846	YPS000696
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18206	54390	CJU100624	30268	66452	PAE203114	42329	78513	YPS003462
18207	54391	CJU100628	30269	66453	PAE203132	42330	78514	YPS003466
18208	54392	CJU100629	30270	66454	PAE203139	42331	78515	YPS003469
18209	54393	CJU100636	30271	66455	PAE203146	42332	78516	YPS003474
18210	54394	CJU100638	30272	66456	PAE203155	42333	78517	YPS003477
18211	54395	CJU100643	30273	66457	PAE203160	42334	78518	YPS003478
18212	54396	CJU100645	30274	66458	PAE203161	42335	78519	YPS003483
18213	54397	CJU100646	30275	66459	PAE203166	42336	78520	YPS003494
18214	54398	CJU100649	30276	66460	PAE203177	42337	78521	YPS003496
18215	54399	CJU100651	30277	66461	PAE203193	42338	78522	YPS003498
18216	54400	CJU100654	30278	66462	PAE203199	42339	78523	YPS003500
18217	54401	CJU100659	30279	66463	PAE203203	42340	78524	YPS003502
18218	54402	CJU100660	30280	66464	PAE203206	42341	78525	YPS003510
18219	54403	CJU100661	30281	66465	PAE203208	42342	78526	YPS003517
18220	54404	CJU100662	30282	66466	PAE203256	42343	78527	YPS003520
18221	54405	CJU100663	30283	66467	PAE203264	42344	78528	YPS003522
18222	54406	CJU100664	30284	66468	PAE203270	42345	78529	YPS003528
18223	54407	CJU100668	30285	66469	PAE203277	42346	78530	YPS003531
18224	54408	CJU100669	30286	66470	PAE203294	42347	78531	YPS003539
18225	54409	CJU100672	30287	66471	PAE203299	42348	78532	YPS003542
18226	54410	CJU100675	30288	66472	PAE203301	42349	78533	YPS003544
18227	54411	CJU100684	30289	66473	PAE203302	42350	78534	YPS003545
18228	54412	CJU100698	30290	66474	PAE203303	42351	78535	YPS003546
18229	54413	CJU100702	30291	66475	PAE203331	42352	78536	YPS003547
18230	54414	CJU100704	30292	66476	PAE203342	42353	78537	YPS003552
18231	54415	CJU100705	30293	66477	PAE203357	42354	78538	YPS003553
18232	54416	CJU100709	30294	66478	PAE203386	42355	78539	YPS003556
18233	54417	CJU100710	30295	66479	PAE203414	42356	78540	YPS003559
18234	54418	CJU100711	30296	66480	PAE203415	42357	78541	YPS003562
18235	54419	CJU100712	30297	66481	PAE203450	42358	78542	YPS003580
18236	54420	CJU100714	30298	66482	PAE203457	42359	78543	YPS003605
18237	54421	CJU100728	30299	66483	PAE203459	42360	78544	YPS003633
18238	54422	CJU100729	30300	66484	PAE203468	42361	78545	YPS003640
18239	54423	CJU100732	30301	66485	PAE203480	42362	78546	YPS003644
18240	54424	CJU100734	30302	66486	PAE203501	42363	78547	YPS003651
18241	54425	CJU100735	30303	66487	PAE203514	42364	78548	YPS003677
18242	54426	CJU100737	30304	66488	PAE203515	42365	78549	YPS003683
18243	54427	CJU100740	30305	66489	PAE203525	42366	78550	YPS003696
18244	54428	CJU100741	30306	66490	PAE203552	42367	78551	YPS003702
18245	54429	CJU100742	30307	66491	PAE203556	42368	78552	YPS003731
18246	54430	CJU100744	30308	66492	PAE203557	42369	78553	YPS003739
18247	54431	CJU100749	30309	66493	PAE203558	42370	78554	YPS003752
18248	54432	CJU100751	30310	66494	PAE203560	42371	78555	YPS003775
18249	54433	CJU100756	30311	66495	PAE203565	42372	78556	YPS003777
18250	54434	CJU100760	30312	66496	PAE203579	42373	78557	YPS003792
18251	54435	CJU100763	30313	66497	PAE203580	42374	78558	YPS003815
18252	54436	CJU100766	30314	66498	PAE203588	42375	78559	YPS003822
18253	54437	CJU100774	30315	66499	PAE203595	42376	78560	YPS003891
18254	54438	CJU100775	30316	66500	PAE203599	42377	78561	YPS003904
18255	54439	CJU100777	30317	66501	PAE203600	42378	78562	YPS003930

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DNA SeqID	Protein SeqID	Gene LocusID	DNA SeqID	Protein SeqID	Gene LocusID	DNA SeqID	Protein SeqID	Gene LocusID
18256	54440	CJU100788	30318	66502	PAE203601	42379	78563	YPS003983
18257	54441	CJU100795	30319	66503	PAE203612	42380	78564	YPS004039
18258	54442	CJU100797	30320	66504	PAE203614	42381	78565	YPS004144
18259	54443	CJU100799	30321	66505	PAE203615	42382	78566	YPS004146
18260	54444	CJU100801	30322	66506	PAE203618	42383	78567	YPS004171
18261	54445	CJU100802	30323	66507	PAE203625	42384	78568	YPS004196
18262	54446	CJU100805	30324	66508	PAE203626	42385	78569	YPS004197
18263	54447	CJU100815	30325	66509	PAE203631	42386	78570	YPS004214
18264	54448	CJU100816	30326	66510	PAE203633	42387	78571	YPS004281
18265	54449	CJU100817	30327	66511	PAE203634	42388	78572	YPS004286
18266	54450	CJU100819	30328	66512	PAE203635	42389	78573	YPS004652
18267	54451	CJU100824	30329	66513	PAE203637	42390	78574	YPS005092
18268	54452	CJU100827	30330	66514	PAE203638	42391	78575	YPS005095
18269	54453	CJU100828	30331	66515	PAE203640	42392	78576	YPS005126
18270	54454	CJU100833	30332	66516	PAE203643	42393	78577	YPS005201
18271	54455	CJU100835	30333	66517	PAE203644	42394	78578	YPS005574
18272	54456	CJU100836	30334	66518	PAE203650	42395	78579	YPS005860
18273	54457	CJU100842	30335	66519	PAE203651	42396	78580	YPS006083
18274	54458	CJU100843	30336	66520	PAE203652	42397	78581	YPS006344
18275	54459	CJU100845						

It will be appreciated that ORFs may also be identified using databases other than PathoSeq. For example, the ORFs may be identified using the methods described in U.S. Provisional Patent Application Serial Number 60/191,078, filed March 21, 2000.

EXAMPLE 4

5 Transfer of Exogenous Nucleic Acid Sequences to other Bacterial Species

The ability of an antisense molecule identified in a first organism to inhibit the proliferation of a second organism (thereby confirming that a gene in the second organism which is homologous to the gene from the first organism is required for proliferation of the second organism) was validated using antisense nucleic acids which inhibit the growth of *E. coli* which were identified using methods similar to those described above. Expression vectors which inhibited growth of *E. coli* upon induction of antisense RNA expression with IPTG were transformed directly into *Enterobacter cloacae*, *Klebsiella pneumonia* or *Salmonella typhimurium*. The transformed cells were then assayed for growth inhibition according to the method of Example 1. After growth in liquid culture, cells were plated at various serial dilutions and a score determined by calculating the log difference in growth for INDUCED vs. UNINDUCED antisense RNA expression as determined by the maximum 10 fold dilution at which a colony was observed. The results of these experiments are listed below in Table II. If there was no effect of antisense RNA expression in a microorganism, the clone is minus in Table II. In contrast, a positive in Table II means that at least 10 fold more cells were required to observe a colony on the induced plate than on the non-induced plate under the conditions used and in that microorganism.

TABLE II
Sensitivity of Other Microorganisms to Antisense Nucleic Acids That Inhibit Proliferation in *E. coli*

Mol. No.	<i>S. typhimurium</i>	<i>E. cloacae</i>	<i>K. pneumoniae</i>
EcXA001	+	+	-
EcXA004	+	-	-
EcXA005	+	+	+
EcXA006	-	-	-
EcXA007	-	+	-
EcXA008	+	-	+
EcXA009	-	-	-
EcXA010	+	+	+
EcXA011	-	+	-
EcXA012	-	+	-
EcXA013	+	+	+
EcXA014	+	+	-
EcXA015	+	+	+
EcXA016	+	+	+
EcXA017	+	+	+
EcXA018	+	+	+
EcXA019	+	+	+
EcXA020	+	+	+
EcXA021	+	+	+
EcXA023	+	+	+
EcXA024	+	-	+

EcXA025	-	-	-
EcXA026	+	+	-
EcXA027	+	+	-
EcXA028	+	-	-
EcXA029	-	-	-
EcXA030	+	+	+
EcXA031	+	-	-
EcXA032	+	+	-
EcXA033	+	+	+
EcXA034	+	+	+
EcXA035	-	-	-
EcXA036	+	-	+
EcXA037	+	+	-
EcXA038	+	+	+
EcXA039	+	-	-
EcXA041	+	+	+
EcXA042	-	+	+
EcXA043	-	-	-
EcXA044	-	-	-
EcXA045	+	+	+
EcXA046	-	-	-
EcXA047	+	+	-
EcXA048	-	-	-
EcXA049	+	-	-
EcXA050	-	-	-
EcXA051	+	-	-
EcXA052	+	-	-
EcXA053	+	+	+
EcXA054	-	-	+
EcXA055	+	-	-
EcXA056	+	-	+
EcXA057	+	+	-
EcXA058	-	-	-
EcXA059	+	+	+
EcXA060	-	-	-
EcXA061	-	-	-
EcXA062	-	-	-
EcXA063	+	+	-
EcXA064	-	-	-
EcXA065	+	+	-
EcXA066	-	-	-
EcXA067	-	+	-
EcXA068	-	-	-
EcXA069	-	+	-
EcXA070	-	-	-
EcXA071	+	-	-
EcXA072	+	-	+
EcXA073	+	+	+
EcXA074	+	+	+
EcXA075	+	-	-
EcXA076	-	+	-

EcXA077	+	+	-
EcXA079	+	+	+
EcXA080	+	-	-
EcXA082	-	+	-
EcXA083	-	-	-
EcXA084	-	+	-
EcXA086	-	-	-
EcXA087	-	-	-
EcXA088	-	-	-
EcXA089	-	-	-
EcXA090	-	-	-
EcXA091	-	-	-
EcXA092	-	-	-
EcXA093	-	-	-
EcXA094	+	+	+
EcXA095	+	+	-
EcXA096	-	-	-
EcXA097	+	-	-
EcXA098	-	-	-
EcXA099	-	-	-
EcXA100	-	-	-
EcXA101	-	-	-
EcXA102	-	-	-
EcXA103	-	+	-
EcXA104	+	+	+
EcXA106	+	+	-
EcXA107	-	-	-
EcXA108	-	-	-
EcXA109	-	-	-
EcXA110	+	+	-
EcXA111	-	-	-
EcXA112	-	+	-
EcXA113	+	+	+
EcXA114	-	+	-
EcXA115	-	+	-
EcXA116	+	+	-
EcXA117	+	-	-
EcXA118	-	-	-
EcXA119	+	+	-
EcXA120	-	-	-
EcXA121	-	-	-
EcXA122	+	-	+
EcXA123	+	-	-
EcXA124	-	-	-
EcXA125	-	-	-
EcXA126	-	-	-
EcXA127	+	+	-
EcXA128	-	-	-
EcXA129	-	+	-
EcXA130	+	+	-
EcXA132	-	-	-

EcXA133	-	-	-
EcXA136	-	-	-
EcXA137	-	-	-
EcXA138	+	-	-
EcXA139	-	-	-
EcXA140	+	-	-
EcXA141	+	-	-
EcXA142	-	-	-
EcXA143	-	+	-
EcXA144	+	+	-
EcXA145	-	-	-
EcXA146	-	-	-
EcXA147	-	-	-
EcXA148	-	-	-
EcXA149	+	+	+
EcXA150	-	-	-
EcXA151	+	-	-
EcXA152	-	-	-
EcXA153	+	+	-
EcXA154	-	-	-
EcXA155	-	-	ND
EcXA156	-	+	-
EcXA157	-	-	-
EcXA158	-	-	-
EcXA159	+	-	-
EcXA160	+	-	-
EcXA162	-	-	-
EcXA163	-	-	-
EcXA164	-	-	-
EcXA165	-	-	-
EcXA166	-	-	-
EcXA167	-	-	-
EcXA168	-	-	-
EcXA169	-	+	-
EcXA171	-	-	-
EcXA172	-	-	-
EcXA173	-	-	-
EcXA174	-	-	-
EcXA175	-	-	-
EcXA176	-	-	-
EcXA178	-	-	-
EcXA179	-	-	-
EcXA180	+	-	-
EcXA181	-	-	-
EcXA182	-	-	-
EcXA183	-	-	-
EcXA184	-	-	-
EcXA185	-	-	-
EcXA186	-	-	-
EcXA187	+	+	+
EcXA189	+	-	-

EcXA190	+	+	+
EcXA191	+	+	-
EcXA192	-	+	-

Thus, the ability of an antisense nucleic acid which inhibits the proliferation of *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Salmonella typhimurium*, *Acinetobacter baumannii*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Corynebacterium diptheriae*, *Enterobacter cloacae*, *Enterococcus faecium*, *Haemophilus influenzae*, *Helicobacter pylori*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella multocida*, *Proteus mirabilis*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella paratyphi*, *Salmonella typhi*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus mutans*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae* or *Yersinia pestis* to inhibit the growth of other organisms may be evaluated by transforming the antisense nucleic acid directly into species other than the organism from which they were obtained. In particular, the ability of the antisense nucleic acid to inhibit the growth of *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diptheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma*

urealyticum, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* or any species falling within the genera of any of the above species may be evaluated. In some embodiments of the present invention, the ability of the antisense nucleic acid to inhibit the growth of an organism other than *E. coli* may be evaluated. In such embodiments, the antisense nucleic acids are inserted into expression vectors functional in the organisms in which the antisense nucleic acids are evaluated.

It will be appreciated that the above methods for evaluating the ability of an antisense nucleic acid to inhibit the proliferation of a heterologous organism may be performed using antisense nucleic acids complementary to any of the proliferation-required nucleic acids from *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Salmonella typhimurium*, *Acinetobacter baumannii*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Corynebacterium diphtheriae*, *Enterobacter cloacae*, *Enterococcus faecium*, *Haemophilus influenzae*, *Helicobacter pylori*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella multocida*, *Proteus mirabilis*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella paratyphi*, *Salmonella typhi*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus mutans*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae* or *Yersinia pestis* (including antisense nucleic acids complementary to SEQ ID NOs.: 6214-42397, such as the antisense nucleic acids of SEQ ID NOs.: 1-6213) or portions thereof, antisense nucleic acids complementary to homologous coding nucleic acids or portions thereof, or homologous antisense nucleic acids.

Those skilled in the art will appreciate that a negative result in a heterologous cell or microorganism does not mean that that cell or microorganism is missing that gene nor does it mean that the gene is unessential. However, a positive result means that the heterologous cell or microorganism contains a homologous gene which is required for proliferation of that cell or microorganism. The homologous gene may be obtained using the methods described herein. For example, the homologous gene may be isolated by performing a PCR procedure using primers based on the antisense sequence which reduced the level or activity of the gene product encoded by the homologous gene or by performing a Southern blot. Those cells that are inhibited by antisense may be used in cell-based assays as described herein for the identification and characterization of compounds in order to develop antibiotics effective in these cells or microorganisms. Those skilled in the art will appreciate that an antisense molecule which works in the microorganism from which it was obtained will not always work in a heterologous cell or microorganism.

EXAMPLE 5

Transfer of Exogenous Nucleic Acid Sequences to Other Bacterial Species Using the *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Salmonella typhimurium*, *Acinetobacter baumannii*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Corynebacterium diptheriae*, *Enterobacter cloacae*, *Enterococcus faecium*, *Haemophilus influenzae*, *Helicobacter pylori*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella multocida*, *Proteus mirabilis*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella paratyphi*, *Salmonella typhi*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus mutans*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae* or *Yersinia pestis* Expression Vectors or Expression Vectors Functional in Bacterial Species Other Than the Foregoing Bacterial Species

The antisense nucleic acids that inhibit the growth of *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Salmonella typhimurium*, *Acinetobacter baumannii*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Corynebacterium diptheriae*, *Enterobacter cloacae*, *Enterococcus faecium*, *Haemophilus influenzae*, *Helicobacter pylori*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella multocida*, *Proteus mirabilis*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella paratyphi*, *Salmonella typhi*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus mutans*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae* or *Yersinia pestis*, or portions thereof, may also be evaluated for their ability to inhibit the growth of cells or microorganisms other than *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Salmonella typhimurium*, *Acinetobacter baumannii*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Corynebacterium diptheriae*, *Enterobacter cloacae*, *Enterococcus faecium*, *Haemophilus influenzae*, *Helicobacter pylori*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*,

Mycobacterium bovis, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella multocida*, *Proteus mirabilis*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella paratyphi*, *Salmonella typhi*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus mutans*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae* or *Yersinia pestis*. For example, the antisense nucleic acids that inhibit the growth of *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Salmonella typhimurium*, *Acinetobacter baumannii*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Corynebacterium diphtheriae*, *Enterobacter cloacae*, *Enterococcus faecium*, *Haemophilus influenzae*, *Helicobacter pylori*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella multocida*, *Proteus mirabilis*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella paratyphi*, *Salmonella typhi*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus mutans*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae* or *Yersinia pestis* may be evaluated for their ability to inhibit the growth of other organisms. In particular, the ability of the antisense nucleic acid to inhibit the growth of *Acinetobacter baumannii*, *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*,

Streptococcus pneumoniae, *Streptococcus mutans*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificans*, *Yersinia enterocolitica*, *Yersinia pestis* or any species falling within the genera of any of the above species may be evaluated. In some embodiments of the present invention, the ability of the antisense nucleic acid to inhibit the growth of an organism other than *E. coli* may be evaluated.

In such methods, expression vectors in which the expression of an antisense nucleic acid that inhibits the growth of *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Salmonella typhimurium*, *Acinetobacter baumannii*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Corynebacterium diphtheriae*, *Enterobacter cloacae*, *Enterococcus faecium*, *Haemophilus influenzae*, *Helicobacter pylori*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella multocida*, *Proteus mirabilis*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella paratyphi*, *Salmonella typhi*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus mutans*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae* or *Yersinia pestis* under the control of an inducible promoter are introduced into the cells or microorganisms in which they are to be evaluated. In some embodiments, the antisense nucleic acids may be evaluated in cells or microorganisms which are closely related to *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Salmonella typhimurium*, *Acinetobacter baumannii*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Corynebacterium diphtheriae*, *Enterobacter cloacae*, *Enterococcus faecium*, *Haemophilus influenzae*, *Helicobacter pylori*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella multocida*, *Proteus mirabilis*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella paratyphi*, *Salmonella typhi*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus mutans*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae* or *Yersinia pestis*. The ability of these antisense nucleic acids to inhibit the growth of the related cells or microorganisms in the presence of the inducer is then measured.

EXAMPLE 6

Identification of Nucleic Acids Homologous to Nucleic Acids Required for the Proliferation of
Staphylococcus aureus in other Bacterial Species

Nucleic acids homologous to proliferation-required nucleic acids from *Staphylococcus aureus* were identified as follows. For example, thirty-nine antisense nucleic acids which inhibited the growth of *Staphylococcus aureus* were identified using methods such as those described herein and were inserted into an expression vector such that their expression was under the control of a xylose-inducible Xyl-T5 promoter. A vector with a reporter gene under control of the Xyl-T5 promoter was used to show that expression from the Xyl-T5 promoter in *Staphylococcus epidermidis* was comparable to that in *Staphylococcus aureus*.

The vectors were introduced into *Staphylococcus epidermidis* by electroporation as follows: *Staphylococcus epidermidis* was grown in liquid culture to mid-log phase and then harvested by centrifugation. The cell pellet was resuspended in 1/3 culture volume of ice-cold EP buffer (0.625 M sucrose, 1 mM MgCl₂, pH=4.0), and then harvested again by centrifugation. The cell pellet was then resuspended with 1/40 volume EP buffer and allowed to incubate on ice for 1 hour. The cells were then frozen for storage at -80°C. For electroporation, 50 µl of thawed electrocompetent cells were combined with 0.5 µg plasmid DNA and then subjected to an electrical pulse of 10 kV/cm, 25 uFarads, 200 ohm using a biorad gene pulser electroporation device. The cells were immediately resuspended with 200 µl outgrowth medium and incubated for 2 hours prior to plating on solid growth medium with drug selection to maintain the plasmid vector. Colonies resulting from overnight growth of these platings were selected, cultured in liquid medium with drug selection, and then subjected to dilution plating analysis as described for *Staphylococcus aureus* in Example 1 above to test growth sensitivity in the presence of the inducer xylose.

The results are shown in Table III below. The first column indicates the Molecule Number of the *Staphylococcus aureus* antisense nucleic acid which was introduced into *Staphylococcus epidermidis*. The second column indicates whether the antisense nucleic acid inhibited the growth of *Staphylococcus epidermidis*, with a "+" indicating that growth was inhibited. Of the 39 *Staphylococcus aureus* antisense nucleic acids evaluated, 20 inhibited the growth of *Staphylococcus epidermidis*.

TABLE III
Sensitivity of Other Microorganisms to Antisense Nucleic Acids That Inhibit Proliferation of
Staphylococcus aureus

Mol. No.	<i>S. epidermidis</i>
SaXA005	+
SaXA007	+
SaXA008	+
SaXA009	+
SaXA010	+
SaXA011	-

SaXA012	-
SaXA013	-
SaXA015	+
SaXA017	-
SaXA022	+
SaXA023	-
SaXA024	-
SaXA025	+
SaXA026	+
SaXA027	-
SaXA027b	-
SaXA02c	-
SaXA028	-
SaXA029	+
SaXA030	+
SaXA032	+
SaXA033	+
SaXA034	-
SaXA035	+
SaXA037	+
SaXA039	-
SaXA042	-
SaXA043	-
SaXA044	-
SaXA045	+
SaXA051	+
SaXA053	-
SaXA056b	-
SaXA059a	+
SaXA060	-
SaXA061	+
SaXA062	+
SaXA063	-
SaXA065	-

Although the results shown above were obtained using a subset of proliferation-required nucleic acids from *Staphylococcus aureus*, it will be appreciated that similar analyses may be performed using the nucleic acids of the present invention to determine whether they inhibit the proliferation of cells or microorganisms other than *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Salmonella typhimurium*, *Acinetobacter baumannii*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Corynebacterium diphtheriae*, *Enterobacter cloacae*, *Enterococcus faecium*, *Haemophilus influenzae*, *Helicobacter pylori*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella multocida*, *Proteus mirabilis*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella paratyphi*, *Salmonella typhi*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus mutans*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae* or *Yersinia pestis*.

Thus, it will be appreciated that the above methods for evaluating the ability of an antisense nucleic acid to inhibit the proliferation of a heterologous organism may be performed using antisense nucleic acids complementary to any of the proliferation-required nucleic acids from *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Salmonella typhimurium*, *Acinetobacter baumannii*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Corynebacterium diphtheriae*, *Enterobacter cloacae*, *Enterococcus faecium*, *Haemophilus influenzae*, *Helicobacter pylori*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella multocida*, *Proteus mirabilis*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella paratyphi*, *Salmonella typhi*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus mutans*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae* or *Yersinia pestis*, (including antisense nucleic acids complementary to SEQ ID NOs.: 6214-42397, such as the antisense nucleic acids of SEQ ID NOs.: 1-6213) or portions thereof, antisense nucleic acids complementary to homologous coding nucleic acids or portions thereof, or homologous antisense nucleic acids.

EXAMPLE 7

Identification of Homologous Nucleic Acids by Functional Complementation

Homologous coding nucleic acids, homologous antisense nucleic acids or nucleic acids encoding homologous polypeptides may be identified as follows. Gene products whose activities may be complemented by a proliferation-required gene product from *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Salmonella typhimurium*, *Acinetobacter baumannii*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Corynebacterium diphtheriae*, *Enterobacter cloacae*, *Enterococcus faecium*, *Haemophilus influenzae*, *Helicobacter pylori*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella multocida*, *Proteus mirabilis*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella paratyphi*, *Salmonella typhi*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus mutans*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae*, *Yersinia pestis* or homologous polypeptides are identified using merodiploids, created by introducing a plasmid or Bacterial Artificial Chromosome into an organism having a mutation in the essential gene which reduces or eliminates the activity of the gene product. In some embodiments, the mutation may be a conditional mutation, such as a temperature sensitive mutation, such that the organism proliferates under permissive conditions but is unable to proliferate under non-permissive conditions in the absence of complementation by the gene on the plasmid or Bacterial Artificial Chromosome. Alternatively, duplications may be constructed as described in Roth et al. (1987) Biosynthesis of Aromatic Amino Acids in *Escherichia coli* and *Salmonella typhimurium*, F. C. Neidhardt, ed., American Society for Microbiology, publisher, pp. 2269-2270. Such methods are familiar to those skilled in the art. Alternatively, homologous coding nucleic acids, homologous antisense nucleic acids or nucleic acids encoding homologous polypeptides may be identified by placing a gene required for proliferation or a nucleic acid complementary to at least a portion of a gene required for proliferation under the control of a regulatable promoter as described above, introducing a plasmid or Bacterial Artificial Chromosome into the cell, and identifying cells which are able to proliferate under conditions which would prevent or reduce proliferation in the absence of the plasmid or Bacterial Artificial Chromosome.

Homologous coding nucleic acids, homologous antisense nucleic acids or nucleic acids encoding homologous polypeptides may be identified using databases as follows.

EXAMPLE 8

Identification of Homologous Nucleic Acids by Database Analysis

As a demonstration of the methodology required to find homologues to an essential gene, fifty-one prokaryotic organisms were analyzed and compared in detail. First, the most reliable source of gene sequences for each organism was assessed by conducting a survey of the public and private data sources. The fifty-one organisms studied are *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Salmonella typhimurium*, *Acinetobacter baumannii*, *Bacillus anthracis*, *Bacteroides fragilis*, *Bordetella pertussis*, *Borrelia burgdorferi*, *Burkholderia cepacia*, *Burkholderia fungorum*, *Burkholderia mallei*, *Campylobacter jejuni*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium acetobutylicum*, *Clostridium botulinum*, *Clostridium difficile*, *Corynebacterium diphtheriae*, *Enterobacter cloacae*, *Enterococcus faecium*, *Haemophilus influenzae*, *Helicobacter pylori*, *Legionella pneumophila*, *Listeria monocytogenes*, *Moraxella catarrhalis*, *Mycobacterium avium*, *Mycobacterium bovis*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Pasteurella multocida*, *Proteus mirabilis*, *Pseudomonas putida*, *Pseudomonas syringae*, *Salmonella paratyphi*, *Salmonella typhi*, *Staphylococcus epidermidis*, *Staphylococcus haemolyticus*, *Streptococcus mutans*, *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Treponema pallidum*, *Ureaplasma urealyticum*, *Vibrio cholerae* and *Yersinia pestis*. Full-length gene protein and nucleotide sequences for these organisms were assembled from various sources. For *Escherichia coli*, *Haemophilus influenzae* and *Helicobacter pylori*, gene sequences were adopted from the public sequencing projects, and derived from the GenPept 115 database (available from NCBI). For *Pseudomonas aeruginosa*, gene sequences were adopted from the *Pseudomonas* genome sequencing project (downloaded from <http://www.pseudomonas.com>). For *Klebsiella pneumoniae*, *Staphylococcus aureus*, *Streptococcus pneumoniae* and *Salmonella typhi*, genomic sequences from PathoSeq v 4.1 (Mar 2000 release) were reanalyzed for ORFs using the gene finding software GeneMark v 2.4a, which was purchased from GenePro Inc. 451 Bishop St., N.W., Suite B, Atlanta, GA, 30318, USA. Similar analyses were conducted for the other organisms using publically available and proprietary databases.

Homologous coding nucleic acids and the homologous polypeptides which they encode may be identified using a "reciprocal" best-hit analysis. To facilitate the identification of homologous coding nucleic acids and homologous polypeptides, paralogous genes within each of 51 organisms were identified and clustered prior to comparison to other organisms. Briefly, the polypeptide sequence of each polypeptide encoded by each open reading frame (ORF) in a given organism was compared to the polypeptide sequence encoded by every other ORF for that organism for each of the 51 pathogenic organisms (PathoSeq Sept 2001 release) using BLASTP 2.09 algorithm without filtering. Simultaneously, the polypeptide sequence encoded by each ORF of an organism was compared to the polypeptide sequences encoded by each of the ORFs in the remaining 51 organisms. Those polypeptides within a single organism that shared a higher degree

of sequence identity to one another than to polypeptide sequences obtained from any other organisms were clustered as "paralog" sequences for "reciprocal" best-hit analysis.

For each reference organism, the 50 homologous coding nucleic acids (and the 50 homologous polypeptides which they encode) was determined by identifying the ORFs in each of the 50 comparison organisms which encode a polypeptide sharing the highest degree of amino acid sequence identity to the polypeptide encoded by the ORF from the reference organism. The accuracy of the identification of the predicted homologous coding nucleic acids (and the homologous polypeptides which they encode) was confirmed by a "reciprocal" BLAST analysis in which the polypeptide sequence of the predicted homologous polypeptide was compared against the polypeptides encoded by each of the ORFS in the reference organism using BLASTP 2.09 algorithm without filtering. Only those polypeptides that share the highest degree of amino acid sequence identity in each portion of the two-way comparison are retained for further analysis.

The best homolog for each of the fifty-one organisms, defined as the most significantly scoring match which also fulfilled the above criteria, was reported in Table IV

Table IV lists the best ORF identified as described above (column labeled Homolog LocusID) that matches the query sequence (column labeled Query LocusID), % identity between the query sequence and the homolog, and the amount of each sequence that aligns together well (columns labeled Query Coverage and Homolog Coverage) for the gene identified in each of the fifty-one organisms evaluated as described above. As described in connection with Table IC, the Locus IDs (ie. both Query Locus ID and Homolog Locus ID) provided in Table IV each comprise a nine digit alpha-numeric identifier that can be used to determine the organism from which the query and homolog sequences were obtained. Specifically, the first letter of the Locus ID corresponds to the first letter of the genus name of the organism described herein from which the Locus was identified and the second and third letters of the Locus ID correspond to the first two letters of the species name of this organism. For example, the identifier EFA205257 describes a gene locus identified from *Enterococcus faecalis*. In those instances where the three letter identifier is the same for different organisms, the exact identity of the organism which corresponds to the Locus ID can be determined by referring to the organism designation in the sequence listing for the coding nucleic acid or polypeptide SEQ ID NO. that corresponds to the particular Locus ID.

TABLE IV

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100001	ECO100001	100%	100%	100%
ECO100001	STY104800	85%	100%	100%
ECO100001	STM104529	85%	100%	100%
ECO100002	ABA101891	29%	40.9%	80.3%
ECO100002	BAN108126	29%	55.5%	98.5%
ECO100002	BAN105795	30%	55.5%	95.8%
ECO100002	BFR11028	36%	98.9%	99.4%
ECO100002	BPT101425	30%	41.5%	81.7%
ECO100002	BCE111633	28%	42.2%	73.4%
ECO100002	BMA100957	30%	41.3%	82.5%
ECO100002	CJU100543	30%	55.5%	97.8%
ECO100002	CDF100035	25%	5.4%	74.4%
ECO100002	CDF100673	25%	54.9%	96.7%
ECO100002	CDP101634	28%	46.1%	95.7%
ECO100002	EBC103170	92%	70.7%	100%
ECO100002	EFA201386	27%	56.2%	99.8%
ECO100002	ECO100002	100%	100%	100%
ECO100002	HIN100088	62%	99.3%	99.8%
ECO100002	HPY101212	32%	41.8%	83.5%
ECO100002	KPN300246	90%	4.1%	76.7%
ECO100002	KPN302085	92%	100%	100%
ECO100002	LMO102676	27%	57.3%	100%
ECO100002	MCA100888	30%	40.9%	80.3%
ECO100002	MAV103162	26%	55.5%	94.8%
ECO100002	MBV103584	28%	41.0%	79.6%
ECO100002	MLP101383	25%	55.5%	94.8%
ECO100002	MTU203655	28%	41.0%	79.6%
ECO100002	NGO100216	30%	8.9%	4.2%
ECO100002	NME201560	30%	8.9%	4.2%
ECO100002	PMU100113	64%	99.3%	99.8%
ECO100002	PRT104264	76%	100%	100%
ECO100002	PAE200903	30%	4.5%	5.6%
ECO100002	PPU106924	31%	40.9%	80.3%
ECO100002	PSY103112	30%	31.7%	82.0%
ECO100002	SPA100167	93%	39.5%	100%
ECO100002	STY100365	94%	100%	100%
ECO100002	STM100038	94%	100%	100%
ECO100002	SAU801327	26%	56.2%	97.6%
ECO100002	SEP201977	26%	56.2%	98.0%
ECO100002	SHA100755	26%	56.2%	99.8%
ECO100002	SMU100555	25%	56.6%	100%
ECO100002	SPN400374	25%	56.1%	98.7%
ECO100002	VCH102329	62%	100%	99.3%
ECO100002	YPS000769	81%	100%	100%
ECO100004	BFR11030	47%	85.3%	93.3%
ECO100004	BPT101337	32%	99.8%	99.4%
ECO100004	BCE114764	28%	97.4%	96.9%
ECO100004	BFU101149	29%	94.9%	94.6%
ECO100004	BMA105857	30%	90.4%	95.0%
ECO100004	CJU100751	29%	90.2%	87.2%
ECO100004	CAC103481	28%	99.5%	95.8%
ECO100004	CBO101914	30%	79.9%	86.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100004	CDF101928	31%	87.9%	85.6%
ECO100004	CDP100440	27%	99.3%	97.9%
ECO100004	EBC102668	92%	80.1%	100%
ECO100004	ECO100004	100%	100%	100%
ECO100004	HIN100086	66%	99.3%	99.5%
ECO100004	HPY100096	28%	89.3%	86.0%
ECO100004	KPN302095	90%	99.3%	99.8%
ECO100004	LPN102575	35%	89.7%	89.8%
ECO100004	MCA103682	29%	99.1%	98.5%
ECO100004	NGO101188	28%	99.1%	98.9%
ECO100004	NME201311	29%	99.1%	98.9%
ECO100004	PMU100115	69%	99.3%	99.8%
ECO100004	PRT104738	78%	99.3%	98.8%
ECO100004	PAE203732	33%	99.8%	98.5%
ECO100004	PPU107824	35%	93.9%	93.2%
ECO100004	PSY103804	34%	99.8%	98.5%
ECO100004	SPA100998	88%	57.0%	100%
ECO100004	STY100371	93%	100%	100%
ECO100004	STM100044	93%	100%	100%
ECO100004	SMU101311	31%	90.0%	87.2%
ECO100004	SPN401875	32%	90.2%	87.7%
ECO100004	VCH102327	68%	99.5%	99.5%
ECO100004	YPS000771	83%	99.3%	99.1%
ECO100005	BCE106023	30%	67.3%	35.5%
ECO100005	BFU106225	33%	74.5%	90.3%
ECO100005	BMA105475	31%	61.2%	52.5%
ECO100005	EBC102669	57%	99.0%	100%
ECO100005	ECO100005	100%	100%	100%
ECO100005	MAV107742	38%	53.1%	50.6%
ECO100005	PAE109842	33%	55.1%	23.9%
ECO100008	BPT101198	53%	98.7%	98.1%
ECO100008	BCE112831	56%	99.7%	90.3%
ECO100008	BFU112516	57%	99.7%	99.7%
ECO100008	BMA101518	57%	98.7%	98.7%
ECO100008	CJU100252	27%	55.2%	49.8%
ECO100008	EBC102672	94%	100%	100%
ECO100008	ECO100008	100%	100%	100%
ECO100008	HIN101098	79%	98.7%	98.7%
ECO100008	HPY101474	28%	58.4%	57.9%
ECO100008	KPN302087	91%	100%	100%
ECO100008	NME201973	31%	47.0%	41.9%
ECO100008	PMU101639	74%	97.8%	98.1%
ECO100008	PMU101602	77%	98.7%	98.7%
ECO100008	PRT104596	86%	100%	100%
ECO100008	PAE202794	60%	97.8%	97.7%
ECO100008	PPU101750	60%	99.4%	99.4%
ECO100008	PSY102944	60%	98.7%	98.4%
ECO100008	SPA100585	92%	62.1%	100%
ECO100008	STY100380	94%	100%	100%
ECO100008	STM100053	94%	100%	100%
ECO100008	SAU504318	30%	30.6%	17.8%
ECO100008	VCH103346	75%	98.7%	98.7%
ECO100008	YPS000773	88%	100%	100%
ECO100009	BPT100950	69%	96.4%	88.9%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100009	BCE102933	73%	96.4%	95.0%
ECO100009	BFU100752	72%	95.4%	88.1%
ECO100009	BMA109380	72%	96.4%	93.2%
ECO100009	CJU100675	50%	95.9%	97.2%
ECO100009	CAC100345	41%	79.5%	90.3%
ECO100009	CBO103886	42%	79.5%	92.0%
ECO100009	CDF101203	35%	78.5%	88.6%
ECO100009	EBC102673	90%	98.5%	98.5%
ECO100009	EFA202344	45%	71.3%	83.8%
ECO100009	ECO100009	100%	100%	100%
ECO100009	HIN100319	79%	96.9%	95.9%
ECO100009	HPY100786	48%	95.9%	99.4%
ECO100009	KPN302084	91%	98.5%	98.5%
ECO100009	MAV104045	37%	75.9%	91.9%
ECO100009	MBV100298	33%	75.9%	90%
ECO100009	MTU200856	33%	75.9%	90%
ECO100009	PMU102003	78%	96.4%	97.9%
ECO100009	PRT105678	82%	99.5%	99.5%
ECO100009	SPA100586	93%	98.5%	98.0%
ECO100009	STY100383	93%	98.5%	98.0%
ECO100009	STM100056	91%	98.5%	98.0%
ECO100009	YPS000774	87%	100%	100%
ECO100013	ECO100013	100%	100%	100%
ECO100013	KPN302079	66%	98.5%	100%
ECO100013	SPA105546	80%	100%	100%
ECO100013	STY106203	82%	100%	100%
ECO100023	ABA106150	60%	92.0%	67.2%
ECO100023	BAN103797	50%	96.6%	95.5%
ECO100023	BFR105539	39%	100%	100%
ECO100023	BPT101291	51%	100%	100%
ECO100023	BBU100232	38%	92.0%	74.8%
ECO100023	BCE112030	47%	98.9%	95.6%
ECO100023	BFU100359	51%	98.9%	93.5%
ECO100023	BMA106459	48%	98.9%	93.5%
ECO100023	CJU101517	34%	100%	100%
ECO100023	CPN201099	31%	94.3%	82.8%
ECO100023	CTR200896	33%	88.5%	75.5%
ECO100023	CAC102146	45%	98.9%	97.7%
ECO100023	CBO100245	39%	98.9%	97.7%
ECO100023	CDF101197	41%	96.6%	81.6%
ECO100023	CDP101196	47%	100%	100%
ECO100023	EBC101439	96%	70.1%	100%
ECO100023	EFA200336	48%	92.0%	95.2%
ECO100023	EFM201993	34%	97.7%	100%
ECO100023	ECO100023	100%	100%	100%
ECO100023	HIN100944	72%	100%	97.8%
ECO100023	HPY100074	33%	100%	97.8%
ECO100023	KPN205579	98%	100%	100%
ECO100023	LMO100322	46%	97.7%	100%
ECO100023	MCA100794	56%	98.9%	97.7%
ECO100023	MAV103835	43%	98.9%	100%
ECO100023	MBV104427	41%	98.9%	97.7%
ECO100023	MLP100381	41%	98.9%	100%
ECO100023	MTU202376	43%	98.9%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100023	MGE100374	30%	97.7%	88.6%
ECO100023	MPN100301	31%	97.7%	89.7%
ECO100023	NGO101642	57%	100%	100%
ECO100023	NME201868	57%	100%	100%
ECO100023	PMU101659	78%	100%	97.8%
ECO100023	PRT102018	83%	98.9%	100%
ECO100023	PAE204561	59%	100%	95.6%
ECO100023	PPU108230	59%	98.9%	93.5%
ECO100023	PSY102689	58%	100%	94.6%
ECO100023	SPA101944	97%	100%	100%
ECO100023	STY101095	97%	100%	100%
ECO100023	SAU801586	40%	90.8%	94.0%
ECO100023	SEP203256	37%	90.8%	90.7%
ECO100023	SHA102295	39%	90.8%	94.0%
ECO100023	SMU102606	41%	97.7%	92.9%
ECO100023	SPN400740	43%	97.7%	94.0%
ECO100023	SPY200946	45%	95.4%	98.7%
ECO100023	UUR100312	40%	88.5%	83.3%
ECO100023	VCH100666	70%	98.9%	100%
ECO100023	YPS003605	87%	98.9%	98.9%
ECO100025	ABA101842	41%	97.8%	97.3%
ECO100025	BAN106284	28%	98.1%	99.4%
ECO100025	BAN101499	35%	99.4%	97.2%
ECO100025	BFR100412	36%	98.4%	98.1%
ECO100025	BPT100434	47%	93.3%	93.1%
ECO100025	BCE109423	47%	98.1%	89.0%
ECO100025	BFU101232	45%	98.1%	92.7%
ECO100025	BMA109546	46%	98.1%	89.0%
ECO100025	CJU100550	26%	91.4%	91.9%
ECO100025	CPN200431	31%	92.0%	90.9%
ECO100025	CTR200362	32%	91.1%	93.9%
ECO100025	CAC102490	31%	89.8%	92.4%
ECO100025	CBO102062	31%	86.3%	97.8%
ECO100025	CDF100874	34%	95.5%	94.8%
ECO100025	CDP100453	30%	94.9%	90.1%
ECO100025	EBC100241	84%	56.9%	98.9%
ECO100025	EFA200587	31%	94.9%	94.3%
ECO100025	EFM201219	33%	97.1%	97.4%
ECO100025	ECO100025	100%	100%	100%
ECO100025	HIN100942	53%	98.1%	98.1%
ECO100025	HPY101070	30%	91.4%	93.6%
ECO100025	KPN300577	86%	91.1%	100%
ECO100025	LPN101116	45%	97.8%	92.7%
ECO100025	LMO100570	34%	92.3%	92.0%
ECO100025	MCA100302	41%	93.3%	93.8%
ECO100025	MAV100301	35%	92.0%	93.5%
ECO100025	MBV101247	35%	91.7%	98.4%
ECO100025	MLP100513	36%	91.7%	91.2%
ECO100025	MTU202748	35%	92.0%	91.5%
ECO100025	MGE100147	28%	89.5%	92.9%
ECO100025	MPN100673	27%	92.0%	96.7%
ECO100025	NGO101768	47%	97.1%	95.3%
ECO100025	NME200577	47%	97.1%	95.6%
ECO100025	PMU101661	58%	98.1%	98.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100025	PRT105259	67%	97.8%	97.8%
ECO100025	PAE204559	55%	98.1%	98.1%
ECO100025	PPU105777	52%	97.1%	95.9%
ECO100025	PSY102686	52%	97.1%	99.7%
ECO100025	SPA101946	88%	98.7%	100%
ECO100025	STY101100	89%	98.7%	98.7%
ECO100025	STM100815	89%	98.7%	98.7%
ECO100025	SAU801272	34%	97.1%	95.4%
ECO100025	SEP201565	35%	98.7%	96.9%
ECO100025	SHA100170	35%	97.1%	95.4%
ECO100025	SMU100956	36%	91.4%	92.5%
ECO100025	SPN401017	33%	92.0%	93.4%
ECO100025	SPY200960	32%	96.8%	96.1%
ECO100025	TPA100878	30%	69.6%	80%
ECO100025	UUR100357	26%	87.2%	86.9%
ECO100025	VCH100668	58%	97.1%	94.1%
ECO100025	YPS000809	75%	99.7%	99.7%
ECO100026	ABA103852	54%	99.8%	100%
ECO100026	BAN106248	37%	92.3%	96.1%
ECO100026	BAN106209	43%	86.5%	99.1%
ECO100026	BFR10500	25%	81.1%	79.2%
ECO100026	BPT100432	51%	99.5%	99.6%
ECO100026	BBU100832	26%	81.8%	74.0%
ECO100026	BCE111670	51%	95.3%	97.0%
ECO100026	BFU101230	51%	99.3%	98.4%
ECO100026	BMA102496	43%	98.5%	94.9%
ECO100026	BMA109115	50%	99.6%	98.7%
ECO100026	CJU100989	40%	96.3%	97.4%
ECO100026	CPN200653	26%	81.7%	73.5%
ECO100026	CTR200283	27%	81.0%	73.4%
ECO100026	CAC102765	27%	90.5%	81.7%
ECO100026	CBO100873	30%	55.1%	96.8%
ECO100026	CDF104554	29%	80.0%	72.4%
ECO100026	CDP101247	28%	89.1%	80.5%
ECO100026	EBC102151	92%	98.2%	100%
ECO100026	EFA202160	44%	98.1%	97.8%
ECO100026	EFM201425	44%	98.5%	98.1%
ECO100026	ECO100026	100%	100%	100%
ECO100026	HPY101401	39%	98.5%	99.2%
ECO100026	KPN300290	95%	4.7%	100%
ECO100026	KPN306610	92%	98.3%	100%
ECO100026	LPN101832	55%	99.9%	99.9%
ECO100026	LMO101679	43%	98.7%	99.2%
ECO100026	MCA103671	52%	0.9%	16.5%
ECO100026	MAV103388	27%	83.7%	74.6%
ECO100026	MBV102555	28%	82.3%	75.3%
ECO100026	MLP100743	24%	89.0%	80.8%
ECO100026	MTU201515	28%	82.3%	75.3%
ECO100026	MGE100354	32%	98.3%	99.4%
ECO100026	MPN100322	33%	89.3%	95.7%
ECO100026	NGO101799	53%	99.7%	100%
ECO100026	NME200578	53%	100%	100%
ECO100026	PMU101662	69%	99.8%	99.7%
ECO100026	PRT101657	80%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100026	PAE204558	57%	100%	100%
ECO100026	PPU109898	56%	100%	100%
ECO100026	PSY102684	54%	98.3%	100%
ECO100026	SPA100667	85%	82.8%	99.5%
ECO100026	STY101103	86%	100%	100%
ECO100026	STM100818	87%	100%	100%
ECO100026	SAU801193	42%	98.3%	99.0%
ECO100026	SEP200928	42%	98.3%	98.7%
ECO100026	SHA101034	41%	98.2%	99.5%
ECO100026	SMU100109	40%	98.5%	98.1%
ECO100026	SPN401501	41%	98.5%	98.1%
ECO100026	SPY201164	42%	95.8%	95.2%
ECO100026	TPA100448	26%	89.6%	81.1%
ECO100026	UUR100414	36%	97.0%	97.8%
ECO100026	VCH100669	67%	100%	100%
ECO100026	YPS000810	83%	100%	100%
ECO100032	BFR102496	39%	97.6%	100%
ECO100032	BCE114725	66%	97.1%	94.6%
ECO100032	BFU101987	64%	97.1%	90.0%
ECO100032	BMA105964	64%	97.1%	94.6%
ECO100032	CJU101410	40%	96.9%	99.5%
ECO100032	CAC100686	41%	96.3%	99.1%
ECO100032	CDF102200	42%	96.3%	98.8%
ECO100032	CDF101392	47%	97.1%	95.3%
ECO100032	CDP100339	45%	98.2%	94.4%
ECO100032	EBC100940	91%	51.8%	100%
ECO100032	EFA201091	45%	97.9%	98.6%
ECO100032	EFM201379	47%	96.9%	97.8%
ECO100032	ECO100032	100%	100%	100%
ECO100032	HPY101220	38%	97.1%	99.2%
ECO100032	KPN306459	80%	100%	100%
ECO100032	LPN100982	58%	97.6%	99.2%
ECO100032	LMO100114	46%	96.6%	96.1%
ECO100032	MCA101274	62%	96.6%	95.9%
ECO100032	MAV103355	43%	98.2%	99.2%
ECO100032	MBV100477	44%	57.6%	97.3%
ECO100032	MLP100326	42%	98.7%	100%
ECO100032	MTU201366	45%	97.6%	98.7%
ECO100032	NGO101672	67%	96.1%	96.6%
ECO100032	NME200564	67%	97.1%	97.6%
ECO100032	PMU101502	65%	97.1%	95.3%
ECO100032	PRT101652	81%	99.2%	97.9%
ECO100032	PAE204754	71%	99.0%	100%
ECO100032	PPU108522	70%	89.8%	100%
ECO100032	PSY107482	68%	64.4%	100%
ECO100032	SPA101379	86%	100%	100%
ECO100032	STY101157	93%	100%	100%
ECO100032	STM100872	94%	100%	100%
ECO100032	SAU801202	45%	97.6%	96.4%
ECO100032	SEP102450	43%	99.2%	98.1%
ECO100032	SHA102129	44%	99.2%	98.1%
ECO100032	SMU100787	43%	97.6%	97.2%
ECO100032	SPN401153	43%	98.2%	98.6%
ECO100032	SPY200619	43%	98.7%	98.9%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100032	VCH102355	82%	99.0%	99.7%
ECO100032	YPS000843	86%	99.7%	97.4%
ECO100033	ABA105447	76%	86.5%	51.8%
ECO100033	BAN106466	36%	92.5%	93.4%
ECO100033	BAN106013	50%	97.2%	73.8%
ECO100033	BFR11696	39%	96.3%	96.2%
ECO100033	BFR10760	40%	39.0%	91.4%
ECO100033	BPT101199	69%	97.1%	73.7%
ECO100033	BCE101906	68%	99.9%	99.9%
ECO100033	BFU114502	68%	99.9%	99.9%
ECO100033	BMA100194	68%	99.9%	99.9%
ECO100033	CJU100250	55%	100%	99.9%
ECO100033	CAC100380	46%	100%	100%
ECO100033	CDF103346	45%	68.9%	81.0%
ECO100033	CDF103290	48%	97.4%	97.7%
ECO100033	CDF102440	47%	97.4%	97.7%
ECO100033	CDP100338	52%	98.4%	98.2%
ECO100033	EBC103143	96%	4.1%	77.8%
ECO100033	EFA201093	49%	98.6%	99.4%
ECO100033	EFM200554	48%	98.6%	99.4%
ECO100033	ECO100033	100%	100%	100%
ECO100033	HPY100903	53%	99.4%	99.7%
ECO100033	KPN306727	95%	92.1%	92.8%
ECO100033	LPN103124	72%	90.9%	74.6%
ECO100033	LMO101147	50%	98.8%	98.5%
ECO100033	MCA101278	70%	99.7%	99.9%
ECO100033	MAV103356	51%	99.9%	99.4%
ECO100033	MBV100481	52%	99.9%	99.6%
ECO100033	MLP100327	51%	99.9%	98.3%
ECO100033	MTU301470	52%	99.9%	99.6%
ECO100033	NGO101630	69%	100%	99.7%
ECO100033	NME200558	69%	100%	99.7%
ECO100033	PMU101505	69%	99.9%	99.9%
ECO100033	PRT101651	90%	100%	99.8%
ECO100033	PAE204752	76%	100%	99.9%
ECO100033	PPU105037	74%	100%	99.6%
ECO100033	PSY104746	75%	100%	99.9%
ECO100033	SPA101378	93%	87.4%	63.3%
ECO100033	STY101163	98%	100%	99.8%
ECO100033	STM100875	98%	100%	99.8%
ECO100033	SAU801203	49%	99.5%	100%
ECO100033	SEP201467	52%	86.8%	35.4%
ECO100033	SHA102130	49%	99.5%	100%
ECO100033	SMU100789	50%	98.4%	99.2%
ECO100033	SPN401152	49%	98.4%	99.2%
ECO100033	SPY200620	49%	98.4%	99.2%
ECO100033	VCH102354	85%	100%	99.6%
ECO100033	YPS000846	92%	100%	99.6%
ECO100040	ECO100040	100%	100%	100%
ECO100040	MAV102307	26%	22.0%	44.2%
ECO100040	PRT105337	87%	100%	100%
ECO100040	SPA102043	92%	54.8%	100%
ECO100040	STY101185	96%	100%	99.8%
ECO100068	BPT100719	25%	79.8%	77.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100068	BCE110446	23%	97.2%	89.3%
ECO100068	BFU104253	25%	59.3%	49.6%
ECO100068	CJU100163	23%	81.0%	82.0%
ECO100068	EBC103044	90%	96.0%	97.5%
ECO100068	ECO100068	100%	100%	100%
ECO100068	HIN100998	50%	99.1%	99.7%
ECO100068	KPN303934	83%	100%	100%
ECO100068	MCA100722	24%	85.6%	85.2%
ECO100068	NGO101933	30%	97.9%	97.3%
ECO100068	NME200270	29%	97.9%	97.3%
ECO100068	PMU100376	49%	95.4%	94.3%
ECO100068	PRT100202	66%	93.9%	94.5%
ECO100068	PAE204684	26%	81.7%	79.7%
ECO100068	PSY105429	22%	88.4%	87.8%
ECO100068	SPA101253	89%	100%	100%
ECO100068	STY101259	91%	100%	100%
ECO100068	TPA100143	31%	91.4%	90.7%
ECO100068	VCH102502	65%	97.6%	97.0%
ECO100068	YPS000940	72%	98.8%	97.9%
ECO100069	BAN110716	37%	7.8%	66.2%
ECO100069	BAN110657	27%	12.0%	60.6%
ECO100069	BAN101932	26%	57.5%	56.3%
ECO100069	EBC103045	79%	100%	100%
ECO100069	ECO100069	100%	100%	100%
ECO100069	KPN303932	78%	100%	100%
ECO100069	LMO101504	24%	94.4%	91.4%
ECO100069	PRT103304	47%	54.3%	100%
ECO100069	SPA101254	81%	99.5%	100%
ECO100069	STY101261	86%	100%	100%
ECO100069	STM100598	38%	99.5%	99.7%
ECO100069	VCH103302	33%	99.5%	99.1%
ECO100069	YPS000941	62%	99.8%	99.8%
ECO100081	BFR12308	32%	53.9%	68.6%
ECO100081	BPT103032	44%	87.5%	90.8%
ECO100081	BCE103942	47%	82.9%	85.9%
ECO100081	BFU100820	48%	82.2%	85.2%
ECO100081	BMA105750	47%	82.2%	85.2%
ECO100081	CAC103463	29%	100%	100%
ECO100081	CBO101902	31%	91.4%	85.9%
ECO100081	CDP101285	34%	93.4%	95.8%
ECO100081	EBC101941	95%	78.9%	100%
ECO100081	EFA202186	34%	88.2%	92.3%
ECO100081	EFM202534	39%	82.2%	83.9%
ECO100081	ECO100081	100%	100%	100%
ECO100081	HIN101103	59%	100%	100%
ECO100081	KPN301855	93%	78.9%	100%
ECO100081	LPN102025	43%	100%	100%
ECO100081	LMO101121	36%	96.7%	96.5%
ECO100081	MAV103918	32%	94.1%	99.3%
ECO100081	MBV101485	31%	94.1%	99.3%
ECO100081	MLP100560	32%	94.1%	99.3%
ECO100081	MTU202132	31%	94.1%	99.3%
ECO100081	MGE100226	27%	98.0%	90.3%
ECO100081	MPN100522	28%	98.7%	99.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100081	NGO100621	40%	91.4%	93.4%
ECO100081	NME201917	40%	91.4%	93.4%
ECO100081	PMU100133	55%	100%	100%
ECO100081	PRT102634	77%	100%	100%
ECO100081	PAE204419	51%	100%	100%
ECO100081	PPU105962	50%	100%	100%
ECO100081	PSY103859	52%	100%	100%
ECO100081	SPA102750	93%	100%	100%
ECO100081	STY103147	93%	100%	100%
ECO100081	STM102859	94%	100%	100%
ECO100081	SAU801178	33%	98.0%	97.9%
ECO100081	SEP200891	32%	98.0%	97.9%
ECO100081	SHA101307	33%	98.0%	97.9%
ECO100081	TPA100379	34%	99.3%	96.6%
ECO100081	UUR100388	25%	96.7%	96.6%
ECO100081	YPS000986	84%	100%	100%
ECO100093	ABA100624	24%	88.0%	82.7%
ECO100093	BAN113055	20%	68.1%	70.9%
ECO100093	BAN105429	21%	68.1%	74.2%
ECO100093	BPT102987	28%	89.1%	94.5%
ECO100093	BCE102722	30%	75%	82%
ECO100093	BFU100406	28%	81.9%	88%
ECO100093	BMA104087	29%	75%	82%
ECO100093	CDP101255	29%	22.8%	31.2%
ECO100093	EBC101799	85%	100%	100%
ECO100093	ECO100093	100%	100%	100%
ECO100093	HIN101115	39%	83.7%	86.6%
ECO100093	KPN301845	88%	100%	100%
ECO100093	LPN103526	29%	85.1%	95.0%
ECO100093	MCA100437	24%	66.3%	74.6%
ECO100093	MAV103267	23%	43.8%	55.3%
ECO100093	MLP100571	24%	34.4%	27.9%
ECO100093	NGO100580	34%	85.9%	94.6%
ECO100093	NME201903	34%	85.9%	94.6%
ECO100093	PMU100145	37%	87.0%	93.4%
ECO100093	PRT102631	61%	93.8%	97.7%
ECO100093	PAE204407	31%	74.6%	70.0%
ECO100093	PPU105995	32%	90.9%	87.2%
ECO100093	PSY103839	33%	83.7%	81.3%
ECO100093	SPA101845	93%	100%	100%
ECO100093	STY103179	93%	100%	100%
ECO100093	STM102891	93%	100%	100%
ECO100093	SEP200899	22%	62.7%	39.8%
ECO100093	SHA100844	23%	62.0%	47.2%
ECO100093	VCH102364	39%	88.0%	90.4%
ECO100093	YPS001020	66%	97.5%	99.6%
ECO100094	ABA100623	30%	96.7%	95.7%
ECO100094	BAN111291	31%	94.3%	89.7%
ECO100094	BAN101900	32%	93.6%	88.2%
ECO100094	BFR102146	24%	79.8%	68.3%
ECO100094	BPT102984	45%	97.4%	98.0%
ECO100094	BBU100299	35%	98.6%	99.3%
ECO100094	BCE109663	46%	98.6%	98.8%
ECO100094	BFU100407	46%	98.6%	98.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100094	BMA104126	47%	98.6%	98.8%
ECO100094	CJU100645	27%	89.8%	80.3%
ECO100094	CAC100288	26%	89.0%	86.6%
ECO100094	CBO102974	28%	89.0%	85.0%
ECO100094	EBC101798	98%	100%	100%
ECO100094	EFA202170	33%	90.5%	83.6%
ECO100094	EFM201888	32%	89.8%	82.8%
ECO100094	ECO100094	100%	100%	100%
ECO100094	HIN101116	52%	100%	100%
ECO100094	HPY100962	25%	92.9%	83.9%
ECO100094	KPN300531	96%	58.3%	100%
ECO100094	LPN103001	44%	100%	100%
ECO100094	LMO101001	32%	95%	89.7%
ECO100094	MCA100438	25%	82.4%	78.9%
ECO100094	NGO100578	41%	97.6%	98.1%
ECO100094	NME201902	42%	97.1%	97.6%
ECO100094	PMU100146	50%	100%	100%
ECO100094	PRT102629	89%	100%	100%
ECO100094	PAE204406	51%	93.6%	92.6%
ECO100094	PPU111774	52%	90%	90.0%
ECO100094	PSY103837	52%	91.7%	92.2%
ECO100094	SPA101844	97%	100%	100%
ECO100094	STY103209	99%	100%	100%
ECO100094	STM102892	99%	100%	100%
ECO100094	SAU801185	24%	88.8%	76.6%
ECO100094	SEP200915	25%	88.8%	77.6%
ECO100094	SHA100845	25%	83.6%	71.9%
ECO100094	SMU100084	31%	89.0%	79.9%
ECO100094	SPN401510	33%	83.3%	74.8%
ECO100094	SPY201171	31%	89.0%	79.7%
ECO100094	TPA100385	33%	93.3%	95.9%
ECO100094	VCH102363	68%	100%	100%
ECO100094	YPS001022	95%	100%	100%
ECO100095	ABA100622	49%	95.8%	93.9%
ECO100095	BAN103024	47%	96.9%	96.4%
ECO100095	BAN112439	48%	96.9%	96.4%
ECO100095	BFR12421	43%	84.1%	74.1%
ECO100095	BPT102981	53%	97.1%	96.4%
ECO100095	BBU100298	47%	97.1%	92.3%
ECO100095	BCE103310	58%	75.7%	100%
ECO100095	BFU100408	52%	98.2%	97.7%
ECO100095	BMA104500	52%	99.7%	99.5%
ECO100095	CJU100646	40%	100%	98.9%
ECO100095	CAC100838	50%	96.9%	95.7%
ECO100095	CBO103263	49%	96.9%	96.5%
ECO100095	CDF102447	48%	98.4%	96.2%
ECO100095	CDP101254	51%	84.6%	77.9%
ECO100095	EBC101797	97%	41.5%	97.5%
ECO100095	EFA202168	51%	90.1%	84.1%
ECO100095	EFM200220	54%	82.0%	75.8%
ECO100095	ECO100095	100%	100%	100%
ECO100095	HIN101117	63%	79.9%	77.9%
ECO100095	HPY100963	40%	79.4%	79.5%
ECO100095	KPN300530	98%	41.8%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100095	LPN100473	71%	9.4%	100%
ECO100095	LMO101235	46%	96.9%	96.2%
ECO100095	MCA101528	55%	85.9%	91.9%
ECO100095	MAV103265	47%	96.6%	97.7%
ECO100095	MBV100533	53%	79.4%	79.9%
ECO100095	MLP100572	45%	96.6%	97.9%
ECO100095	MTU202116	53%	79.4%	79.9%
ECO100095	MGE100229	34%	54.6%	55.6%
ECO100095	MPN100519	32%	54.0%	53.4%
ECO100095	NGO100577	48%	96.9%	95.2%
ECO100095	NME201901	48%	96.9%	95.2%
ECO100095	PMU100147	62%	87.5%	82.7%
ECO100095	PRT102627	94%	48.8%	100%
ECO100095	PAE204405	57%	100%	100%
ECO100095	PPU105993	58%	100%	100%
ECO100095	PSY103835	57%	100%	100%
ECO100095	SPA100031	91%	67.1%	98.1%
ECO100095	STY103211	98%	100%	100%
ECO100095	STM102893	98%	100%	100%
ECO100095	SAU801186	52%	81.2%	79.0%
ECO100095	SEP200917	45%	97.4%	95.2%
ECO100095	SHA100846	45%	97.4%	95.2%
ECO100095	SMU100085	51%	89.6%	78.1%
ECO100095	SPN401509	56%	80.7%	73.5%
ECO100095	SPY201170	54%	82.0%	71.3%
ECO100095	TPA100386	49%	79.4%	72.7%
ECO100095	VCH102362	75%	100%	100%
ECO100095	YPS001023	94%	100%	100%
ECO100096	ABA100621	49%	71.5%	100%
ECO100096	BFR100706	38%	88.5%	63.3%
ECO100096	BPT102979	52%	97.7%	98.0%
ECO100096	BCE106802	54%	97.4%	97.0%
ECO100096	BFU106497	53%	97.4%	97.0%
ECO100096	BMA100406	55%	97.4%	97.0%
ECO100096	CJU100121	42%	94.1%	95.9%
ECO100096	CPN200093	36%	89.2%	95.8%
ECO100096	CTR200809	38%	90.8%	95.5%
ECO100096	EBC100070	97%	37.4%	100%
ECO100096	EFA204185	36%	16.4%	7.8%
ECO100096	ECO100096	100%	100%	100%
ECO100096	HIN101118	77%	99.7%	99.7%
ECO100096	HPY101035	42%	95.4%	96.9%
ECO100096	KPN300609	94%	76.7%	100%
ECO100096	MCA100416	54%	97.0%	97.7%
ECO100096	NGO101976	48%	96.4%	96.4%
ECO100096	NME200247	49%	96.4%	96.4%
ECO100096	PMU100148	77%	99.7%	99.7%
ECO100096	PRT100138	86%	90.8%	100%
ECO100096	PAE204404	57%	99.7%	100%
ECO100096	PPU111772	56%	99.7%	100%
ECO100096	PSY103834	56%	99.7%	100%
ECO100096	SPA100700	87%	100%	100%
ECO100096	STY103212	98%	100%	100%
ECO100096	STM102894	98%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100096	VCH102361	73%	100%	100%
ECO100096	YPS001024	92%	100%	98.1%
ECO100102	BPT102719	31%	100%	99.2%
ECO100102	BCE111292	30%	91.5%	91.2%
ECO100102	BFU101371	31%	98.4%	98.8%
ECO100102	BMA106052	30%	98.4%	98.8%
ECO100102	EBC103445	80%	100%	100%
ECO100102	ECO100102	100%	100%	100%
ECO100102	KPN301732	76%	97.6%	100%
ECO100102	LPN101018	24%	93.9%	92.7%
ECO100102	PRT104002	53%	98.4%	97.2%
ECO100102	PPU100250	45%	16.2%	97.6%
ECO100102	SPA101560	89%	100%	100%
ECO100102	STY103218	89%	100%	100%
ECO100102	VCH102393	40%	97.6%	97.6%
ECO100102	YPS000901	67%	100%	98.8%
ECO100113	BAN100380	31%	84.6%	98.2%
ECO100113	BMA109038	39%	90.6%	63.6%
ECO100113	CDF100440	28%	89.0%	86.6%
ECO100113	EBC103453	92%	100%	100%
ECO100113	ECO100113	100%	100%	100%
ECO100113	KPN307947	90%	24.0%	92.4%
ECO100113	KPN301741	93%	100%	98.1%
ECO100113	LMO100648	28%	89.4%	95.2%
ECO100113	MAV105850	25%	90.6%	92%
ECO100113	MAV106443	25%	91.7%	94.7%
ECO100113	MAV106442	28%	86.6%	85%
ECO100113	NGO100599	34%	96.9%	94.6%
ECO100113	NME201814	34%	96.9%	94.2%
ECO100113	PRT106136	79%	98.8%	96.2%
ECO100113	PAE204765	47%	97.6%	97.7%
ECO100113	PPU100113	46%	97.6%	98.8%
ECO100113	SPA100332	95%	100%	100%
ECO100113	STY103289	96%	100%	100%
ECO100113	STM102972	96%	100%	100%
ECO100113	VCH102380	65%	98.8%	98.0%
ECO100113	YPS000871	86%	99.6%	99.6%
ECO100115	ABA105536	46%	33.7%	68.0%
ECO100115	BAN101075	31%	0.2%	45.1%
ECO100115	BAN101226	36%	17.1%	43.7%
ECO100115	BPT100902	56%	0.2%	43.0%
ECO100115	BCE106716	56%	21.1%	4.3%
ECO100115	BFU100111	53%	25.9%	13.8%
ECO100115	BMA108930	53%	20.8%	55.4%
ECO100115	CJU100863	21%	4.3%	34.7%
ECO100115	CDP100400	34%	98.7%	98.2%
ECO100115	EBC102752	90%	100%	100%
ECO100115	EFA202405	34%	37.1%	59.6%
ECO100115	EFM201990	32%	37.1%	60.1%
ECO100115	ECO100115	100%	100%	100%
ECO100115	HIN101204	68%	34.6%	58.6%
ECO100115	KPN301446	91%	100%	100%
ECO100115	LPN100774	45%	10.3%	53.9%
ECO100115	LMO102367	35%	37.1%	60.1%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100115	MCA101150	39%	19.0%	44.2%
ECO100115	MAV103601	31%	1.6%	33.2%
ECO100115	MTU405582	32%	50.2%	84.6%
ECO100115	MTU400129	32%	64.4%	99.8%
ECO100115	MGE100278	25%	16.5%	26.3%
ECO100115	MPN100447	27%	3.2%	46.0%
ECO100115	NGO100078	53%	15.6%	38.0%
ECO100115	NME201414	56%	33.2%	19.6%
ECO100115	PMU100894	72%	100%	100%
ECO100115	PRT102280	78%	100%	100%
ECO100115	PAE205011	54%	83.0%	99.3%
ECO100115	PPU105100	54%	18.7%	59.2%
ECO100115	PSY103646	52%	20.2%	43.8%
ECO100115	SPA100283	80%	60.5%	100%
ECO100115	STY103294	93%	100%	100%
ECO100115	STM102974	93%	100%	100%
ECO100115	SAU101783	36%	39.8%	77.6%
ECO100115	SPY200777	30%	3.8%	35.4%
ECO100115	VCH102378	74%	100%	99.1%
ECO100115	YPS000863	79%	14.0%	37.7%
ECO100116	ABA101766	38%	95.6%	96.4%
ECO100116	BAN101609	33%	96.4%	97.0%
ECO100116	BAN103383	44%	96.4%	97.0%
ECO100116	BFR10034	33%	94.1%	98.2%
ECO100116	BFR11786	32%	94.1%	98.7%
ECO100116	BPT100905	63%	99.6%	79.2%
ECO100116	BCE110691	66%	97.9%	79.7%
ECO100116	BFU100082	65%	99.4%	92.9%
ECO100116	BMA107694	65%	99.6%	80.0%
ECO100116	CPN201018	35%	93.0%	94.1%
ECO100116	CTR200835	38%	93.0%	94.0%
ECO100116	CBO103777	35%	93.5%	95.2%
ECO100116	CBO103904	37%	94.7%	97.0%
ECO100116	CDF102926	38%	94.7%	95.7%
ECO100116	CDP100695	36%	96.6%	98.7%
ECO100116	EBC102751	97%	100%	100%
ECO100116	EFA202404	43%	96.4%	97.4%
ECO100116	EFM201020	42%	96.4%	97.4%
ECO100116	ECO100116	100%	100%	100%
ECO100116	HIN101203	81%	100%	99.2%
ECO100116	KPN301447	96%	100%	99.8%
ECO100116	LPN100879	62%	100%	100%
ECO100116	LMO101821	43%	95.4%	96.4%
ECO100116	MCA101643	37%	98.1%	98.8%
ECO100116	MAV101768	37%	95.6%	97.0%
ECO100116	MBV103409	37%	97.0%	98.7%
ECO100116	MLP101416	34%	97.0%	98.7%
ECO100116	MTU200460	37%	97.0%	98.7%
ECO100116	MGE100277	32%	93.7%	96.3%
ECO100116	MPN100448	33%	93.7%	96.3%
ECO100116	NGO100074	63%	99.4%	81.1%
ECO100116	NME201415	63%	99.4%	81.1%
ECO100116	PMU100893	88%	100%	100%
ECO100116	PRT102281	90%	100%	99.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100116	PAE201586	42%	98.5%	99.4%
ECO100116	PPU103115	40%	98.5%	99.4%
ECO100116	PSY104859	41%	98.5%	99.4%
ECO100116	SPA100336	96%	83.5%	100%
ECO100116	STY103295	98%	100%	99.8%
ECO100116	STM103004	98%	100%	100%
ECO100116	SAU801096	44%	95.6%	96.4%
ECO100116	SEP200806	45%	95.6%	96.4%
ECO100116	SHA100679	44%	95.6%	96.8%
ECO100116	SMU101480	36%	93.2%	74.7%
ECO100116	SPN401048	38%	93.2%	76.5%
ECO100116	SPY200778	35%	97.5%	77.7%
ECO100116	VCH102377	89%	100%	99.8%
ECO100116	YPS000861	93%	100%	99.8%
ECO100117	BPT103682	29%	59.3%	100%
ECO100117	BCE104746	29%	31.9%	62.8%
ECO100117	BFU101391	43%	46.8%	46.8%
ECO100117	BFU100907	41%	49.3%	57.2%
ECO100117	EBC102750	48%	89.5%	100%
ECO100117	EFA200061	22%	25.8%	20.0%
ECO100117	EFA201265	22%	25.8%	20.0%
ECO100117	ECO100117	100%	100%	100%
ECO100117	KPN305987	52%	91.2%	96.4%
ECO100117	MCA102218	28%	10.9%	46.5%
ECO100117	PPU101283	36%	77.3%	91.2%
ECO100117	SPA101490	56%	88.8%	100%
ECO100117	STY103296	58%	87.8%	98.0%
ECO100117	SAU800401	27%	13.1%	11.6%
ECO100117	SPN401793	29%	14.1%	22.7%
ECO100118	ABA100442	74%	99.3%	98.7%
ECO100118	BPT102269	72%	99.1%	99.5%
ECO100118	BCE109527	73%	99.3%	99.8%
ECO100118	BFU107948	74%	99.3%	98.1%
ECO100118	CJU100774	60%	98.4%	99.2%
ECO100118	EBC106332	96%	82.5%	100%
ECO100118	ECO100118	100%	100%	100%
ECO100118	HPY100766	61%	98.4%	99.2%
ECO100118	KPN300389	95%	18.2%	90.2%
ECO100118	KPN300864	96%	93.5%	100%
ECO100118	MCA101955	73%	95.5%	99.3%
ECO100118	NGO101334	74%	99.3%	99.8%
ECO100118	NME201620	74%	99.3%	99.8%
ECO100118	PMU100204	81%	99.9%	99.5%
ECO100118	PRT101310	88%	100%	100%
ECO100118	PAE201786	79%	99.0%	98.8%
ECO100118	PPU111285	79%	96.3%	96.0%
ECO100118	PSY101607	78%	99.0%	96.3%
ECO100118	SPA100508	94%	60%	100%
ECO100118	STY103298	96%	100%	100%
ECO100118	STM103008	96%	100%	100%
ECO100118	TPA100176	31%	13.3%	37.0%
ECO100118	VCH100593	82%	99.7%	99.7%
ECO100118	YPS000857	90%	100%	100%
ECO100135	ECO100135	100%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100135	SPA106733	29%	40.3%	97.3%
ECO100135	STY103389	32%	98.5%	97.2%
ECO100136	ECO100136	100%	100%	100%
ECO100136	SPA109709	36%	58.6%	98.2%
ECO100136	STY103420	37%	86.4%	84.8%
ECO100139	ABA100394	33%	96.0%	97.9%
ECO100139	ABA100739	36%	92.5%	97.6%
ECO100139	BFU103132	30%	68.4%	77.5%
ECO100139	BFU103304	38%	76.4%	92.9%
ECO100139	BFU103222	33%	94.7%	87.3%
ECO100139	ECO100139	100%	100%	100%
ECO100139	KPN302863	35%	94.3%	96.5%
ECO100139	PRT105280	35%	93.9%	93.8%
ECO100139	PAE204081	35%	93.2%	94.2%
ECO100139	SPA104033	45%	96.4%	100%
ECO100139	STY103424	60%	98.3%	98.4%
ECO100139	SHA101318	19%	16.4%	31.5%
ECO100139	SPY100688	22%	23.1%	53.9%
ECO100139	TPA100432	23%	19.5%	46.1%
ECO100139	YPS000524	36%	93.1%	91.7%
ECO100140	ABA100736	35%	95.1%	96.7%
ECO100140	ABA100392	40%	88.2%	88.2%
ECO100140	BPT101284	41%	87.0%	75.9%
ECO100140	BFU103245	39%	94.7%	97.9%
ECO100140	BFU103302	47%	93.9%	93.5%
ECO100140	ECO100140	100%	100%	100%
ECO100140	KPN302865	39%	91.5%	93.6%
ECO100140	PRT105676	42%	95.9%	90.7%
ECO100140	PAE204082	39%	87.0%	85.1%
ECO100140	PPU101843	34%	43.9%	81.8%
ECO100140	PSY105016	36%	87.0%	76.6%
ECO100140	SPA104034	48%	97.2%	95.2%
ECO100140	STY103425	57%	100%	100%
ECO100140	YPS000522	41%	96.7%	92.3%
ECO100142	ABA105477	47%	88.1%	85.6%
ECO100142	BAN112513	43%	84.3%	77.8%
ECO100142	BFR100366	39%	84.9%	88.9%
ECO100142	BPT101655	40%	88.7%	85.3%
ECO100142	BCE102263	49%	49.7%	62.9%
ECO100142	BFU102640	37%	99.4%	85.7%
ECO100142	BMA109305	39%	95.0%	87.4%
ECO100142	CJU100058	29%	79.9%	80.3%
ECO100142	CAC103001	38%	84.9%	48.7%
ECO100142	CBO100107	41%	87.4%	90.7%
ECO100142	CDF102980	37%	86.2%	50.6%
ECO100142	CDP100654	36%	93.7%	90.6%
ECO100142	EBC102063	85%	88.1%	100%
ECO100142	ECO100142	100%	100%	100%
ECO100142	HIN100063	56%	99.4%	98.1%
ECO100142	HPY101019	31%	86.2%	83.4%
ECO100142	KPN308497	77%	100%	100%
ECO100142	LPN102612	37%	88.1%	98.6%
ECO100142	LMO102140	42%	84.9%	84.3%
ECO100142	MCA100865	38%	99.4%	98.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100142	MAV104005	38%	88.7%	78.0%
ECO100142	MBV102400	33%	84.3%	73.9%
ECO100142	MLP100158	35%	80.5%	70.2%
ECO100142	MTU203554	33%	84.3%	73.9%
ECO100142	NGO101986	42%	84.3%	81.1%
ECO100142	NME200881	43%	84.3%	81.1%
ECO100142	PMU100865	57%	92.5%	88.5%
ECO100142	PRT102518	62%	97.5%	95.2%
ECO100142	PAE204724	51%	96.9%	94.4%
ECO100142	PPU108440	48%	99.4%	99.4%
ECO100142	PSY105158	53%	96.9%	93.3%
ECO100142	SPA104025	80%	98.1%	100%
ECO100142	STY103427	89%	90.6%	90.6%
ECO100142	SAU800516	40%	89.9%	89.9%
ECO100142	SEP201849	43%	87.4%	86.8%
ECO100142	SHA100112	41%	87.4%	86.8%
ECO100142	SMU100995	42%	86.2%	77.7%
ECO100142	SPN400269	36%	97.5%	55.2%
ECO100142	SPY200833	44%	87.4%	83.1%
ECO100142	VCH100582	58%	100%	95.2%
ECO100142	YPS000787	65%	93.1%	93.1%
ECO100144	ABA104779	45%	93.8%	91.9%
ECO100144	BPT100055	48%	88.6%	96.8%
ECO100144	BCE107846	45%	88.6%	95.6%
ECO100144	BFU114519	47%	83.1%	86.6%
ECO100144	BMA109098	46%	81.8%	88.9%
ECO100144	EBC102068	78%	92.9%	90.2%
ECO100144	ECO100144	100%	100%	100%
ECO100144	KPN306084	76%	92.9%	97.6%
ECO100144	MCA102257	34%	88.3%	93.8%
ECO100144	NGO101470	46%	91.9%	98.6%
ECO100144	NME201975	45%	91.9%	98.6%
ECO100144	PAE204720	48%	92.2%	96.9%
ECO100144	PPU108420	50%	93.8%	96.3%
ECO100144	PSY105149	44%	81.8%	96.9%
ECO100144	SPA104029	79%	80.5%	98.4%
ECO100144	STY103460	81%	96.4%	99.7%
ECO100144	VCH100584	56%	96.4%	98.0%
ECO100144	YPS000781	71%	91.2%	87.5%
ECO100145	ABA104294	63%	95.4%	81.5%
ECO100145	BAN111357	29%	69.5%	51.8%
ECO100145	BAN107715	31%	69.5%	46.5%
ECO100145	BPT100533	37%	94.7%	92.2%
ECO100145	BBU100167	29%	74.2%	92%
ECO100145	BCE102976	45%	78.8%	85.5%
ECO100145	BFU114180	43%	78.8%	84.9%
ECO100145	BMA106451	46%	78.8%	85.5%
ECO100145	CJU100114	26%	76.8%	97.5%
ECO100145	CTR200677	23%	74.2%	85.8%
ECO100145	CAC101598	27%	71.5%	58.5%
ECO100145	CBO101773	30%	63.6%	54.1%
ECO100145	CDF100661	32%	32.5%	30.1%
ECO100145	EBC102067	98%	100%	100%
ECO100145	ECO100145	100%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100145	HIN100061	75%	94.0%	97.9%
ECO100145	KPN304195	98%	100%	100%
ECO100145	LPN103126	72%	88.1%	84.2%
ECO100145	MCA101582	62%	86.1%	93.5%
ECO100145	NGO101937	45%	82.1%	89.1%
ECO100145	NME200203	45%	82.1%	89.1%
ECO100145	PMU100863	80%	94.0%	97.9%
ECO100145	PRT101562	94%	100%	100%
ECO100145	PAE204719	76%	86.8%	88.5%
ECO100145	PPU108418	68%	85.4%	83.8%
ECO100145	PSY100089	76%	74.2%	96.6%
ECO100145	SPA104031	97%	30.5%	100%
ECO100145	STY103461	98%	100%	100%
ECO100145	SAU801431	32%	31.1%	80.3%
ECO100145	SPY200759	50%	19.9%	34.7%
ECO100145	TPA100095	29%	56.3%	65%
ECO100145	VCH100585	85%	95.4%	97.3%
ECO100145	YPS000779	94%	100%	100%
ECO100148	CDP101536	34%	89.7%	99.0%
ECO100148	EBC102064	78%	69.9%	100%
ECO100148	ECO100148	100%	100%	100%
ECO100148	KPN304202	81%	98.2%	100%
ECO100148	PRT101564	55%	97.8%	99.6%
ECO100148	PAE203958	47%	97.6%	99.4%
ECO100148	PPU107649	45%	96.7%	99.5%
ECO100148	PSY108786	45%	97.6%	96.6%
ECO100148	SPA101069	75%	100%	100%
ECO100148	STY103465	84%	98.7%	100%
ECO100148	STM103140	84%	100%	100%
ECO100148	VCH100590	48%	97.9%	99.5%
ECO100148	YPS000776	65%	98.1%	98.6%
ECO100150	ABA103956	29%	98.5%	99.0%
ECO100150	BFR104161	21%	22.4%	18.2%
ECO100150	BFR100416	25%	19.0%	17.3%
ECO100150	BFR10467	21%	20.3%	20.2%
ECO100150	BFR11841	27%	16.1%	17.5%
ECO100150	BFR101776	25%	17.0%	16.1%
ECO100150	BFR103964	23%	20.5%	20.3%
ECO100150	BFR104855	31%	11.8%	13.2%
ECO100150	BFR100601	22%	44.0%	33.4%
ECO100150	BFR10065	27%	16.3%	36.7%
ECO100150	BFR103068	20%	21.4%	22.6%
ECO100150	BFR104786	21%	26.6%	24.0%
ECO100150	BFR10126	22%	86.9%	79.2%
ECO100150	BPT101854	38%	93.2%	83.9%
ECO100150	BCE111433	33%	82.6%	98.4%
ECO100150	BFU107418	24%	98.4%	96.3%
ECO100150	BMA109111	34%	95.9%	94.8%
ECO100150	EBC101242	89%	96.5%	100%
ECO100150	ECO100150	100%	100%	100%
ECO100150	HIN101435	26%	39.2%	87.2%
ECO100150	KPN304208	60%	100%	100%
ECO100150	MCA102097	23%	23.2%	19.8%
ECO100150	MBV102043	29%	9.1%	35.6%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100150	MTU202942	29%	9.1%	37.6%
ECO100150	PRT104914	33%	99.7%	98.9%
ECO100150	PAE202464	38%	91.7%	80.7%
ECO100150	PPU105337	38%	94.4%	97.9%
ECO100150	PSY101285	37%	97.3%	97.2%
ECO100150	SPA100272	91%	47.4%	100%
ECO100150	STY104553	35%	98.1%	99.3%
ECO100150	STM103144	73%	100%	100%
ECO100150	TPA100587	29%	14.1%	47.5%
ECO100150	VCH100198	32%	91.3%	90.7%
ECO100150	YPS000978	26%	96.5%	98.1%
ECO100151	BFR105362	32%	78.5%	82.5%
ECO100151	BFU102313	62%	98.1%	88.1%
ECO100151	CJU101278	38%	89.8%	94.0%
ECO100151	EFA201996	42%	87.5%	91.6%
ECO100151	ECO100151	100%	100%	100%
ECO100151	HPY100874	31%	90.9%	94.9%
ECO100151	KPN304210	92%	100%	100%
ECO100151	PRT102499	36%	89.8%	94.0%
ECO100151	PPU100161	42%	86.0%	87.6%
ECO100151	SPA100271	75%	67.5%	100%
ECO100151	STY103469	91%	100%	100%
ECO100151	STM103175	92%	100%	100%
ECO100151	SMU100116	38%	90.2%	88.4%
ECO100151	VCH100199	45%	92.1%	85.6%
ECO100151	YPS000155	79%	100%	100%
ECO100153	BAN110904	27%	94.4%	45.6%
ECO100153	BAN110932	31%	94.4%	94.7%
ECO100153	BCE113442	30%	4.2%	94.8%
ECO100153	BFU103716	31%	100%	95.5%
ECO100153	BMA103709	31%	99.5%	94.9%
ECO100153	CDP100079	29%	40.2%	95.7%
ECO100153	EBC105792	81%	1.4%	98.6%
ECO100153	ECO100153	100%	100%	100%
ECO100153	KPN304213	83%	100%	100%
ECO100153	SPA103168	82%	21.2%	98.9%
ECO100153	STY103491	90%	98.8%	95.2%
ECO100153	STM103177	90%	98.8%	95.2%
ECO100153	VCH100201	36%	97.4%	97.5%
ECO100153	YPS000152	68%	98.8%	98.2%
ECO100158	ABA104905	27%	65.0%	51.6%
ECO100158	BAN107089	25%	77.4%	65.7%
ECO100158	BFR101755	22%	61.7%	44.9%
ECO100158	BPT100813	34%	91.0%	84.2%
ECO100158	BCE101181	40%	62.8%	77.5%
ECO100158	BFU105758	34%	90.2%	83.2%
ECO100158	BMA108052	36%	94.7%	83.5%
ECO100158	CJU101523	28%	73.3%	73.1%
ECO100158	CAC103091	21%	60.2%	45.6%
ECO100158	CBO101985	29%	72.9%	64.1%
ECO100158	CDP100163	27%	64.3%	53.1%
ECO100158	EBC102140	77%	99.2%	99.2%
ECO100158	ECO100158	100%	100%	100%
ECO100158	HIN101441	22%	66.2%	56.1%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100158	HPY101538	24%	74.4%	55.8%
ECO100158	KPN308672	72%	99.6%	99.6%
ECO100158	LMO101056	29%	89.1%	81.3%
ECO100158	PRT105976	50%	95.9%	95.7%
ECO100158	PAE204042	30%	93.6%	95.1%
ECO100158	PPU104488	29%	94.4%	94.4%
ECO100158	PSY103310	25%	51.9%	44.0%
ECO100158	SPA102649	75%	76.3%	99.5%
ECO100158	STY103497	80%	100%	100%
ECO100158	SAU800609	27%	89.5%	85.4%
ECO100158	SEP200175	28%	85.3%	81.7%
ECO100158	SHA101549	26%	89.5%	83.2%
ECO100158	SPY201383	20%	74.1%	68.4%
ECO100158	VCH102346	37%	90.2%	89.1%
ECO100158	YPS000147	54%	97.0%	92.9%
ECO100161	BAN110062	37%	59.3%	71.5%
ECO100161	BAN107077	36%	78.9%	67.6%
ECO100161	BFR11675	39%	75.7%	74.7%
ECO100161	BPT102297	41%	74.3%	85.3%
ECO100161	BBU100104	34%	93.9%	92.1%
ECO100161	BCE109327	36%	95.6%	92.1%
ECO100161	BMA103894	36%	94.7%	91.5%
ECO100161	CJU101153	38%	95.1%	94.7%
ECO100161	CTR200205	40%	77.6%	75.5%
ECO100161	CBO100298	43%	57.6%	67.1%
ECO100161	EBC102486	91%	100%	100%
ECO100161	EFA202055	34%	92.2%	78.0%
ECO100161	EFM201658	36%	48.3%	95.8%
ECO100161	ECO100161	100%	100%	100%
ECO100161	HPY101002	42%	79.1%	88.9%
ECO100161	KPN304180	90%	100%	100%
ECO100161	LPN103539	41%	93.5%	95.2%
ECO100161	LMO101189	36%	60.3%	60.8%
ECO100161	MAV103189	34%	56.1%	53.4%
ECO100161	MBV100882	36%	56.1%	51.3%
ECO100161	MLP100663	35%	57.2%	51.4%
ECO100161	MTU201206	35%	56.1%	49.0%
ECO100161	PAE200765	38%	77.8%	99.6%
ECO100161	PSY102326	38%	73.4%	96.8%
ECO100161	SPA102656	90%	100%	96.5%
ECO100161	STY103840	92%	100%	100%
ECO100161	STM103213	92%	100%	100%
ECO100161	SAU801728	40%	57.6%	65.8%
ECO100161	SEP202073	41%	61.8%	73.1%
ECO100161	SHA100568	40%	59.1%	67.3%
ECO100161	SMU101421	38%	57.6%	72.6%
ECO100161	SPY201695	33%	69.8%	87.2%
ECO100161	TPA100832	34%	89.2%	88.7%
ECO100161	VCH100556	58%	100%	99.8%
ECO100161	YPS000135	75%	100%	100%
ECO100167	ABA104028	40%	94.6%	95.9%
ECO100167	BPT101104	38%	88.9%	91.7%
ECO100167	BCE102413	35%	83.9%	99.6%
ECO100167	BFU101941	36%	68.2%	99.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100167	BMA110028	36%	92.7%	95.5%
ECO100167	CDP101162	26%	47.1%	60.8%
ECO100167	EBC103102	90%	64.9%	99.5%
ECO100167	ECO100167	100%	100%	100%
ECO100167	HIN101684	46%	92.8%	95.6%
ECO100167	KPN306317	88%	97.2%	99.8%
ECO100167	LPN101443	37%	94.9%	98.1%
ECO100167	MCA101007	33%	95.1%	96.2%
ECO100167	MAV103401	24%	48.3%	90.3%
ECO100167	MBV102319	25%	93.8%	97.3%
ECO100167	MTU202880	25%	93.8%	97.3%
ECO100167	NGO100301	33%	92.1%	95.7%
ECO100167	NME201261	33%	92.2%	95.8%
ECO100167	PMU100460	46%	96.7%	99.3%
ECO100167	PRT104542	66%	77.3%	97.3%
ECO100167	PAE203656	42%	96.2%	96.1%
ECO100167	PPU105172	41%	93.7%	94.1%
ECO100167	PSY104380	42%	94.7%	94.8%
ECO100167	SPA100030	76%	41.9%	97.4%
ECO100167	STY103845	92%	100%	100%
ECO100167	VCH102228	53%	96.9%	98.0%
ECO100167	YPS001121	76%	98.8%	96.5%
ECO100169	ABA104000	72%	92.1%	88.8%
ECO100169	BAN100446	53%	76.8%	95.7%
ECO100169	BAN110084	53%	97.9%	98.7%
ECO100169	BFR104950	47%	97.1%	84.2%
ECO100169	BPT101108	59%	97.9%	97.2%
ECO100169	BBU100122	47%	92.5%	85.8%
ECO100169	BCE101166	55%	97.9%	98.0%
ECO100169	BFU101939	59%	92.5%	89.2%
ECO100169	BMA101604	56%	97.1%	98.8%
ECO100169	CJU101107	52%	98.8%	89.7%
ECO100169	CPN200048	43%	92.1%	79.8%
ECO100169	CTR200051	45%	88.8%	75.8%
ECO100169	CAC101756	52%	93.4%	97.0%
ECO100169	CBO103187	53%	93.4%	97.0%
ECO100169	CDF101764	54%	97.5%	99.2%
ECO100169	CDP101120	50%	93.4%	85.0%
ECO100169	EBC103098	97%	100%	100%
ECO100169	EFA200418	51%	99.2%	91.2%
ECO100169	ECO100169	100%	100%	100%
ECO100169	HIN100892	82%	100%	95.6%
ECO100169	HPY101531	47%	98.8%	90.9%
ECO100169	KPN301398	98%	95.0%	100%
ECO100169	LPN100646	57%	99.2%	94.9%
ECO100169	LMO100442	53%	99.2%	96.0%
ECO100169	MCA101251	67%	92.1%	81.9%
ECO100169	MAV106404	52%	92.9%	81.2%
ECO100169	MBV102282	52%	92.9%	78.0%
ECO100169	MLP100973	52%	92.9%	80.9%
ECO100169	MTU202852	52%	92.9%	78.0%
ECO100169	MGE100072	36%	92.1%	78.5%
ECO100169	MPN100623	39%	92.5%	76.2%
ECO100169	NGO100893	53%	99.2%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100169	NME200306	52%	99.2%	100%
ECO100169	PMU101984	84%	100%	95.2%
ECO100169	PRT105507	90%	100%	100%
ECO100169	PAE203654	73%	99.6%	97.2%
ECO100169	PPU107884	70%	93.8%	92.2%
ECO100169	PSY108183	72%	93.8%	84.6%
ECO100169	SPA101195	97%	100%	100%
ECO100169	STY103848	97%	100%	100%
ECO100169	STM103561	97%	100%	100%
ECO100169	SAU801256	51%	93.4%	88.2%
ECO100169	SEP201549	52%	93.4%	85.9%
ECO100169	SHA100713	50%	70.1%	81.2%
ECO100169	SMU100628	49%	99.6%	92.0%
ECO100169	SPN402017	48%	100%	93.1%
ECO100169	SPY201599	50%	100%	94.5%
ECO100169	TPA100599	48%	94.2%	78.0%
ECO100169	UUR100024	36%	91.3%	63.3%
ECO100169	VCH102226	82%	100%	100%
ECO100169	YPS001127	93%	100%	100%
ECO100170	ABA106144	54%	98.2%	97.9%
ECO100170	BAN110110	37%	94.3%	97.2%
ECO100170	BAN103067	47%	98.9%	99.0%
ECO100170	BFR10353	32%	90.5%	97.9%
ECO100170	BPT101109	49%	98.2%	97.9%
ECO100170	BBU100121	33%	87.6%	92.8%
ECO100170	BCE107064	48%	98.2%	96.9%
ECO100170	BFU100280	49%	98.2%	96.9%
ECO100170	BMA107429	49%	98.2%	96.9%
ECO100170	CJU101106	35%	98.2%	99.4%
ECO100170	CPN200047	33%	92.6%	99.6%
ECO100170	CTR200050	35%	86.9%	91.8%
ECO100170	CAC101812	44%	98.9%	99.3%
ECO100170	CBO101301	42%	98.6%	99.0%
ECO100170	CDF101762	43%	99.3%	100%
ECO100170	CDP101115	43%	92.9%	99.6%
ECO100170	EBC103096	95%	100%	100%
ECO100170	EFA200421	41%	99.3%	99.7%
ECO100170	ECO100170	100%	100%	100%
ECO100170	HIN100893	71%	98.9%	98.6%
ECO100170	HPY101532	36%	99.3%	100%
ECO100170	KPN301399	96%	100%	100%
ECO100170	LPN100716	52%	98.2%	98.6%
ECO100170	LMO102014	45%	99.6%	100%
ECO100170	MCA101252	52%	98.2%	97.6%
ECO100170	MAV106405	40%	92.9%	99.6%
ECO100170	MBV102285	39%	92.9%	99.6%
ECO100170	MLP100972	37%	92.9%	99.6%
ECO100170	MTU202851	39%	92.9%	99.6%
ECO100170	MGE100443	39%	97.2%	98.0%
ECO100170	MPN100211	40%	97.2%	98.0%
ECO100170	NGO100890	50%	99.3%	99.6%
ECO100170	NME200305	50%	99.3%	99.6%
ECO100170	PMU101985	74%	99.3%	99.6%
ECO100170	PRT104501	74%	99.3%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100170	PAE203653	57%	98.2%	97.6%
ECO100170	PPU107887	58%	98.2%	97.6%
ECO100170	PSY104373	58%	98.2%	97.6%
ECO100170	SPA101193	96%	100%	100%
ECO100170	STY103870	96%	100%	100%
ECO100170	STM103563	96%	100%	100%
ECO100170	SAU801257	43%	99.3%	100%
ECO100170	SEP201550	43%	98.2%	99.3%
ECO100170	SHA100714	43%	98.2%	99.3%
ECO100170	SMU100627	38%	98.2%	97.7%
ECO100170	SPN402016	39%	98.2%	97.7%
ECO100170	SPY201600	38%	98.2%	97.7%
ECO100170	TPA100598	30%	90.8%	95.9%
ECO100170	UUR100520	39%	97.9%	99.0%
ECO100170	VCH102225	70%	98.2%	98.9%
ECO100170	YPS001128	77%	100%	100%
ECO100171	ABA101328	60%	99.2%	100%
ECO100171	BAN107431	43%	97.5%	98.3%
ECO100171	BAN103009	48%	97.5%	98.3%
ECO100171	BFR104169	53%	90.0%	98.6%
ECO100171	BPT101110	55%	95.9%	97.1%
ECO100171	BCE109906	58%	95.9%	97.5%
ECO100171	BFU100279	57%	95.9%	97.5%
ECO100171	BMA109323	57%	95.9%	97.5%
ECO100171	CJU101199	49%	92.9%	94.1%
ECO100171	CPN200046	38%	96.3%	94.0%
ECO100171	CTR200049	38%	88.4%	88.2%
ECO100171	CAC103602	49%	96.7%	97.9%
ECO100171	CBO103420	47%	97.5%	97.9%
ECO100171	CDF101760	47%	97.1%	98.7%
ECO100171	CDP101114	44%	97.9%	96.7%
ECO100171	EBC103094	97%	100%	100%
ECO100171	EFA200424	48%	97.1%	97.9%
ECO100171	ECO100171	100%	100%	100%
ECO100171	HIN101042	77%	97.5%	99.2%
ECO100171	HPY100764	51%	93.8%	94.6%
ECO100171	KPN301400	98%	100%	100%
ECO100171	LPN101596	61%	95.9%	93.9%
ECO100171	LMO102234	47%	96.7%	97.1%
ECO100171	MCA100778	60%	98.3%	98.8%
ECO100171	MAV106392	46%	96.3%	87.2%
ECO100171	MBV102299	45%	96.3%	88.5%
ECO100171	MLP100970	46%	96.3%	82.8%
ECO100171	MTU202845	45%	96.3%	88.5%
ECO100171	MGE100444	35%	90.9%	90.5%
ECO100171	MPN100210	34%	95.0%	97.9%
ECO100171	NGO100888	53%	95.9%	96.7%
ECO100171	NME200304	53%	95.9%	96.7%
ECO100171	PMU101986	79%	98.3%	97.9%
ECO100171	PRT104887	91%	99.6%	99.2%
ECO100171	PAE203652	69%	97.9%	96.3%
ECO100171	PPU102433	69%	97.9%	95.5%
ECO100171	PSY104372	69%	96.7%	94.3%
ECO100171	SPA101722	94%	47.3%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100171	STY103871	98%	100%	100%
ECO100171	STM103564	98%	100%	100%
ECO100171	SAU801258	44%	96.7%	97.5%
ECO100171	SEP201551	45%	100%	100%
ECO100171	SHA100715	45%	100%	90.9%
ECO100171	SMU101143	47%	97.5%	96.3%
ECO100171	SPN400845	49%	97.9%	96.0%
ECO100171	SPY200331	48%	97.5%	97.5%
ECO100171	TPA100098	31%	25.3%	24.3%
ECO100171	UUR100519	35%	96.3%	98.7%
ECO100171	VCH102224	85%	100%	99.2%
ECO100171	YPS001129	90%	100%	100%
ECO100179	ABA101312	39%	97.7%	99.1%
ECO100179	BFR105934	35%	97.1%	96.0%
ECO100179	BPT101128	42%	91.5%	89.3%
ECO100179	BCE111319	41%	99.1%	98.3%
ECO100179	BFU114742	39%	96.5%	92.7%
ECO100179	BMA109885	39%	97.4%	96.1%
ECO100179	CJU100537	34%	95.3%	99.7%
ECO100179	CPN200450	34%	98.5%	94.7%
ECO100179	CTR200507	33%	99.1%	96.9%
ECO100179	CBO103766	28%	23.8%	84.3%
ECO100179	EBC103091	89%	100%	100%
ECO100179	ECO100179	100%	100%	100%
ECO100179	HIN100894	65%	98.5%	99.1%
ECO100179	HPY100193	31%	90.9%	91.4%
ECO100179	KPN301403	92%	90.6%	100%
ECO100179	LPN102597	35%	99.1%	99.7%
ECO100179	MCA100324	44%	87.7%	90.8%
ECO100179	NGO100826	38%	97.7%	96.3%
ECO100179	NME200082	38%	97.7%	96.3%
ECO100179	PMU101994	65%	98.2%	98.5%
ECO100179	PRT101247	80%	100%	99.7%
ECO100179	PAE203644	51%	98.2%	94.9%
ECO100179	PPU101150	49%	98.5%	95.7%
ECO100179	PSY104345	50%	98.2%	95.4%
ECO100179	SPA100512	85%	83.6%	58.2%
ECO100179	STY103879	95%	100%	100%
ECO100179	STM103592	95%	100%	100%
ECO100179	VCH102216	64%	100%	97.2%
ECO100179	YPS001147	82%	99.7%	100%
ECO100180	ABA101324	44%	94.0%	100%
ECO100180	BAN112058	43%	56.3%	92.2%
ECO100180	BAN101529	48%	92.1%	95.1%
ECO100180	BPT101129	51%	92.1%	94.7%
ECO100180	BCE105358	58%	96.0%	94.2%
ECO100180	BFU107782	52%	96.0%	93.5%
ECO100180	BFU105730	55%	96.7%	94.8%
ECO100180	BMA107929	57%	96.0%	94.2%
ECO100180	CJU100245	47%	90.1%	94.5%
ECO100180	CPN200094	44%	92.1%	91.5%
ECO100180	CTR200808	43%	90.1%	89.5%
ECO100180	CAC102008	45%	89.4%	94.3%
ECO100180	CBO103374	45%	90.7%	93.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100180	CDF104046	51%	25.8%	97.5%
ECO100180	CDF101479	42%	57.6%	95.5%
ECO100180	CDF100018	52%	78.8%	96.7%
ECO100180	EBC103090	93%	39.1%	78.7%
ECO100180	EBC100020	91%	57.0%	84.3%
ECO100180	EBC100023	91%	57.0%	84.3%
ECO100180	EFA203430	50%	90.1%	95.0%
ECO100180	EFM202041	50%	90.1%	96.4%
ECO100180	ECO100180	100%	100%	100%
ECO100180	HIN101039	68%	92.7%	93.9%
ECO100180	HPY101356	46%	88.7%	86.8%
ECO100180	KPN301913	97%	100%	100%
ECO100180	LPN101746	52%	84.8%	89.0%
ECO100180	LMO100873	51%	93.4%	96.5%
ECO100180	MCA100038	44%	96.0%	83.4%
ECO100180	MBV105275	29%	45.0%	31.9%
ECO100180	NGO100839	55%	92.7%	94.0%
ECO100180	NME200083	55%	92.7%	94.0%
ECO100180	PMU101995	70%	96.7%	95.4%
ECO100180	PRT101246	83%	97.4%	85.5%
ECO100180	PAE203643	54%	94.0%	98.6%
ECO100180	PPU101164	57%	92.1%	96.6%
ECO100180	PSY104344	56%	94.0%	98.6%
ECO100180	SPA100773	99%	100%	100%
ECO100180	STY103910	99%	100%	100%
ECO100180	STM103593	98%	100%	100%
ECO100180	SAU802098	46%	89.4%	91.1%
ECO100180	SEP204192	44%	89.4%	91.7%
ECO100180	SHA100083	38%	35.8%	93.1%
ECO100180	SMU100534	46%	92.1%	97.1%
ECO100180	SPN400384	46%	92.1%	97.1%
ECO100180	SPY201345	46%	92.1%	97.8%
ECO100180	VCH102215	64%	97.4%	96.1%
ECO100180	YPS001148	89%	100%	83.4%
ECO100183	ABA101887	65%	93.4%	98.9%
ECO100183	BAN111817	53%	82.3%	68.9%
ECO100183	BAN113438	54%	90.9%	69.6%
ECO100183	BFR12457	51%	88.4%	87.6%
ECO100183	BPT101141	58%	93.4%	92.0%
ECO100183	BBU100046	37%	89.4%	98.3%
ECO100183	BCE104245	60%	94.4%	87.4%
ECO100183	BFU105066	58%	92.4%	74.2%
ECO100183	BMA107189	60%	94.4%	87.4%
ECO100183	CJU100010	38%	87.9%	88.5%
ECO100183	CPN200642	41%	96.0%	88.8%
ECO100183	CTR200293	46%	92.4%	84.3%
ECO100183	CAC100322	41%	89.4%	71.7%
ECO100183	CBO102656	41%	91.9%	69.1%
ECO100183	CDF100890	49%	88.9%	69.0%
ECO100183	CDP101132	45%	79.8%	93.6%
ECO100183	EBC102552	89%	100%	100%
ECO100183	EFA201281	50%	91.9%	71.0%
ECO100183	EFM202475	51%	91.9%	72.1%
ECO100183	ECO100183	100%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100183	HIN101036	72%	96.5%	98.0%
ECO100183	HPY101305	33%	92.9%	91.9%
ECO100183	KPN301923	89%	100%	99.5%
ECO100183	LPN101418	62%	90.9%	93.2%
ECO100183	LMO102644	47%	91.9%	69.3%
ECO100183	MCA101524	38%	90.9%	85.8%
ECO100183	MAV102888	46%	91.4%	76.6%
ECO100183	MBV102296	48%	91.4%	69.3%
ECO100183	MLP100982	48%	91.4%	75.4%
ECO100183	MTU202864	48%	91.4%	69.3%
ECO100183	NGO100782	61%	92.9%	95.4%
ECO100183	NME200070	61%	92.9%	95.4%
ECO100183	PMU101998	72%	96.5%	97.5%
ECO100183	PRT101243	75%	98.5%	99.5%
ECO100183	PAE203640	71%	94.4%	93.0%
ECO100183	PPU101167	72%	92.4%	88.4%
ECO100183	PSY106718	71%	92.4%	82.4%
ECO100183	STY103913	92%	100%	100%
ECO100183	STM103626	92%	100%	100%
ECO100183	SAU801244	44%	92.9%	71.8%
ECO100183	SEP201538	45%	91.4%	69.2%
ECO100183	SHA101009	43%	91.4%	70.6%
ECO100183	SMU100101	45%	93.4%	71.9%
ECO100183	SPN401044	49%	91.4%	69.5%
ECO100183	SPY200888	46%	90.9%	69.2%
ECO100183	UUR100400	35%	38.9%	25.3%
ECO100183	VCH102212	73%	93.9%	90.3%
ECO100183	YPS001153	84%	97.5%	97.5%
ECO100184	ABA101411	48%	99.6%	96.4%
ECO100184	BAN112326	36%	99.2%	99.5%
ECO100184	BFR102018	33%	96.8%	95.0%
ECO100184	BPT101552	48%	99.7%	99.3%
ECO100184	BBU100578	38%	99.2%	98.1%
ECO100184	BCE115231	49%	99.9%	100%
ECO100184	BFU107633	47%	99.9%	99.7%
ECO100184	BMA101634	48%	99.9%	100%
ECO100184	CJU100668	39%	89.9%	88.7%
ECO100184	CPN200079	37%	92.5%	89.8%
ECO100184	CTR200821	36%	92.5%	90.0%
ECO100184	CAC103161	39%	90.5%	91.0%
ECO100184	CBO100607	34%	99.7%	99.8%
ECO100184	CBO101196	35%	99.6%	99.2%
ECO100184	CDF101163	40%	92.2%	91.0%
ECO100184	CDP101233	34%	98.8%	99.1%
ECO100184	EBC102553	94%	100%	100%
ECO100184	EFA202115	32%	96.2%	96.7%
ECO100184	EFM200294	32%	99.1%	99.5%
ECO100184	ECO100184	100%	100%	100%
ECO100184	HIN100720	71%	99.9%	99.8%
ECO100184	HPY101439	39%	92.5%	91.3%
ECO100184	KPN301922	95%	100%	100%
ECO100184	LPN102982	56%	99.6%	99.7%
ECO100184	LMO100629	35%	99.4%	99.8%
ECO100184	MCA102321	49%	89.4%	86.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100184	MAV100203	34%	7.7%	90.7%
ECO100184	MAV103371	35%	99.2%	99.5%
ECO100184	MBV102577	35%	97.8%	99.1%
ECO100184	MLP100747	35%	99.2%	99.5%
ECO100184	MTU201526	36%	98.8%	98.7%
ECO100184	MGE100266	27%	72.6%	89.6%
ECO100184	MPN100459	36%	18.4%	19.4%
ECO100184	NGO101860	47%	99.9%	100%
ECO100184	NME200585	47%	99.9%	100%
ECO100184	PMU100034	71%	99.9%	99.8%
ECO100184	PRT101242	85%	98.6%	100%
ECO100184	PAE203638	58%	99.5%	99.6%
ECO100184	PPU100137	58%	99.9%	99.9%
ECO100184	PSY104339	57%	99.5%	99.6%
ECO100184	SPA100912	92%	99.3%	100%
ECO100184	STY103914	96%	100%	100%
ECO100184	STM103627	96%	100%	100%
ECO100184	SAU801703	33%	93.0%	93.8%
ECO100184	SEP201707	33%	92.0%	92.4%
ECO100184	SHA100359	33%	96.0%	94.2%
ECO100184	SMU101018	30%	90.8%	92.0%
ECO100184	SPN400795	31%	95.3%	95.0%
ECO100184	SPY200987	29%	96.2%	96.8%
ECO100184	TPA100661	39%	92.8%	90.7%
ECO100184	UUR100419	29%	87.0%	94.4%
ECO100184	VCH102211	76%	100%	99.6%
ECO100184	YPS001155	88%	100%	99.1%
ECO100185	ABA100308	57%	80.9%	94.1%
ECO100185	BAN105768	55%	97.8%	95.4%
ECO100185	BPT101398	64%	99.4%	97.8%
ECO100185	BCE106451	64%	99.4%	97.2%
ECO100185	BFU100947	64%	99.4%	97.2%
ECO100185	BMA107589	64%	99.4%	97.2%
ECO100185	CJU100411	49%	98.4%	97.8%
ECO100185	CPN200335	44%	98.7%	96.3%
ECO100185	CTR200529	45%	98.7%	96.3%
ECO100185	CAC100492	52%	81.8%	95.3%
ECO100185	CBO102220	51%	89.3%	50.3%
ECO100185	CDF101403	50%	96.6%	97.1%
ECO100185	EBC102554	96%	100%	100%
ECO100185	BFA200247	52%	79.6%	96.9%
ECO100185	EFM200190	55%	81.5%	99.6%
ECO100185	ECO100185	100%	100%	100%
ECO100185	HIN100386	74%	99.7%	99.7%
ECO100185	HPY100550	48%	98.1%	96.8%
ECO100185	KPN301921	96%	100%	100%
ECO100185	LPN101352	62%	84.0%	99.3%
ECO100185	LMO100159	52%	98.4%	97.8%
ECO100185	MCA100190	60%	80.3%	100%
ECO100185	MLP100072	28%	46.4%	27.9%
ECO100185	NGO100369	64%	98.1%	97.2%
ECO100185	NME201237	64%	98.1%	97.2%
ECO100185	PMU100292	75%	99.7%	99.7%
ECO100185	PRT100667	69%	99.7%	99.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100185	PRT101241	88%	99.7%	99.7%
ECO100185	PAE203637	69%	99.4%	99.4%
ECO100185	PPU101171	67%	99.4%	99.7%
ECO100185	PSY108491	67%	99.4%	99.1%
ECO100185	SPA100816	80%	88.4%	100%
ECO100185	STY103916	97%	100%	100%
ECO100185	STM103628	97%	100%	100%
ECO100185	SAU801700	52%	97.8%	98.4%
ECO100185	SEP201704	52%	97.8%	98.4%
ECO100185	SHA100923	52%	97.8%	98.1%
ECO100185	SMU100529	54%	79.9%	98.0%
ECO100185	SPN400387	50%	79.9%	98.4%
ECO100185	SPY201342	52%	79.9%	98.0%
ECO100185	VCH102210	75%	99.7%	99.7%
ECO100185	YPS001157	90%	99.7%	99.7%
ECO100193	CJU100189	40%	16.1%	23.4%
ECO100193	ECO100193	100%	100%	100%
ECO100193	KPN300059	73%	55.8%	100%
ECO100193	KPN301914	66%	88.7%	92.5%
ECO100193	TPA100217	26%	29.1%	82.4%
ECO100193	YPS000139	43%	83.6%	84.2%
ECO100194	ABA100529	68%	99.3%	100%
ECO100194	BAN100354	47%	99.0%	99.3%
ECO100194	BAN103931	51%	99.8%	100%
ECO100194	BFR100495	28%	33.2%	0.2%
ECO100194	BPT102439	60%	96.7%	96.5%
ECO100194	BBU100401	28%	87.1%	65.4%
ECO100194	BCE111561	67%	38.6%	99.5%
ECO100194	BFU106495	56%	99.8%	99.1%
ECO100194	BMA104091	56%	99.8%	99.1%
ECO100194	CJU100505	45%	99.7%	99.6%
ECO100194	CPN200251	43%	97.4%	97.5%
ECO100194	CTR200662	39%	99.7%	97.9%
ECO100194	CAC100467	49%	98.4%	97.4%
ECO100194	CBO100123	28%	98.6%	98.3%
ECO100194	CDF100404	47%	12.8%	76.6%
ECO100194	CDF100250	47%	98.6%	97.5%
ECO100194	CDP100483	40%	99.5%	99.1%
ECO100194	EBC102546	93%	99.8%	100%
ECO100194	EFA200454	47%	96.7%	95.8%
ECO100194	EFM201684	47%	99.0%	98.6%
ECO100194	ECO100194	100%	100%	100%
ECO100194	HIN100709	75%	99.7%	99.5%
ECO100194	HPY100234	39%	99.8%	99.7%
ECO100194	KPN301911	94%	96.0%	100%
ECO100194	LPN102483	71%	16.4%	100%
ECO100194	LMO100624	49%	99.0%	98.8%
ECO100194	MCA101839	60%	98.4%	99.5%
ECO100194	MAV102826	40%	97.4%	97.6%
ECO100194	MBV103229	40%	97.4%	97.6%
ECO100194	MLP100951	27%	93.0%	73.1%
ECO100194	MTU202807	40%	97.7%	97.3%
ECO100194	NGO100106	60%	98.4%	98.4%
ECO100194	NME201412	60%	98.4%	98.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100194	PMU101370	76%	99.0%	98.9%
ECO100194	PRT101177	79%	99.7%	99.8%
ECO100194	PAE200955	71%	99.7%	99.6%
ECO100194	PPU108855	68%	96.5%	99.6%
ECO100194	PSY105509	67%	99.8%	99.8%
ECO100194	SPA100809	89%	98.4%	100%
ECO100194	STY103990	95%	100%	100%
ECO100194	SAU801263	44%	99.5%	99.1%
ECO100194	SEP201556	46%	99.8%	99.5%
ECO100194	SHA101150	47%	98.3%	97.9%
ECO100194	SMU101082	40%	99.0%	99.2%
ECO100194	SPN400243	42%	99.0%	99.0%
ECO100194	SPY201510	41%	99.0%	98.9%
ECO100194	TPA100158	40%	93.7%	93.7%
ECO100194	VCH100859	71%	99.0%	99.1%
ECO100194	YPS002005	84%	99.8%	99.8%
ECO100195	ABA103785	37%	94.5%	93.0%
ECO100195	BAN110343	34%	40%	58.0%
ECO100195	CBO101676	39%	39.6%	91.4%
ECO100195	CDF101307	33%	43.8%	65.2%
ECO100195	EBC102547	82%	100%	100%
ECO100195	ECO100195	100%	100%	100%
ECO100195	HIN100489	51%	94.5%	92.9%
ECO100195	KPN301908	85%	100%	100%
ECO100195	MCA100700	39%	74.9%	93.7%
ECO100195	NGO100030	42%	98.7%	98.2%
ECO100195	NME200229	42%	96.2%	95.6%
ECO100195	PMU101170	54%	93.6%	89.4%
ECO100195	PRT101178	62%	100%	100%
ECO100195	PAE203386	48%	90.2%	89.6%
ECO100195	PPU108086	47%	90.2%	90%
ECO100195	PSY104415	45%	95.3%	95.2%
ECO100195	SPA100206	89%	37.9%	100%
ECO100195	STY103991	88%	100%	100%
ECO100195	VCH100860	52%	98.3%	99.1%
ECO100195	YPS002007	71%	100%	100%
ECO100197	ABA101419	34%	88.6%	99.2%
ECO100197	ABA101431	41%	81.9%	81.2%
ECO100197	BAN110744	44%	91.5%	96.2%
ECO100197	BAN101917	44%	94.5%	96.3%
ECO100197	BPT102034	47%	100%	100%
ECO100197	BCE106577	56%	87.1%	80.3%
ECO100197	BFU102067	50%	96.3%	95.9%
ECO100197	BMA104983	54%	97.0%	96.3%
ECO100197	CJU100709	37%	85.6%	89.9%
ECO100197	CJU101125	41%	80.4%	81.3%
ECO100197	CJU100710	42%	84.9%	87.9%
ECO100197	CJU100711	45%	82.3%	86.0%
ECO100197	CPN200473	31%	93.0%	93.8%
ECO100197	CAC100740	40%	95.2%	93.4%
ECO100197	CBO102481	33%	92.3%	92.6%
ECO100197	CBO101824	41%	94.5%	94.1%
ECO100197	CBO103909	45%	91.9%	92.2%
ECO100197	CDF100529	43%	97.8%	98.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100197	CDP100114	31%	98.2%	91.7%
ECO100197	CDP100115	32%	94.5%	88.3%
ECO100197	EBC102539	96%	100%	100%
ECO100197	EFA201785	40%	98.2%	97.5%
ECO100197	EFM201963	38%	98.2%	97.2%
ECO100197	ECO100197	100%	100%	100%
ECO100197	HIN100600	60%	98.9%	99.6%
ECO100197	HPY101541	42%	97.4%	97.8%
ECO100197	KPN301905	95%	100%	100%
ECO100197	LPN100686	45%	95.2%	98.8%
ECO100197	LMO100978	47%	94.5%	93.8%
ECO100197	MCA103679	55%	98.5%	99.3%
ECO100197	NGO101326	37%	96.3%	94.1%
ECO100197	NME200471	38%	96.3%	94.1%
ECO100197	PMU101730	58%	98.9%	99.6%
ECO100197	PRT100159	78%	100%	100%
ECO100197	PAE205500	47%	78.6%	81.2%
ECO100197	PPU101952	47%	78.6%	82.4%
ECO100197	PSY101363	51%	78.6%	82.1%
ECO100197	SPA101556	37%	88.2%	87.3%
ECO100197	STY103993	96%	100%	100%
ECO100197	STM100616	37%	88.2%	87.3%
ECO100197	SAU800839	36%	97.0%	98.2%
ECO100197	SEP201451	37%	97.0%	98.1%
ECO100197	SHA100334	38%	92.6%	93.0%
ECO100197	SHA101832	35%	97.0%	97.4%
ECO100197	SMU100488	33%	93.4%	93.6%
ECO100197	SPN400147	35%	96.7%	97.5%
ECO100197	SPY200233	36%	100%	100%
ECO100197	TPA100812	34%	98.9%	98.5%
ECO100197	VCH100889	68%	100%	97.8%
ECO100197	YPS002011	90%	100%	100%
ECO100198	ABA101423	45%	100%	99.1%
ECO100198	BAN105551	52%	76.0%	81.3%
ECO100198	BAN106583	47%	96.3%	94.6%
ECO100198	BPT103178	52%	100%	100%
ECO100198	BCE112661	54%	98.2%	100%
ECO100198	BFU102065	54%	100%	95.2%
ECO100198	BMA106456	54%	98.2%	100%
ECO100198	CJU100712	44%	89.4%	64.0%
ECO100198	CPN200472	36%	95.9%	94.1%
ECO100198	CAC101527	43%	96.3%	95.9%
ECO100198	CBO103376	48%	95.9%	98.6%
ECO100198	CDF100530	48%	92.6%	92.2%
ECO100198	CDP100111	39%	94.5%	91.1%
ECO100198	EBC102541	97%	100%	100%
ECO100198	EFA201706	46%	93.5%	89.0%
ECO100198	EFM202483	44%	94.9%	91.2%
ECO100198	ECO100198	100%	100%	100%
ECO100198	HPY101554	43%	96.3%	96.7%
ECO100198	KPN301904	95%	100%	100%
ECO100198	LPN101477	53%	99.1%	99.1%
ECO100198	LMO100259	45%	98.2%	95.5%
ECO100198	MCA103062	45%	98.6%	93.9%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100198	NGO101323	43%	96.3%	91.7%
ECO100198	NME200470	43%	96.3%	91.7%
ECO100198	PMU101729	49%	95.4%	90.8%
ECO100198	PRT100130	83%	100%	100%
ECO100198	PAE202349	48%	98.6%	98.6%
ECO100198	PPU109980	50%	97.7%	100%
ECO100198	PSY103687	48%	98.2%	94.7%
ECO100198	SPA100613	90%	85.3%	100%
ECO100198	STY103994	92%	97.7%	100%
ECO100198	STM100618	44%	93.5%	92.7%
ECO100198	SAU800463	50%	95.9%	95.0%
ECO100198	SEP201771	50%	95.9%	95.0%
ECO100198	SHA100333	46%	98.6%	89.0%
ECO100198	SMU100477	40%	97.2%	90.8%
ECO100198	SPN400150	41%	94.5%	88.7%
ECO100198	SPY200235	42%	94.5%	92.7%
ECO100198	TPA100118	40%	95.4%	95.0%
ECO100198	VCH100890	53%	96.8%	93.3%
ECO100198	YPS002016	90%	100%	100%
ECO100201	ABA104598	65%	100%	100%
ECO100201	BPT102715	65%	100%	100%
ECO100201	BCE100085	66%	99.3%	93.6%
ECO100201	EBC100779	90%	85.4%	97.9%
ECO100201	ECO100201	100%	100%	100%
ECO100201	KPN301057	90%	100%	100%
ECO100201	PRT104732	81%	100%	100%
ECO100201	PAE204164	65%	99.3%	97.4%
ECO100201	PPU111521	67%	100%	100%
ECO100201	SPA101642	90%	100%	100%
ECO100201	STY104030	91%	100%	100%
ECO100201	STM103710	92%	100%	100%
ECO100201	YPS002027	75%	100%	100%
ECO100223	BAN108547	31%	33.0%	38.5%
ECO100223	BAN105487	31%	44.4%	80%
ECO100223	ECO100223	100%	100%	100%
ECO100223	VCH100877	26%	64.8%	54.4%
ECO100223	YPS002852	49%	94.3%	84.2%
ECO100236	ABA101495	43%	99.5%	97.9%
ECO100236	BAN105079	42%	96.2%	95.7%
ECO100236	BAN100068	43%	98.6%	98.1%
ECO100236	BFR101900	41%	97.1%	96.9%
ECO100236	BPT102346	44%	99.8%	98.3%
ECO100236	BCE107136	45%	98.3%	89.0%
ECO100236	BMA109567	45%	98.3%	89.7%
ECO100236	CJU100520	38%	97.6%	97.8%
ECO100236	CAC102032	47%	97.8%	96.7%
ECO100236	CDP101216	45%	96.2%	93.5%
ECO100236	EBC103210	88%	100%	100%
ECO100236	EFA200208	46%	99.8%	99.3%
ECO100236	EFM200382	46%	99.5%	99.0%
ECO100236	ECO100236	100%	100%	100%
ECO100236	HIN101211	62%	99.8%	99.8%
ECO100236	KPN302476	86%	100%	100%
ECO100236	LPN100519	40%	98.1%	97.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100236	LMO101153	46%	99.5%	99.0%
ECO100236	MAV103439	48%	96.9%	90.1%
ECO100236	MBV104414	47%	96.6%	93.3%
ECO100236	MLP100899	45%	97.8%	96.8%
ECO100236	MTU202391	47%	96.6%	93.3%
ECO100236	NGO101136	44%	97.8%	97.4%
ECO100236	NME201166	45%	97.8%	97.4%
ECO100236	PMU100936	65%	99.8%	99.0%
ECO100236	PRT105196	71%	99.8%	99.8%
ECO100236	PAE204004	48%	99.5%	97.9%
ECO100236	PPU112135	43%	96.2%	98.5%
ECO100236	PSY105063	45%	99.5%	97.4%
ECO100236	SPA104265	83%	100%	100%
ECO100236	STY104449	86%	100%	100%
ECO100236	STM103861	86%	100%	100%
ECO100236	SMU101435	48%	99.8%	99.3%
ECO100236	SPN400833	46%	97.4%	97.1%
ECO100236	SPY201284	47%	99.5%	99.0%
ECO100236	TPA100346	44%	97.6%	97.9%
ECO100236	VCH102239	58%	99.8%	99.3%
ECO100236	YPS002651	72%	100%	99.5%
ECO100239	BFU102395	50%	89.2%	65.3%
ECO100239	EBC103227	98%	63.9%	100%
ECO100239	ECO102590	81%	90.5%	89.4%
ECO100239	ECO101961	81%	93.7%	100%
ECO100239	ECO100239	100%	100%	100%
ECO100239	LPN103162	46%	66.5%	95.5%
ECO100239	SEP200678	37%	43.7%	65.7%
ECO100240	EBC103228	85%	100%	72.0%
ECO100240	ECO100240	100%	100%	100%
ECO100240	KPN202940	29%	86.8%	94.4%
ECO100240	KPN204064	29%	87.5%	95.7%
ECO100240	KPN200664	29%	86.8%	94.4%
ECO100240	PRT102844	43%	73.7%	100%
ECO100245	EBC103236	92%	99.7%	100%
ECO100245	ECO100245	100%	100%	100%
ECO100245	NME200125	22%	84.0%	81.8%
ECO100255	ABA104682	35%	80.8%	32.0%
ECO100255	ECO100255	100%	100%	100%
ECO100255	HIN100123	69%	83.3%	28.0%
ECO100255	PMU100956	75%	85.8%	25.5%
ECO100255	PRT102521	90%	85.8%	26.2%
ECO100255	VCH103408	81%	85.8%	25%
ECO100256	EBC101194	98%	31.7%	100%
ECO100256	EBC101311	92%	47.3%	98.8%
ECO100256	EBC103715	88%	58.1%	100%
ECO100256	EBC103943	90%	74.9%	100%
ECO100256	EBC104524	90%	74.9%	100%
ECO100256	EBC103604	99%	100%	100%
ECO100256	ECO100266	100%	100%	100%
ECO100256	ECO100256	100%	100%	100%
ECO100256	KPN302635	99%	100%	100%
ECO100256	KPN301602	99%	100%	100%
ECO100256	KPN303307	99%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100256	KPN306562	99%	100%	100%
ECO100256	KPN308721	99%	100%	100%
ECO100256	KPN302324	99%	100%	100%
ECO100256	KPN301774	99%	100%	100%
ECO100256	KPN301257	97%	47.9%	100%
ECO100256	KPN300832	91%	56.3%	100%
ECO100256	KPN302225	100%	65.9%	100%
ECO100256	KPN300593	96%	98.8%	100%
ECO100256	KPN302471	99%	100%	100%
ECO100256	KPN300357	99%	100%	100%
ECO100256	KPN300875	99%	100%	100%
ECO100256	STY100327	99%	100%	100%
ECO100256	STY104877	99%	100%	100%
ECO100256	STY104954	99%	100%	100%
ECO100257	EBC103602	100%	100%	100%
ECO100257	ECO100257	100%	100%	100%
ECO100257	ECO100267	100%	100%	100%
ECO100257	KPN302325	100%	100%	100%
ECO100257	KPN308692	100%	100%	100%
ECO100257	KPN306262	100%	100%	100%
ECO100257	KPN301718	98%	58.2%	89.8%
ECO100257	KPN301773	100%	82.4%	90.4%
ECO100257	KPN305294	95%	100%	100%
ECO100257	KPN302468	100%	100%	100%
ECO100257	KPN300876	100%	100%	100%
ECO100257	KPN301600	100%	100%	100%
ECO100257	KPN303306	100%	100%	100%
ECO100257	KPN302228	100%	100%	100%
ECO100257	NGO100079	32%	81.3%	38.4%
ECO100257	STY100087	100%	100%	100%
ECO100257	STY105122	100%	100%	100%
ECO100257	STY104783	100%	100%	100%
ECO100262	BFR11395	35%	96.3%	98.5%
ECO100262	EBC102936	98%	100%	100%
ECO100262	ECO100262	100%	100%	100%
ECO100262	SPN401706	27%	21.1%	25.4%
ECO100298	BAN105357	48%	100%	100%
ECO100298	BAN100434	51%	100%	99.6%
ECO100298	BFR102281	32%	100%	99.6%
ECO100298	BCE100671	35%	99.6%	91.3%
ECO100298	BFU114123	36%	98.7%	98.3%
ECO100298	BMA102603	37%	98.7%	98.3%
ECO100298	CJU100066	33%	99.2%	95.9%
ECO100298	CDP101095	42%	99.6%	92.7%
ECO100298	EFA201476	44%	98.7%	92.9%
ECO100298	ECO100298	100%	100%	100%
ECO100298	HPY100137	36%	100%	98.8%
ECO100298	NGO101247	35%	99.6%	91.5%
ECO100298	NME201508	35%	99.6%	91.5%
ECO100298	PMU101853	73%	100%	100%
ECO100298	PRT100774	72%	100%	100%
ECO100298	PRT101849	78%	99.6%	97.1%
ECO100315	BCE100919	27%	28.8%	31.5%
ECO100315	EBC101762	85%	99.4%	98.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100315	ECO100315	100%	100%	100%
ECO100350	ECO100350	100%	100%	100%
ECO100361	ABA100700	46%	97.0%	95.2%
ECO100361	BAN101055	43%	93.7%	97.5%
ECO100361	BAN100517	51%	93.1%	95.1%
ECO100361	BPT100922	45%	93.7%	94.7%
ECO100361	BCE101370	45%	93.7%	96.4%
ECO100361	BFU101599	44%	94.9%	97.0%
ECO100361	BMA104829	46%	93.7%	96.4%
ECO100361	CJU100923	51%	94.3%	98.2%
ECO100361	CPN200001	45%	92.8%	94.6%
ECO100361	CTR200001	43%	93.4%	94.9%
ECO100361	CAC102676	49%	94.3%	99.1%
ECO100361	CBO101832	48%	93.4%	96.9%
ECO100361	CDF102168	49%	94.6%	98.5%
ECO100361	CDP100775	49%	94.9%	98.8%
ECO100361	EBC102698	93%	66.9%	100%
ECO100361	ECO100361	100%	100%	100%
ECO100361	HPY100160	51%	94.0%	98.1%
ECO100361	KPN308372	91%	96.7%	100%
ECO100361	LPN101016	50%	93.4%	95.2%
ECO100361	LMO100837	51%	95.2%	98.8%
ECO100361	MCA101135	46%	93.1%	95.2%
ECO100361	MAV107884	48%	93.4%	97.2%
ECO100361	MBV102362	47%	93.4%	96.9%
ECO100361	MLP101436	46%	93.1%	96.0%
ECO100361	MTU200510	47%	93.4%	96.4%
ECO100361	NGO100861	43%	93.4%	94.1%
ECO100361	NME200933	44%	93.4%	94.1%
ECO100361	PMU101692	41%	93.7%	94.1%
ECO100361	PRT102370	77%	95.2%	98.2%
ECO100361	PAE205238	40%	93.7%	94.7%
ECO100361	PPU110651	76%	94.3%	97.5%
ECO100361	PSY101277	42%	94.0%	95.2%
ECO100361	SPA101546	90%	85.4%	99.6%
ECO100361	STY104591	93%	96.7%	100%
ECO100361	SAU801668	49%	92.8%	96.9%
ECO100361	SEP201642	49%	92.8%	96.9%
ECO100361	SHA101765	42%	58.5%	98.0%
ECO100361	VCH100105	44%	93.7%	92.2%
ECO100361	YPS000599	43%	93.7%	94.1%
ECO100362	ECO100362	100%	100%	100%
ECO100366	BFR101178	24%	34.9%	57.0%
ECO100366	CJU100896	19%	55.0%	36.6%
ECO100366	CDP102949	27%	21.6%	9.1%
ECO100366	EBC102756	70%	96.6%	100%
ECO100366	ECO100366	100%	100%	100%
ECO100366	LPN101403	23%	25.9%	39.1%
ECO100366	PRT103239	21%	51.8%	36.1%
ECO100366	SPA101548	89%	70.7%	100%
ECO100366	STY104592	89%	97.0%	47.2%
ECO100366	STM104306	91%	100%	47.8%
ECO100367	EBC102015	28%	77.0%	100%
ECO100367	EBC102758	51%	91.0%	97.6%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100367	ECO100367	100%	100%	100%
ECO100367	KPN304631	34%	78.8%	100%
ECO100367	SPA101549	68%	98.6%	100%
ECO100367	STY104593	71%	93.2%	100%
ECO100367	STM104307	71%	93.2%	100%
ECO100381	EBC102823	83%	96.8%	96.8%
ECO100381	ECO100381	100%	100%	100%
ECO100381	KPN304881	79%	98.4%	98.4%
ECO100381	STY100328	95%	98.4%	98.4%
ECO100381	STM104352	93%	98.4%	98.4%
ECO100390	ABA100709	34%	73.5%	72.5%
ECO100390	BAN111886	25%	64.5%	73.0%
ECO100390	BAN113193	23%	98.5%	97.9%
ECO100390	BFR11820	28%	96%	99.2%
ECO100390	BPT100403	35%	21.2%	23.5%
ECO100390	BBU100828	26%	82.8%	82.6%
ECO100390	BCE105254	23%	22.8%	24.4%
ECO100390	BFU106002	34%	21.5%	23.4%
ECO100390	CAC100402	26%	84%	85.3%
ECO100390	CBO100412	26%	92.2%	92.2%
ECO100390	CDF103755	25%	89.5%	92.6%
ECO100390	CDP101084	24%	62%	58.7%
ECO100390	EBC101912	81%	99.8%	98.3%
ECO100390	EFA200864	26%	97.2%	97.9%
ECO100390	EFM200128	24%	96%	99.5%
ECO100390	ECO100390	100%	100%	100%
ECO100390	KPN308651	78%	99.8%	99.5%
ECO100390	LMO102080	27%	96.8%	97.6%
ECO100390	MCA101153	32%	95.8%	90.7%
ECO100390	MAV100736	24%	62%	58.2%
ECO100390	MLP100687	27%	21.2%	23.0%
ECO100390	MTU406882	27%	21.2%	30.2%
ECO100390	PRT101271	55%	96.8%	96.3%
ECO100390	PAE204279	31%	92%	91.4%
ECO100390	PPU105701	33%	92%	92.2%
ECO100390	PSY101474	31%	99.8%	99.5%
ECO100390	SPA101178	81%	100%	98.3%
ECO100390	STY100355	83%	100%	100%
ECO100390	SAU801345	23%	97.8%	98.9%
ECO100390	SEP202011	21%	97.8%	98.9%
ECO100390	SHA100866	23%	72.2%	73.8%
ECO100390	SPN201925	26%	16%	16.3%
ECO100390	TPA100619	26%	63.2%	62.9%
ECO100390	VCH103245	28%	72.8%	74.4%
ECO100390	YPS002608	60%	98.8%	96.9%
ECO100394	ABA104913	59%	99.6%	97.2%
ECO100394	BAN112358	49%	94.7%	95.8%
ECO100394	BAN100163	52%	98.2%	97.6%
ECO100394	BCE101232	61%	94.7%	100%
ECO100394	BMA101593	62%	95.2%	96.0%
ECO100394	EBC101456	91%	54.9%	100%
ECO100394	EFA201477	33%	98.7%	98%
ECO100394	ECO100394	100%	100%	100%
ECO100394	KPN304910	93%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100394	MPN100528	22%	71.8%	65.7%
ECO100394	PRT102253	60%	96.9%	97.6%
ECO100394	PAE205092	63%	95.6%	94.2%
ECO100394	PPU106756	60%	93.2%	95.3%
ECO100394	PSY101310	63%	96.9%	97.2%
ECO100394	SPA101112	94%	98.0%	99.6%
ECO100394	STY100389	95%	99.6%	99.8%
ECO100394	STM100031	95%	99.6%	99.8%
ECO100394	YPS002596	81%	98.7%	97.4%
ECO100395	BAN101050	31%	73.1%	70.0%
ECO100395	BAN109230	33%	73.1%	69.8%
ECO100395	BFR12473	26%	64.0%	70.0%
ECO100395	CAC100478	27%	64.1%	82.9%
ECO100395	CDF104139	31%	74.4%	71.2%
ECO100395	EBC101457	84%	79.0%	100%
ECO100395	EFA202423	30%	68.6%	65.8%
ECO100395	EFM200019	29%	82.5%	82.5%
ECO100395	ECO100395	100%	100%	100%
ECO100395	KPN304911	79%	99.5%	99.5%
ECO100395	LMO100614	31%	73.2%	70.7%
ECO100395	SPA105253	92%	4.5%	90%
ECO100395	SPA101113	81%	44.1%	100%
ECO100395	STY100390	83%	99.8%	99.8%
ECO100395	STM100032	83%	99.8%	99.8%
ECO100395	SPN400948	29%	72.9%	70.0%
ECO100395	SPY201005	32%	75.0%	73.0%
ECO100395	YPS002575	57%	99.5%	99.0%
ECO100402	BAN107351	47%	26.1%	35.6%
ECO100402	BFR102271	29%	60.9%	24.5%
ECO100402	EBC103463	93%	100%	100%
ECO100402	ECO100402	100%	100%	100%
ECO100402	KPN301340	90%	100%	97.5%
ECO100402	PRT101447	89%	100%	100%
ECO100402	PPU108585	56%	88.7%	79.7%
ECO100402	PSY105486	56%	88.7%	79.0%
ECO100402	SPA103227	96%	100%	100%
ECO100402	STY100420	96%	100%	100%
ECO100402	STM100071	96%	100%	100%
ECO100402	YPS000205	82%	98.3%	100%
ECO100404	EBC101277	64%	58.8%	100%
ECO100404	ECO100404	100%	100%	100%
ECO100404	KPN303448	70%	88.4%	97.8%
ECO100404	SPA103216	73%	89.9%	100%
ECO100404	STY100423	74%	89.9%	100%
ECO100407	ABA103638	62%	91.7%	91.0%
ECO100407	BAN110020	44%	96.2%	100%
ECO100407	BAN104354	54%	96.2%	97.4%
ECO100407	BFR104554	42%	88.5%	83.5%
ECO100407	BPT100012	39%	94.9%	85.5%
ECO100407	BCE102848	40%	96.2%	84.8%
ECO100407	BFU108808	42%	96.8%	86.9%
ECO100407	BMA102272	41%	93.6%	81.5%
ECO100407	CJU100351	50%	98.7%	100%
ECO100407	CPN200977	27%	98.7%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100407	CTR200105	37%	99.4%	98.7%
ECO100407	CAC100789	52%	98.7%	98.7%
ECO100407	CBO101079	57%	98.7%	99.4%
ECO100407	CDF101258	55%	97.4%	95.6%
ECO100407	CDP100290	42%	94.2%	92.3%
ECO100407	EBC101280	98%	100%	100%
ECO100407	ECO100407	100%	100%	100%
ECO100407	HIN101269	76%	100%	90.2%
ECO100407	HPY100002	50%	99.4%	99.4%
ECO100407	KPN308524	100%	100%	87.2%
ECO100407	LPN100108	43%	90.4%	90.3%
ECO100407	MCA103693	60%	90.4%	85.4%
ECO100407	MAV100814	44%	91.7%	85.9%
ECO100407	MBV102145	44%	91.7%	87.5%
ECO100407	MLP100346	42%	90.4%	88.8%
ECO100407	MTU201397	44%	91.7%	90.9%
ECO100407	NGO100984	45%	96.8%	94.3%
ECO100407	NME200821	44%	96.8%	94.3%
ECO100407	PMU100731	73%	100%	99.4%
ECO100407	PRT100213	83%	99.4%	99.4%
ECO100407	PAE204050	56%	100%	98.1%
ECO100407	PPU104481	57%	100%	98.1%
ECO100407	PSY108754	52%	100%	98.1%
ECO100407	SPA108738	90%	100%	90.2%
ECO100407	STY100427	91%	100%	100%
ECO100407	STM100098	91%	100%	100%
ECO100407	SAU801767	58%	82.7%	96.2%
ECO100407	SEP202131	56%	96.2%	97.4%
ECO100407	SHA101039	58%	94.9%	96.7%
ECO100407	SPN400161	54%	100%	100%
ECO100407	VCH102234	65%	98.7%	89.0%
ECO100407	YPS002509	86%	99.4%	99.4%
ECO100408	ABA101072	44%	97.8%	91.3%
ECO100408	BAN105057	32%	87.8%	93.1%
ECO100408	BAN110216	35%	87.8%	93.1%
ECO100408	BFR105998	27%	62.6%	28.6%
ECO100408	BPT100014	45%	95.0%	88.3%
ECO100408	BBU100107	33%	85.6%	86.2%
ECO100408	BCE111817	43%	97.8%	93.8%
ECO100408	BFU113008	42%	97.1%	93.8%
ECO100408	BMA102557	44%	97.8%	93.8%
ECO100408	CJU100350	34%	89.9%	93.9%
ECO100408	CPN200850	23%	91.4%	78.5%
ECO100408	CTR200214	25%	90.6%	79.3%
ECO100408	CAC103566	31%	87.8%	91.1%
ECO100408	CBO100362	33%	89.2%	97.2%
ECO100408	CDF101805	31%	66.9%	55.6%
ECO100408	CDP100352	32%	91.4%	66.8%
ECO100408	EBC101281	93%	100%	100%
ECO100408	EFA202204	34%	87.8%	81.5%
ECO100408	EFM100580	31%	90.6%	91.3%
ECO100408	ECO100408	100%	100%	100%
ECO100408	HIN101270	54%	95.7%	92.4%
ECO100408	HPY100001	30%	89.9%	90.6%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100408	KPN308025	94%	100%	100%
ECO100408	LPN101606	40%	93.5%	88.4%
ECO100408	LMO102626	37%	91.4%	96.1%
ECO100408	MCA103036	34%	94.2%	82.3%
ECO100408	MAV101907	36%	87.8%	80.8%
ECO100408	MBV101339	34%	87.8%	43.4%
ECO100408	MLP100320	35%	89.2%	67.4%
ECO100408	MTU202496	34%	87.8%	80.8%
ECO100408	NGO100982	42%	96.4%	95.0%
ECO100408	NME200820	42%	96.4%	95.0%
ECO100408	PMU100730	63%	95.7%	92.4%
ECO100408	PRT103311	74%	74.8%	100%
ECO100408	PAE204049	55%	96.4%	84.3%
ECO100408	PPU111159	53%	96.4%	80.7%
ECO100408	PSY102195	51%	96.4%	81.2%
ECO100408	SPA103662	94%	40.3%	100%
ECO100408	STY100428	96%	100%	100%
ECO100408	STM100099	96%	100%	100%
ECO100408	SAU801524	34%	88.5%	95.3%
ECO100408	SEP200894	35%	88.5%	95.3%
ECO100408	SHA100990	34%	88.5%	96.1%
ECO100408	SMU101206	31%	89.9%	90.2%
ECO100408	SPN400390	34%	89.9%	87.0%
ECO100408	SPY201398	30%	89.9%	88%
ECO100408	TPA101005	35%	90.6%	91.5%
ECO100408	UUR100302	28%	54.0%	59.8%
ECO100408	VCH102233	53%	97.1%	95.5%
ECO100408	YPS002505	84%	99.3%	100%
ECO100409	ABA105144	46%	98.2%	99.3%
ECO100409	BFR11172	30%	97.5%	95.9%
ECO100409	BPT100016	43%	98.2%	93.8%
ECO100409	BCE110120	53%	52%	85%
ECO100409	BFU102731	49%	97.8%	97.3%
ECO100409	BMA107273	44%	96.9%	99.1%
ECO100409	CJU101376	27%	82.5%	88.6%
ECO100409	CDP100279	31%	74.8%	72.3%
ECO100409	EBC101282	84%	99.4%	100%
ECO100409	ECO100409	100%	100%	100%
ECO100409	HIN101271	52%	99.1%	93.9%
ECO100409	KPN303432	84%	99.4%	100%
ECO100409	LPN101227	52%	82.2%	83.3%
ECO100409	MCA103652	39%	91.7%	99.7%
ECO100409	MAV101439	35%	82.8%	82.4%
ECO100409	MBV102049	36%	82.8%	81.4%
ECO100409	MLP101022	35%	81.8%	82.5%
ECO100409	MTU202939	36%	82.8%	81.4%
ECO100409	NGO100695	42%	97.8%	99.1%
ECO100409	NME201944	43%	97.8%	99.1%
ECO100409	PMU100729	53%	99.1%	99.7%
ECO100409	PRT100038	67%	99.1%	98.8%
ECO100409	PAE204048	45%	98.8%	98.8%
ECO100409	PPU104483	45%	98.2%	98.1%
ECO100409	PSY102181	47%	99.1%	99.4%
ECO100409	SPA103660	87%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100409	STY100439	87%	100%	100%
ECO100409	STM100100	88%	100%	100%
ECO100409	VCH102232	54%	99.1%	96.1%
ECO100409	YPS002502	75%	99.7%	98.5%
ECO100424	ABA103655	43%	93.7%	96.9%
ECO100424	BAN111570	28%	72.4%	88.2%
ECO100424	BAN110867	33%	85.1%	92.4%
ECO100424	BPT102774	55%	85.7%	88.8%
ECO100424	BCE104834	59%	78.1%	93.5%
ECO100424	BFU101934	57%	83.2%	93.5%
ECO100424	BMA107732	57%	88.6%	92.6%
ECO100424	BMA109512	56%	89.5%	97.2%
ECO100424	CDP100360	28%	24.8%	21.0%
ECO100424	EBC101217	95%	100%	100%
ECO100424	ECO100424	100%	100%	100%
ECO100424	KPN303418	85%	47.9%	100%
ECO100424	LMO100640	34%	94.0%	81.0%
ECO100424	MAV102952	26%	39.0%	37.5%
ECO100424	MBV101465	22%	42.9%	27.2%
ECO100424	MTU202140	22%	42.9%	25%
ECO100424	PRT103954	67%	98.4%	98.4%
ECO100424	PAE201316	57%	95.2%	90.0%
ECO100424	PPU101498	57%	97.5%	99.7%
ECO100424	PSY104255	56%	96.5%	96.5%
ECO100424	SPA102308	76%	100%	100%
ECO100424	STY100721	95%	100%	99.1%
ECO100424	SAU801061	35%	81.0%	68.0%
ECO100424	SEP200354	38%	81.0%	66.6%
ECO100424	SHA100551	40%	58.4%	59.5%
ECO100424	YPS001897	66%	96.5%	99.7%
ECO100430	ABA101466	71%	93.6%	91.3%
ECO100430	BAN100418	59%	22.6%	96.9%
ECO100430	BAN109620	38%	94.3%	97.8%
ECO100430	BAN107278	65%	68.2%	93.4%
ECO100430	BAN111361	61%	96.5%	96.4%
ECO100430	BFR100135	54%	86.1%	94.8%
ECO100430	BPT100486	71%	100%	93.2%
ECO100430	BBU100611	53%	96.7%	95.8%
ECO100430	BCE114986	74%	97.4%	97.6%
ECO100430	BFU100995	73%	97.4%	97.6%
ECO100430	BMA101609	73%	97.4%	97.6%
ECO100430	CJU100247	55%	94.6%	96.2%
ECO100430	CPN201004	57%	96.0%	98.3%
ECO100430	CTR200078	57%	96.0%	98.3%
ECO100430	CAC101555	61%	96.9%	94.7%
ECO100430	CBO100837	62%	97.4%	93.7%
ECO100430	CDF102979	61%	96.5%	97.8%
ECO100430	CDP101237	61%	96.2%	96.7%
ECO100430	EBC101545	95%	98.3%	100%
ECO100430	EFA202273	60%	95.5%	96.6%
ECO100430	EFM101238	60%	96.5%	97.6%
ECO100430	ECO100430	100%	100%	100%
ECO100430	HIN100694	69%	97.4%	100%
ECO100430	HPY101354	51%	94.3%	97.1%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100430	KPN301083	98%	100%	100%
ECO100430	LMO102362	62%	96.2%	96.2%
ECO100430	MCA101655	65%	93.4%	97.0%
ECO100430	MAV102304	62%	96.0%	96.0%
ECO100430	MBV101048	61%	96.9%	96.9%
ECO100430	MLP100910	61%	96.2%	96.2%
ECO100430	MTU202421	61%	96.9%	96.9%
ECO100430	NGO101085	69%	94.1%	97.8%
ECO100430	NME201444	69%	94.1%	97.8%
ECO100430	PMU101977	73%	94.6%	98.1%
ECO100430	PRT101501	88%	100%	100%
ECO100430	PAE201801	77%	98.3%	97.9%
ECO100430	PPU109917	77%	98.8%	98.4%
ECO100430	PSY107890	77%	98.3%	97.9%
ECO100430	SPA102998	97%	98.8%	99.8%
ECO100430	STY100725	97%	100%	100%
ECO100430	STM100438	98%	100%	100%
ECO100430	SAU801674	61%	94.1%	94.0%
ECO100430	SEP201649	61%	94.1%	94.0%
ECO100430	SHA100379	56%	44.8%	92.5%
ECO100430	SMU100958	59%	94.1%	96.6%
ECO100430	SPN401426	58%	96.7%	98.8%
ECO100430	SPY200660	59%	94.1%	96.8%
ECO100430	TPA100504	56%	93.6%	95.4%
ECO100430	VCH101891	84%	100%	100%
ECO100430	YPS001881	92%	100%	100%
ECO100431	ABA100033	61%	24.2%	90.3%
ECO100431	ABA105304	55%	97.6%	95.2%
ECO100431	BAN104528	44%	96.9%	99.6%
ECO100431	BAN103992	53%	97.7%	96.3%
ECO100431	BFR11925	45%	97.4%	94.3%
ECO100431	BPT100489	68%	98.2%	95.5%
ECO100431	BBU100612	39%	97.7%	97.3%
ECO100431	BCE108504	69%	98.2%	95.3%
ECO100431	BFU100993	70%	98.5%	95.5%
ECO100431	BMA107557	69%	99.4%	96.6%
ECO100431	CJU100999	39%	97.1%	98.4%
ECO100431	CPN200737	40%	97.8%	95.1%
ECO100431	CTR200613	40%	97.1%	94.6%
ECO100431	CAC100342	47%	97.1%	98.1%
ECO100431	CBO101096	50%	98.0%	99.6%
ECO100431	CDF102998	52%	97.2%	97.3%
ECO100431	EBC101544	98%	54.5%	100%
ECO100431	ECO100431	100%	100%	100%
ECO100431	HIN100442	74%	98.3%	96.3%
ECO100431	HPY101359	39%	97.1%	98.9%
ECO100431	KPN301084	96%	62.6%	100%
ECO100431	MCA100771	52%	98.9%	96.8%
ECO100431	MAV107390	50%	47.6%	95.6%
ECO100431	MLP100403	40%	8.2%	19.4%
ECO100431	MGE100244	41%	96.2%	98.2%
ECO100431	MPN100504	40%	96.2%	98.2%
ECO100431	NGO100249	65%	98.1%	95.5%
ECO100431	NME201277	65%	98.9%	97.0%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100431	PMU101978	75%	99.4%	96.8%
ECO100431	PRT101500	88%	100%	100%
ECO100431	PAE201802	70%	97.8%	96.0%
ECO100431	PPU106533	70%	97.8%	96.0%
ECO100431	PSY103927	69%	97.8%	96.0%
ECO100431	SPA102997	99%	100%	98.4%
ECO100431	STY100726	99%	100%	100%
ECO100431	STM100439	99%	100%	100%
ECO100431	SPN401780	25%	15.9%	41.4%
ECO100431	SPY101613	24%	13.8%	42.9%
ECO100431	TPA100519	43%	98.3%	87.7%
ECO100431	UUR100350	40%	96.7%	99.0%
ECO100431	VCH101890	82%	100%	99.6%
ECO100431	YPS001875	91%	100%	100%
ECO100435	ABA106138	24%	96.2%	84.2%
ECO100435	BFR102134	27%	79.5%	78.4%
ECO100435	BFU104105	26%	95.5%	83.9%
ECO100435	CAC102936	39%	55.3%	54.1%
ECO100435	EBC102273	87%	99.2%	99.2%
ECO100435	ECO100435	100%	100%	100%
ECO100435	KPN302385	85%	98.5%	97.7%
ECO100435	LPN102857	30%	85.6%	83.1%
ECO100435	MCA100454	24%	78.8%	64.6%
ECO100435	MAV107513	22%	97.0%	94.2%
ECO100435	MBV101527	26%	96.2%	92.8%
ECO100435	MTU202439	26%	96.2%	92.8%
ECO100435	NGO101290	40%	96.2%	97.6%
ECO100435	NME200457	40%	96.2%	97.6%
ECO100435	PRT106164	55%	97.0%	94.8%
ECO100435	SPA102993	93%	100%	100%
ECO100435	STY100750	94%	100%	100%
ECO100435	STM100443	94%	100%	100%
ECO100435	SPN401264	26%	75.8%	33.1%
ECO100435	TPA100154	37%	90.2%	88.8%
ECO100435	YPS001867	69%	99.2%	97.0%
ECO100445	BAN103966	24%	61.1%	4.8%
ECO100445	BAN105784	24%	61.1%	43.0%
ECO100445	BMA103371	31%	43.7%	23.7%
ECO100445	CJU101094	30%	44.2%	93.3%
ECO100445	EBC101949	75%	81.6%	98.1%
ECO100445	ECO100445	100%	100%	100%
ECO100445	KPN302393	70%	84.2%	98.8%
ECO100445	MAV100663	25%	55.3%	53.0%
ECO100445	PAE203672	38%	54.2%	77.3%
ECO100445	PPU105141	40%	52.1%	74.2%
ECO100445	PSY107733	35%	53.2%	98.1%
ECO100445	SPA103161	84%	100%	100%
ECO100445	STY100781	88%	100%	100%
ECO100445	STM100473	88%	100%	100%
ECO100445	VCH101045	43%	47.9%	63.6%
ECO100445	YPS001806	55%	87.4%	94.2%
ECO100448	ECO100448	100%	100%	100%
ECO100448	KPN302401	62%	48.5%	100%
ECO100448	PAE202198	27%	94.8%	95.1%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100448	PPU101997	30%	97.1%	93.8%
ECO100448	SPA103158	77%	49.2%	100%
ECO100448	STY100783	67%	99.2%	99.6%
ECO100453	ABA101792	57%	99.1%	99.3%
ECO100453	BPT100257	67%	98.8%	97.6%
ECO100453	BCE114545	66%	24.5%	84.0%
ECO100453	BCE104032	66%	99.5%	98.6%
ECO100453	BFU105569	65%	100%	98.2%
ECO100453	BMA106830	66%	99.9%	98.2%
ECO100453	EBC103991	92%	100%	100%
ECO100453	ECO100453	100%	100%	100%
ECO100453	HIN100875	32%	97.9%	97.4%
ECO100453	KPN303893	91%	100%	100%
ECO100453	LPN101626	40%	98.9%	99.4%
ECO100453	MCA100461	56%	99.9%	99.7%
ECO100453	MAV103904	24%	18.5%	20.4%
ECO100453	MBV105073	23%	19.9%	19.1%
ECO100453	MTU201501	23%	19.5%	16.7%
ECO100453	NGO100607	48%	99.9%	98.7%
ECO100453	NME201818	49%	99.9%	98.7%
ECO100453	PMU101132	31%	97.6%	97.1%
ECO100453	PRT104879	75%	99.3%	99.2%
ECO100453	PAE200425	70%	98.5%	98.6%
ECO100453	PPU101135	65%	99.0%	98.7%
ECO100453	PSY103933	65%	99.3%	99.5%
ECO100453	STY100789	94%	99.9%	99.9%
ECO100453	YPS001789	84%	99.8%	99.6%
ECO100456	BCE114237	32%	23.7%	57.2%
ECO100456	BFU101219	28%	27.1%	67.2%
ECO100456	CPN200570	19%	22.7%	58.7%
ECO100456	CTR100201	19%	37.5%	48.0%
ECO100456	CDP102443	27%	12.8%	29.9%
ECO100456	EBC103983	84%	97.2%	99.9%
ECO100456	ECO100456	100%	100%	100%
ECO100456	HIN100185	35%	97.2%	98.4%
ECO100456	KPN300148	83%	14.6%	100%
ECO100456	KPN303886	83%	99.7%	97.9%
ECO100456	LPN100506	21%	82.6%	90.8%
ECO100456	MLP100103	19%	19.0%	26.4%
ECO100456	MPN100367	22%	38.7%	9.5%
ECO100456	PMU100358	38%	97.7%	98.5%
ECO100456	PRT105555	48%	97.3%	98.3%
ECO100456	PAE205017	39%	97.1%	97.0%
ECO100456	PPU102036	40%	97.4%	98.5%
ECO100456	PSY103682	41%	94.7%	93.7%
ECO100456	SPA102914	88%	95.2%	100%
ECO100456	STY100812	89%	99.8%	99.8%
ECO100456	STM100504	89%	99.7%	99.7%
ECO100456	UUR100392	24%	13.8%	11.3%
ECO100456	YPS001764	59%	97.4%	96.3%
ECO100457	EBC106191	73%	84.9%	73.8%
ECO100457	ECO100457	100%	100%	100%
ECO100457	KPN303890	75%	84.9%	78.9%
ECO100457	PRT105806	58%	94.3%	94.1%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100457	SPA102916	80%	92.5%	92.7%
ECO100457	STY100814	80%	92.5%	92.7%
ECO100457	VCH101828	58%	81.1%	61.4%
ECO100457	YPS003930	57%	84.9%	88.2%
ECO100458	CDP100984	27%	56%	24.8%
ECO100458	EBC103989	56%	100%	100%
ECO100458	ECO100458	100%	100%	100%
ECO100458	KPN300488	55%	92%	100%
ECO100458	KPN303892	59%	100%	100%
ECO100458	PMU100990	20%	97.1%	95.1%
ECO100458	PRT104644	35%	98.3%	97.2%
ECO100458	PAE108407	28%	88.6%	23.8%
ECO100458	SPA102917	72%	97.7%	100%
ECO100458	VCH101827	32%	81.1%	79.1%
ECO100458	YPS001761	36%	98.3%	97.2%
ECO100464	ABA105152	52%	99.7%	99.4%
ECO100464	BFR105086	32%	90.2%	82.4%
ECO100464	BPT101320	59%	99.2%	98.1%
ECO100464	BBU100559	41%	98.4%	93.4%
ECO100464	BCE101760	60%	99.4%	99.1%
ECO100464	BFU107645	61%	99.5%	98.9%
ECO100464	BMA108677	61%	98.7%	99.2%
ECO100464	CJU100481	43%	98.4%	98.8%
ECO100464	CAC101040	39%	98.4%	99.0%
ECO100464	CBO103036	41%	42.6%	99.6%
ECO100464	CDF102736	29%	96.0%	95.7%
ECO100464	EBC103981	91%	100%	100%
ECO100464	ECO100464	100%	100%	100%
ECO100464	HIN100103	75%	99.5%	98.7%
ECO100464	HPY100206	45%	98.6%	98.4%
ECO100464	KPN303864	91%	100%	100%
ECO100464	LPN102583	62%	99.5%	99.2%
ECO100464	LMO102556	23%	98.6%	98.2%
ECO100464	MCA100562	50%	98.6%	98.6%
ECO100464	MAV101501	48%	97.1%	96.7%
ECO100464	MBV105727	45%	98.4%	98.0%
ECO100464	MLP100990	45%	98.4%	98.0%
ECO100464	MTU202265	45%	98.4%	98.0%
ECO100464	NGO100474	25%	19.9%	34.3%
ECO100464	NME200399	25%	19.9%	18.6%
ECO100464	PMU101024	76%	99.2%	98.4%
ECO100464	PRT105522	81%	99.7%	99.0%
ECO100464	PAE201595	61%	99.4%	98.4%
ECO100464	PPU101233	60%	99.4%	98.7%
ECO100464	PSY105027	60%	99.4%	98.7%
ECO100464	SPA100495	91%	91.7%	99.7%
ECO100464	STY100841	94%	100%	98.7%
ECO100464	STM100533	94%	100%	98.7%
ECO100464	TPA100974	41%	98.4%	98.7%
ECO100464	VCH100968	69%	99.2%	98.1%
ECO100464	YPS001737	86%	100%	99.7%
ECO100465	ABA102578	62%	99.5%	99.1%
ECO100465	BAN108855	43%	100%	98.6%
ECO100465	BAN106781	47%	100%	98.6%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100465	BFR10586	39%	98.6%	96.8%
ECO100465	BPT101280	60%	99.5%	99.1%
ECO100465	BBU100416	35%	99.5%	98.1%
ECO100465	BCE114693	65%	96.3%	96.4%
ECO100465	BFU106856	65%	96.3%	96.4%
ECO100465	BMA102106	65%	96.7%	96.8%
ECO100465	CJU100600	25%	98.1%	94.3%
ECO100465	CPN200508	34%	83.6%	83.6%
ECO100465	CTR200398	32%	94.9%	83.0%
ECO100465	CAC102891	48%	100%	99.1%
ECO100465	CBO103787	51%	100%	98.6%
ECO100465	CDF102350	52%	100%	96.4%
ECO100465	CDP100003	40%	86.4%	87.3%
ECO100465	EBC103984	96%	100%	100%
ECO100465	EFA201978	45%	99.5%	98.6%
ECO100465	EFM200623	45%	99.5%	99.1%
ECO100465	ECO100465	100%	100%	100%
ECO100465	HIN100331	71%	100%	100%
ECO100465	HPY100611	30%	61.2%	72.3%
ECO100465	KPN303865	96%	100%	100%
ECO100465	LPN102084	55%	99.5%	99.1%
ECO100465	LMO102187	46%	99.5%	98.6%
ECO100465	MCA101231	61%	99.5%	98.6%
ECO100465	MAV102071	38%	100%	99.4%
ECO100465	MBV101628	37%	100%	99.4%
ECO100465	MLP101114	39%	86.4%	87.3%
ECO100465	MTU200730	37%	100%	99.4%
ECO100465	MGE100174	34%	84.6%	84.6%
ECO100465	MPN100646	32%	86.0%	86.5%
ECO100465	NGO100911	62%	100%	99.5%
ECO100465	NME200954	64%	100%	99.5%
ECO100465	PMU100284	71%	99.5%	99.5%
ECO100465	PRT104973	81%	100%	100%
ECO100465	PAE203684	64%	96.7%	96.7%
ECO100465	PPU107935	64%	96.7%	96.8%
ECO100465	PSY104919	60%	81.3%	96.2%
ECO100465	SPA100230	92%	100%	91.8%
ECO100465	STY100842	96%	100%	100%
ECO100465	STM100555	96%	100%	100%
ECO100465	SAU802229	47%	99.5%	98.6%
ECO100465	SEP200243	47%	99.5%	98.6%
ECO100465	SHA100179	47%	99.5%	98.1%
ECO100465	SMU100597	43%	85.0%	85.8%
ECO100465	SPN400210	38%	99.5%	98.1%
ECO100465	SPY200058	40%	99.5%	98.1%
ECO100465	TPA100588	38%	98.6%	97.2%
ECO100465	UUR100253	33%	99.5%	98.1%
ECO100465	VCH100969	73%	99.5%	99.5%
ECO100465	YPS001716	87%	100%	100%
ECO100468	ABA104316	27%	50.7%	63.8%
ECO100468	EBC103990	93%	100%	100%
ECO100468	ECO100468	100%	100%	100%
ECO100468	KPN303867	89%	100%	100%
ECO100468	MCA101546	24%	57.4%	72.1%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100468	PRT103854	82%	100%	100%
ECO100468	SPA107646	92%	100%	100%
ECO100468	STY100845	94%	100%	100%
ECO100468	STM100558	94%	100%	100%
ECO100468	VCH103521	69%	100%	100%
ECO100468	VCH101110	75%	100%	100%
ECO100468	YPS001600	83%	100%	100%
ECO100469	ABA105707	48%	97.3%	97.0%
ECO100469	BAN105697	24%	61.3%	85.4%
ECO100469	BAN103529	27%	63.6%	89.8%
ECO100469	BAN105257	27%	67.6%	93.7%
ECO100469	BFR10916	30%	63.8%	48.5%
ECO100469	BFR11614	32%	69.9%	50.9%
ECO100469	BBU100446	21%	69.4%	57.9%
ECO100469	BCE111018	51%	97.7%	97.5%
ECO100469	BMA106790	50%	99.3%	98.4%
ECO100469	CBO103826	23%	65.9%	91.1%
ECO100469	CDP101177	26%	90.1%	93.7%
ECO100469	EBC105058	92%	98.2%	98.4%
ECO100469	EFM201852	28%	67.9%	96.1%
ECO100469	ECO100469	100%	100%	100%
ECO100469	KPN309208	91%	100%	100%
ECO100469	MAV102680	29%	64.9%	93.2%
ECO100469	MBV104698	29%	61.5%	86.2%
ECO100469	MLP100477	27%	61.5%	86.5%
ECO100469	MTU203193	29%	61.5%	86.2%
ECO100469	PRT101586	71%	98.0%	95.4%
ECO100469	PAE205513	62%	98.0%	97.0%
ECO100469	PPU103619	33%	68.3%	64.0%
ECO100469	SPA103965	83%	98.2%	100%
ECO100469	STY100846	94%	99.6%	99.6%
ECO100469	SAU401722	23%	66.8%	85.2%
ECO100469	TPA100056	23%	37.6%	47.1%
ECO100469	YPS001597	79%	98.2%	97.3%
ECO100473	BCE112818	22%	90.5%	79.4%
ECO100473	BFU105062	27%	87.5%	92.5%
ECO100473	BMA109015	23%	55.7%	93.1%
ECO100473	CAC101805	21%	87.1%	80.6%
ECO100473	EBC101032	70%	51.1%	100%
ECO100473	ECO100473	100%	100%	100%
ECO100473	KPN305997	67%	96.2%	99.2%
ECO100473	PRT105875	47%	99.2%	97.8%
ECO100473	SPA101218	64%	100%	100%
ECO100473	STY100870	65%	100%	100%
ECO100473	VCH102186	33%	88.6%	80.2%
ECO100473	YPS001582	56%	99.2%	97.4%
ECO100475	ABA101879	41%	7.2%	16.0%
ECO100475	BAN105978	44%	57.4%	98.6%
ECO100475	BAN110321	44%	69.3%	100%
ECO100475	BFR10291	39%	86.6%	98.1%
ECO100475	BPT102136	41%	6.8%	15.8%
ECO100475	BCE110602	43%	73.5%	97.9%
ECO100475	BFU113139	47%	72.8%	81.7%
ECO100475	BMA106854	46%	73.3%	73.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100475	CJU101080	30%	86.9%	89.4%
ECO100475	CAC100879	39%	18.9%	7.9%
ECO100475	CBO102754	38%	99.2%	99.5%
ECO100475	CDF102644	39%	4.6%	16.2%
ECO100475	CDP100778	38%	5.2%	7.9%
ECO100475	EBC100331	89%	4.2%	19.6%
ECO100475	EFA201855	39%	19.2%	7.9%
ECO100475	EFM201092	37%	87.5%	98.5%
ECO100475	ECO100475	100%	100%	100%
ECO100475	HIN100276	37%	3.2%	10.7%
ECO100475	HPY101055	32%	88.0%	99.6%
ECO100475	KPN308679	87%	6.6%	18.6%
ECO100475	LPN101141	44%	77.7%	89.0%
ECO100475	LPN101253	45%	77.7%	88.7%
ECO100475	LMO100878	37%	1.4%	12.6%
ECO100475	MCA100406	36%	87.5%	95.5%
ECO100475	MAV100988	36%	72.9%	81.5%
ECO100475	MBV103852	44%	77.7%	79.7%
ECO100475	MLP101222	34%	87.4%	96.5%
ECO100475	MTU200960	44%	77.7%	81.9%
ECO100475	NGO100160	39%	86.7%	98.1%
ECO100475	NME201398	40%	87.2%	98.6%
ECO100475	PMU101892	39%	2.9%	10.9%
ECO100475	PRT105140	72%	27.5%	12.7%
ECO100475	PAE203917	41%	7.1%	16.3%
ECO100475	PPU108258	41%	99.6%	98.6%
ECO100475	PSY102170	42%	7.0%	21.1%
ECO100475	SPA101217	84%	86.8%	100%
ECO100475	STY100871	93%	99.9%	99.9%
ECO100475	STM104228	42%	4.4%	8.3%
ECO100475	SAU802557	38%	99.9%	99.5%
ECO100475	SEP201193	37%	7.2%	16.6%
ECO100475	SHA100292	40%	73.9%	100%
ECO100475	SMU100795	41%	4.4%	8.9%
ECO100475	SPN400641	43%	72.1%	79.3%
ECO100475	SPY201317	41%	4.6%	8.9%
ECO100475	TPA101026	34%	3.7%	9.8%
ECO100475	UUR100203	28%	76.9%	92.9%
ECO100475	VCH102181	50%	9.0%	19.3%
ECO100475	YPS001578	66%	7.3%	22.9%
ECO100485	ABA102979	44%	78.8%	90.3%
ECO100485	BPT100402	42%	86.5%	82.4%
ECO100485	BCE103660	39%	98.1%	60.3%
ECO100485	BFU101347	38%	93.3%	90.2%
ECO100485	BMA107037	42%	86.1%	81.2%
ECO100485	CAC101080	25%	84.1%	98.9%
ECO100485	CBO103052	27%	48.6%	52.1%
ECO100485	CDF104317	23%	79.3%	92.3%
ECO100485	EBC103361	92%	90.9%	100%
ECO100485	EFA202370	25%	74.0%	85.1%
ECO100485	ECO100485	100%	100%	100%
ECO100485	KPN303861	87%	100%	95.4%
ECO100485	LMO100084	26%	80.3%	96.4%
ECO100485	NGO100490	35%	75.5%	71.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100485	NME201781	35%	75.5%	71.8%
ECO100485	PRT104443	57%	89.4%	97.9%
ECO100485	PAE202854	49%	91.3%	95.5%
ECO100485	PPU111360	45%	93.8%	91.2%
ECO100485	PSY100343	47%	75%	98.8%
ECO100485	SPA101077	87%	98.1%	94.9%
ECO100485	STY100879	89%	98.1%	100%
ECO100485	SPY201146	27%	84.1%	55.6%
ECO100485	VCH103503	56%	90.9%	88.8%
ECO100485	YPS001527	71%	98.1%	98.1%
ECO100488	ABA100225	26%	47.2%	31.6%
ECO100488	ABA100477	26%	27.1%	80.5%
ECO100488	BAN104847	21%	28.1%	4.3%
ECO100488	BAN109223	31%	7.2%	48.7%
ECO100488	BAN101440	31%	7.6%	43.5%
ECO100488	BAN110288	23%	20.8%	3.8%
ECO100488	BFR104422	59%	1.9%	27%
ECO100488	BCE108121	26%	28.9%	68.0%
ECO100488	BCE104951	26%	49.5%	30.5%
ECO100488	BFU107935	29%	21.0%	31.4%
ECO100488	BFU100092	51%	6.2%	98.9%
ECO100488	BFU100109	28%	9.3%	60.6%
ECO100488	BFU102581	29%	11.2%	4.4%
ECO100488	BMA107682	26%	25.9%	53.9%
ECO100488	CAC100404	28%	7.9%	39.1%
ECO100488	EBC107494	33%	21.5%	50.7%
ECO100488	EBC103412	28%	21.5%	25.6%
ECO100488	EBC104888	26%	28.5%	68.9%
ECO100488	ECO100686	77%	23.5%	70.2%
ECO100488	ECO101427	86%	41.4%	86.8%
ECO100488	ECO100683	77%	88.2%	89.3%
ECO100488	ECO103515	77%	88.2%	90.6%
ECO100488	ECO103405	74%	99.6%	99.7%
ECO100488	ECO100488	100%	100%	100%
ECO100488	MAV107400	23%	19.1%	20.6%
ECO100488	PRT103688	29%	7.3%	73.6%
ECO100488	PRT103361	31%	7.6%	75.1%
ECO100488	PRT103421	25%	11.2%	4.4%
ECO100488	PAE202682	31%	88.3%	88.8%
ECO100488	PPU107712	30%	7.6%	94.3%
ECO100488	PPU109654	27%	6.8%	73.5%
ECO100488	PPU110484	28%	12.0%	92.3%
ECO100488	PPU107101	28%	10.9%	38.6%
ECO100488	PPU109653	28%	41.0%	73.7%
ECO100488	PPU109652	25%	32.9%	38.8%
ECO100488	PPU110482	29%	53.6%	54.8%
ECO100488	PSY108533	33%	4.9%	83.6%
ECO100488	PSY101322	55%	4.1%	24.3%
ECO100488	PSY105816	47%	7.2%	45.3%
ECO100488	PSY102083	25%	44.4%	45.2%
ECO100488	SPA106438	38%	2.5%	16.8%
ECO100488	SPA100247	26%	53.2%	67.7%
ECO100488	STY104094	26%	30.2%	50.1%
ECO100488	STY104095	30%	59.5%	51.1%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100488	STM103807	42%	8.0%	50.8%
ECO100488	STM103806	26%	40.7%	49.6%
ECO100488	YPS002860	25%	84.9%	75.6%
ECO100490	ABA100225	43%	36.9%	5.8%
ECO100490	ABA100477	45%	38.6%	10.5%
ECO100490	BAN101440	31%	39.4%	37.8%
ECO100490	BAN109223	31%	39.4%	44.2%
ECO100490	BAN110288	33%	39.4%	4.4%
ECO100490	BCE104951	36%	50.4%	8.6%
ECO100490	BCE108121	46%	39.0%	10.1%
ECO100490	BFU100092	48%	36.9%	97.8%
ECO100490	BFU102581	51%	39.0%	6.1%
ECO100490	BFU100109	47%	41.1%	14.2%
ECO100490	BMA107682	35%	38.6%	8.0%
ECO100490	CAC100404	32%	35.6%	30.3%
ECO100490	EBC103412	43%	38.1%	33.2%
ECO100490	ECO100686	73%	39.8%	19.7%
ECO100490	ECO103517	66%	45.8%	45.5%
ECO100490	ECO103515	75%	39.4%	6.8%
ECO100490	ECO103405	76%	39.8%	6.7%
ECO100490	ECO100683	76%	39.4%	6.7%
ECO100490	ECO100488	80%	39.4%	6.5%
ECO100490	ECO101427	42%	92.4%	31.4%
ECO100490	ECO100490	100%	100%	100%
ECO100490	PRT103361	33%	38.6%	65.5%
ECO100490	PRT103421	45%	39.4%	7.7%
ECO100490	PAE202682	51%	39.4%	7.0%
ECO100490	PPU107712	49%	23.3%	63.2%
ECO100490	PPU107101	48%	38.6%	22.0%
ECO100490	PPU110482	46%	39.0%	6.6%
ECO100490	PPU109652	45%	40.7%	6.4%
ECO100490	PSY101322	55%	24.6%	23.9%
ECO100490	PSY105816	46%	39.0%	40.8%
ECO100490	PSY102083	47%	39.0%	5.8%
ECO100490	SPA106438	46%	37.3%	40%
ECO100490	STY104095	48%	38.6%	10.8%
ECO100490	STY104094	51%	37.3%	6.6%
ECO100490	STM103806	49%	37.7%	6.7%
ECO100490	STM103807	49%	37.7%	37.0%
ECO100490	YPS002860	47%	39.4%	6.4%
ECO100491	ECO100491	100%	100%	100%
ECO100499	ABA104957	38%	99.6%	97.3%
ECO100499	BCE100249	55%	98.4%	94.4%
ECO100499	BFU102476	53%	98.4%	95.1%
ECO100499	BFU114367	56%	98.4%	94.4%
ECO100499	ECO100499	100%	100%	100%
ECO100499	PAE201500	59%	98.4%	97.7%
ECO100499	PPU107167	57%	98.4%	97.7%
ECO100499	SPA103879	83%	100%	100%
ECO100499	STY100931	84%	100%	100%
ECO100499	STM100624	84%	100%	100%
ECO100500	ABA103985	44%	98.6%	99.0%
ECO100500	BPT100453	34%	93.5%	99.3%
ECO100500	BCE106184	65%	99.0%	97.0%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100500	BFU104727	64%	99.7%	96.0%
ECO100500	EFA200236	38%	95.9%	94.9%
ECO100500	BFM201855	40%	96.2%	95.6%
ECO100500	ECO100500	100%	100%	100%
ECO100500	HPY200581	30%	97.3%	98.6%
ECO100500	LMO101779	41%	95.9%	98.3%
ECO100500	PAE201499	62%	99.3%	98.3%
ECO100500	PPU100008	63%	99.3%	98.0%
ECO100500	SPA103880	90%	100%	100%
ECO100500	STY100932	91%	100%	100%
ECO100500	STM100645	91%	100%	100%
ECO100501	ECO100501	100%	100%	100%
ECO100501	STM104546	57%	53.3%	58.3%
ECO100502	ABA104757	29%	99.3%	89.2%
ECO100502	BCE108546	28%	98.2%	82.9%
ECO100502	BFU103203	26%	96.3%	79.2%
ECO100502	BMA100176	27%	96.3%	79.2%
ECO100502	EBC101321	30%	36.8%	93.7%
ECO100502	EFA202073	53%	97.9%	86.5%
ECO100502	ECO100502	100%	100%	100%
ECO100502	KPN301121	28%	96.8%	84.7%
ECO100502	PAE200475	30%	98.2%	74.4%
ECO100502	PPU107187	28%	96.3%	78.9%
ECO100502	PSY103157	26%	95.4%	85.9%
ECO100502	SPA103881	91%	100%	90.3%
ECO100502	STM100647	92%	100%	100%
ECO100502	YPS002040	27%	96.8%	85.4%
ECO100522	EBC104095	61%	93.5%	100%
ECO100522	ECO100522	100%	100%	100%
ECO100522	LPN101710	27%	35.2%	30.8%
ECO100522	PRT104641	26%	77.4%	75.5%
ECO100522	PRT103064	29%	92.2%	95.5%
ECO100522	PRT105670	29%	98.3%	97.8%
ECO100522	PRT105544	30%	95.7%	98.6%
ECO100522	PRT105082	33%	93.5%	95.9%
ECO100522	PRT101027	42%	97.0%	96.9%
ECO100522	PRT101728	46%	96.1%	94.0%
ECO100522	PRT105207	46%	93.0%	93.0%
ECO100522	SPA101492	64%	96.5%	93.7%
ECO100522	STY101296	62%	99.6%	99.6%
ECO100522	STM101010	61%	99.6%	99.6%
ECO100523	BBU100344	26%	17.1%	36.2%
ECO100523	BMA102682	37%	95.0%	95.5%
ECO100523	CDF100539	22%	18.0%	56.5%
ECO100523	EBC104108	65%	95.6%	99.3%
ECO100523	ECO100523	100%	100%	100%
ECO100523	KPN201537	39%	95.8%	98.7%
ECO100523	MAV108170	24%	20.3%	37.6%
ECO100523	PRT104636	44%	97.5%	99.3%
ECO100523	SPA103196	72%	68.5%	100%
ECO100523	STY101297	69%	98.6%	98.5%
ECO100523	STM101011	70%	98.6%	98.5%
ECO100523	SAU300377	26%	11.5%	52.7%
ECO100541	EBC101703	52%	98.4%	95.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100541	ECO100541	100%	100%	100%
ECO100541	PRT105258	53%	48.8%	98.4%
ECO100541	PRT100296	49%	96.9%	93.2%
ECO100541	YPS000017	65%	94.5%	93.0%
ECO100549	ECO100549	100%	100%	100%
ECO100554	ABA101274	33%	40.6%	26.5%
ECO100554	ABA101204	39%	31.7%	23.0%
ECO100554	ABA104217	29%	37.8%	27.6%
ECO100554	BFR101004	32%	28.9%	11.4%
ECO100554	BFR105341	35%	31.3%	13.8%
ECO100554	BCE106065	29%	29.7%	67.3%
ECO100554	BCE113842	31%	49.8%	33.2%
ECO100554	BMA107995	26%	31.3%	22.3%
ECO100554	BMA105539	32%	31.7%	38.9%
ECO100554	ECO101470	28%	92.4%	89.7%
ECO100554	ECO103438	36%	93.6%	96.3%
ECO100554	ECO100554	100%	100%	100%
ECO100554	LPN103151	28%	32.9%	24.5%
ECO100554	MBV100183	26%	55.4%	37.6%
ECO100554	MTU301482	26%	55.4%	36.9%
ECO100554	NME102614	33%	29.7%	24.6%
ECO100554	PRT101349	35%	39.8%	39.5%
ECO100554	PRT104740	34%	51.8%	48.0%
ECO100554	PAE202094	29%	33.3%	25%
ECO100554	PAE203213	31%	30.5%	22.6%
ECO100554	PPU102277	25%	37.8%	26.4%
ECO100554	PPU101064	31%	30.5%	21.5%
ECO100554	SPA100934	36%	50.6%	51.4%
ECO100554	SPA103838	40%	49.8%	40.1%
ECO100554	STY102368	37%	49.0%	48.6%
ECO100554	STY102403	33%	73.9%	64.9%
ECO100554	STM103734	40%	49.8%	40.1%
ECO100554	SMU100002	29%	37.8%	27.9%
ECO100554	VCH100823	29%	49.0%	44.2%
ECO100555	BFU112796	28%	18.3%	36.0%
ECO100555	EBC102973	48%	100%	97.1%
ECO100555	ECO100555	100%	100%	100%
ECO100555	LPN101913	38%	97.8%	98.7%
ECO100555	PPU103428	23%	56.8%	38.8%
ECO100555	SPA103146	46%	100%	100%
ECO100555	STY101101	46%	100%	100%
ECO100555	YPS000286	40%	91.5%	90.4%
ECO100557	ABA102872	22%	69.9%	59.8%
ECO100557	ECO100557	100%	100%	100%
ECO100557	PPU111671	33%	99.3%	98.9%
ECO100557	PSY102041	25%	73.3%	70.7%
ECO100560	BAN106854	24%	24.4%	90.1%
ECO100560	BAN112348	33%	23.8%	76.5%
ECO100560	BAN100221	25%	74.8%	77.7%
ECO100560	BAN103717	26%	62.5%	96.9%
ECO100560	BAN100334	26%	57.1%	93.3%
ECO100560	BAN102939	26%	74.8%	76.4%
ECO100560	BAN113334	25%	63.5%	84.6%
ECO100560	BAN102333	27%	68.8%	71.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100560	BAN110951	28%	62.5%	67.8%
ECO100560	BFR10765	27%	59.6%	63.9%
ECO100560	BFR103543	27%	64.0%	68.4%
ECO100560	BPT104047	31%	97.9%	96.7%
ECO100560	BCE114206	31%	97.9%	97.4%
ECO100560	BFU111283	42%	61.7%	63.6%
ECO100560	BFU103037	32%	97.7%	98.6%
ECO100560	BMA100332	31%	98.3%	98.1%
ECO100560	CAC102666	28%	60.6%	62.2%
ECO100560	CDF100992	28%	52.7%	65.7%
ECO100560	EBC104519	56%	99.8%	97.8%
ECO100560	ECO100560	100%	100%	100%
ECO100560	KPN302405	66%	98.5%	98.3%
ECO100560	LPN102226	32%	63.3%	88.0%
ECO100560	LMO102551	24%	99.8%	98.6%
ECO100560	PAE202808	41%	68.3%	72.7%
ECO100560	PPU101821	35%	97.7%	98.4%
ECO100560	PPU101984	35%	97.9%	96.4%
ECO100560	PSY104285	40%	67.3%	70.9%
ECO100560	SAU801414	23%	95%	96.5%
ECO100560	YPS003206	35%	67.1%	69.3%
ECO100572	ECO100572	100%	100%	100%
ECO100572	ECO100016	100%	100%	100%
ECO100572	ECO102351	100%	100%	99.5%
ECO100572	KPN301837	28%	24.6%	33.5%
ECO100572	KPN301756	28%	24.6%	25.9%
ECO100572	PPU112458	31%	21.6%	17.3%
ECO100572	PPU110183	31%	21.6%	18.0%
ECO100572	PPU100534	31%	21.6%	17.3%
ECO100572	PPU111918	31%	21.6%	17.3%
ECO100572	PPU111424	31%	21.6%	17.3%
ECO100572	PPU109580	31%	21.6%	17.3%
ECO100572	STY100108	28%	24.6%	25.9%
ECO100582	BAN107042	36%	24.8%	26.5%
ECO100582	BAN100797	25%	61.9%	58.9%
ECO100582	BAN107954	22%	56.0%	61.5%
ECO100582	BAN107919	23%	84.3%	79.6%
ECO100582	CAC102393	22%	47.5%	43.3%
ECO100582	CDF102033	25%	37.7%	36.8%
ECO100582	EBC100468	78%	74.8%	100%
ECO100582	EFA205322	25%	90.6%	88.1%
ECO100582	ECO100582	100%	100%	100%
ECO100582	KPN304825	84%	96.2%	96.2%
ECO100582	PRT102496	24%	69.8%	63.2%
ECO100582	PAE204156	41%	97.8%	98.0%
ECO100582	SPA102125	76%	100%	100%
ECO100582	STY101372	79%	100%	100%
ECO100582	SHA100136	24%	88.4%	86.1%
ECO100582	SPY200281	22%	81.4%	76.5%
ECO100582	VCH100763	36%	96.5%	92%
ECO100582	YPS002778	53%	92.1%	86.9%
ECO100584	ABA103671	56%	98.5%	98.7%
ECO100584	BAN111652	41%	98.7%	99.8%
ECO100584	BAN104146	48%	98.7%	98.1%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100584	BCE105183	43%	65.1%	93.5%
ECO100584	EBC100728	73%	81.9%	100%
ECO100584	ECO100584	100%	100%	100%
ECO100584	KPN304829	81%	98.7%	98.9%
ECO100584	MAV100968	42%	98.7%	96.7%
ECO100584	MBV101299	37%	97.4%	95.3%
ECO100584	MTU202348	39%	97.4%	93.6%
ECO100584	PAE204226	46%	98.7%	96.7%
ECO100584	PSY105284	42%	90.7%	92.5%
ECO100584	SPA100882	82%	99.6%	100%
ECO100584	STY101374	85%	99.6%	99.4%
ECO100584	STM101106	86%	99.6%	99.6%
ECO100584	VCH100759	48%	98.5%	98.0%
ECO100584	YPS002354	42%	93.7%	95.0%
ECO100593	EBC102628	50%	99%	99.3%
ECO100593	ECO100593	100%	100%	100%
ECO100593	KPN303370	48%	97.7%	94.2%
ECO100593	SPA103039	53%	99.3%	99.3%
ECO100593	STY101394	54%	99.3%	99.3%
ECO100619	EBC101386	61%	100%	83.9%
ECO100619	ECO100619	100%	100%	100%
ECO100619	KPN302688	50%	100%	89.3%
ECO100619	SPA102530	61%	100%	100%
ECO100619	STY101451	68%	100%	83.9%
ECO100632	ABA105508	56%	99.5%	99.1%
ECO100632	BAN102826	43%	99.3%	99.5%
ECO100632	BFR10298	34%	99.5%	99.9%
ECO100632	BPT102350	48%	99.8%	99.9%
ECO100632	BBU100250	38%	99.5%	99.6%
ECO100632	BCE103321	49%	99.9%	100%
ECO100632	BMA109061	49%	99.9%	94.6%
ECO100632	CJU101017	43%	99.4%	99.6%
ECO100632	CPN200606	41%	99.5%	99.9%
ECO100632	CTR200474	40%	99.5%	99.9%
ECO100632	CAC101070	40%	99.0%	99.1%
ECO100632	CBO100961	40%	98.8%	99.0%
ECO100632	CDF103555	44%	99.4%	99.5%
ECO100632	CDP101454	36%	99.0%	97.1%
ECO100632	EBC100539	92%	55.2%	100%
ECO100632	EFA200538	42%	99.3%	99.5%
ECO100632	EFM200610	43%	99.3%	99.5%
ECO100632	ECO100632	100%	100%	100%
ECO100632	HIN100900	72%	99.9%	99.8%
ECO100632	HPY101524	42%	98.8%	99.3%
ECO100632	KPN300581	97%	18.4%	96.3%
ECO100632	KPN302684	95%	99.8%	100%
ECO100632	LPN103327	54%	100%	100%
ECO100632	LMO100611	42%	99.3%	99.5%
ECO100632	MCA102972	49%	99.7%	99.0%
ECO100632	MAV103767	37%	96.3%	90.9%
ECO100632	MBV104696	37%	96.2%	92.8%
ECO100632	MLP100028	36%	99.9%	97.7%
ECO100632	MTU200041	37%	96.2%	93.0%
ECO100632	MGE100272	34%	99.4%	99.6%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100632	MPN100453	34%	99.4%	99.5%
ECO100632	NGO100059	57%	99.9%	99.8%
ECO100632	NME200518	55%	99.9%	100%
ECO100632	PMU101214	72%	99.8%	99.8%
ECO100632	PRT102887	80%	100%	100%
ECO100632	PAE203984	57%	99.8%	99.8%
ECO100632	PPU108817	57%	99.8%	99.8%
ECO100632	PSY105072	57%	99.8%	99.8%
ECO100632	SPA100430	93%	58.6%	98.8%
ECO100632	STY101466	95%	100%	100%
ECO100632	SAU801760	42%	99.3%	99.5%
ECO100632	SEP202121	42%	99.3%	99.5%
ECO100632	SHA100631	42%	99.3%	99.5%
ECO100632	SMU100492	40%	99.4%	99.5%
ECO100632	SPN400235	42%	99.4%	99.5%
ECO100632	SPY200128	42%	99.4%	99.5%
ECO100632	TPA100579	39%	98.8%	99.2%
ECO100632	UUR100373	34%	99.4%	99.9%
ECO100632	VCH100940	75%	99.8%	95.7%
ECO100632	YPS001199	84%	100%	100%
ECO100645	ABA101420	41%	99.0%	100%
ECO100645	BPT102527	46%	98.3%	96.7%
ECO100645	BCE104111	65%	100%	99%
ECO100645	BFU109692	45%	99.0%	85.4%
ECO100645	BMA102165	72%	86.8%	100%
ECO100645	EBC102933	91%	100%	100%
ECO100645	ECO100645	100%	100%	100%
ECO100645	KPN300407	91%	41.7%	100%
ECO100645	KPN302708	89%	100%	100%
ECO100645	PRT102877	75%	100%	100%
ECO100645	PAE201341	58%	97.4%	97.7%
ECO100645	PPU101496	57%	96.4%	97.4%
ECO100645	PSY105194	55%	96.4%	94.8%
ECO100645	SPA102587	95%	92.1%	100%
ECO100645	STY101796	93%	100%	98.1%
ECO100645	YPS001209	78%	100%	100%
ECO100647	ABA104991	36%	96.5%	92.3%
ECO100647	BPT100972	30%	94.1%	98.1%
ECO100647	BBU100236	28%	32.4%	32.1%
ECO100647	BCE102700	33%	92.2%	82.3%
ECO100647	BFU103489	32%	95.9%	92.9%
ECO100647	BMA107358	31%	70.3%	97.8%
ECO100647	CJU101021	23%	53.7%	55.1%
ECO100647	CPN200092	23%	95.3%	92.1%
ECO100647	CTR200810	28%	35.2%	34.9%
ECO100647	CAC101602	24%	29.7%	62.6%
ECO100647	CDP101117	24%	81.6%	90.6%
ECO100647	EBC102934	85%	99.6%	100%
ECO100647	ECO100647	100%	100%	100%
ECO100647	HIN100288	44%	97.1%	95.4%
ECO100647	HPY100177	23%	60.5%	66.8%
ECO100647	KPN302711	83%	100%	100%
ECO100647	LPN102781	30%	84.6%	98.6%
ECO100647	MCA100961	36%	96.3%	94.9%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100647	MAV106114	25%	97.3%	82.0%
ECO100647	MBV102260	26%	97.1%	94.9%
ECO100647	MLP100891	24%	96.9%	79.2%
ECO100647	MTU202018	26%	97.1%	57.9%
ECO100647	NGO101835	31%	97.1%	96.5%
ECO100647	NME200849	31%	97.1%	96.5%
ECO100647	PMU101032	45%	96.3%	94.0%
ECO100647	PRT102866	61%	96.5%	97.2%
ECO100647	PAE203981	40%	95.7%	95.1%
ECO100647	PPU107601	41%	94.3%	94.7%
ECO100647	PSY105070	41%	95.1%	95.7%
ECO100647	SPA102458	85%	76.2%	100%
ECO100647	STY101797	87%	100%	100%
ECO100647	TPA100249	25%	69.9%	72.0%
ECO100647	TPA100413	25%	75.6%	76.6%
ECO100647	VCH100942	48%	99.0%	99.2%
ECO100647	YPS001211	65%	99.6%	99.2%
ECO100648	ABA106059	43%	83.6%	89.6%
ECO100648	BFR10598	34%	86.6%	57.9%
ECO100648	BPT100973	42%	91.8%	89.8%
ECO100648	BBU100059	37%	79.8%	90.7%
ECO100648	BCE102638	45%	90.4%	88.1%
ECO100648	BFU103492	45%	88.4%	82.6%
ECO100648	BMA100300	44%	95.5%	89.3%
ECO100648	CPN200241	32%	70.5%	53.5%
ECO100648	CTR200696	30%	77.4%	60.7%
ECO100648	CDP100549	33%	91.1%	64.0%
ECO100648	EBC102935	94%	100%	100%
ECO100648	EFM200835	33%	85.6%	56.1%
ECO100648	ECO100648	100%	100%	100%
ECO100648	HIN100287	63%	97.3%	95.7%
ECO100648	KPN302676	96%	100%	92.7%
ECO100648	LPN103355	47%	86.3%	88.4%
ECO100648	LMO101012	30%	89.0%	61.8%
ECO100648	MCA100807	40%	93.8%	94.8%
ECO100648	MAV100201	36%	76.0%	51.8%
ECO100648	MBV102614	37%	76.0%	52.0%
ECO100648	MTU202330	37%	76.0%	52.0%
ECO100648	MGE100148	26%	66.8%	45.5%
ECO100648	MPN100672	25%	66.8%	45.5%
ECO100648	NGO101904	51%	90.8%	96.4%
ECO100648	NME200659	51%	90.8%	96.4%
ECO100648	PMU101033	64%	95.9%	93%
ECO100648	PRT102899	84%	99.3%	98.6%
ECO100648	PAE203980	51%	91.4%	96.1%
ECO100648	PPU112260	52%	91.4%	96.1%
ECO100648	PSY105068	52%	91.4%	95.7%
ECO100648	SPA102459	96%	100%	100%
ECO100648	STY101798	97%	100%	100%
ECO100648	SPN401776	34%	76.0%	49.7%
ECO100648	SPY200275	34%	79.1%	52.0%
ECO100648	TPA100641	35%	78.8%	86.0%
ECO100648	VCH100943	66%	96.9%	96.6%
ECO100648	YPS001216	86%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100652	BFR100448	41%	10.0%	16.5%
ECO100652	BPT101695	33%	97.7%	98.5%
ECO100652	EBC100475	77%	91.8%	100%
ECO100652	ECO100652	100%	100%	100%
ECO100652	KPN302701	78%	100%	100%
ECO100652	MBV101815	24%	79.8%	76.2%
ECO100652	MTU201729	24%	80.6%	68.9%
ECO100652	PMU101002	50%	98.5%	98.5%
ECO100652	PRT102895	60%	98.5%	97.7%
ECO100652	SPA102463	83%	100%	100%
ECO100652	STY101812	85%	100%	100%
ECO100652	STM101551	85%	100%	100%
ECO100652	VCH100947	52%	99.7%	96.7%
ECO100652	YPS001221	63%	99.5%	99.2%
ECO100659	BFR10535	28%	87.9%	90.3%
ECO100659	BMA106268	32%	16.5%	22.1%
ECO100659	CBO102186	30%	74.6%	96.5%
ECO100659	CDP101325	27%	70.4%	90.2%
ECO100659	EBC101470	91%	100%	100%
ECO100659	EFM101256	25%	92.9%	95.3%
ECO100659	ECO100659	100%	100%	100%
ECO100659	KPN301178	88%	100%	100%
ECO100659	LMO100695	30%	82.3%	82.2%
ECO100659	MAV103808	23%	79.8%	62.5%
ECO100659	MBV102332	22%	79.8%	78.8%
ECO100659	MTU408202	22%	79.8%	78.8%
ECO100659	PMU100683	54%	97.8%	98.3%
ECO100659	PRT100305	70%	98.5%	98.3%
ECO100659	PSY101979	30%	18.0%	33.3%
ECO100659	PSY105778	23%	49.8%	60.1%
ECO100659	SPA101689	93%	100%	100%
ECO100659	STY101819	94%	100%	100%
ECO100659	SMU100070	28%	74.1%	96.3%
ECO100659	SPN201158	27%	80.0%	83.9%
ECO100659	SPY201178	29%	74.9%	97.2%
ECO100659	VCH100976	60%	98.3%	99.0%
ECO100659	YPS001229	78%	99.8%	99.0%
ECO100661	BAN112647	36%	79.7%	93.1%
ECO100661	BAN106376	34%	90.6%	87.0%
ECO100661	BFR104796	64%	98.9%	97.4%
ECO100661	BBU100151	60%	98.5%	97.8%
ECO100661	BFU102111	22%	44.4%	19.7%
ECO100661	CAC101312	36%	92.9%	100%
ECO100661	CBO103757	38%	94.0%	98.0%
ECO100661	CDF100159	38%	40.6%	89.9%
ECO100661	CDF100928	38%	94.0%	98.0%
ECO100661	CDP101713	44%	79.7%	81.9%
ECO100661	EBC101472	93%	100%	100%
ECO100661	EFA201130	34%	92.9%	100%
ECO100661	EFM201449	33%	92.9%	100%
ECO100661	ECO100661	100%	100%	100%
ECO100661	HIN100134	74%	97.4%	95.9%
ECO100661	KPN301180	93%	100%	100%
ECO100661	LMO102723	39%	76.7%	83.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100661	MLP100363	25%	59.8%	64.0%
ECO100661	MTU401062	23%	76.3%	80.6%
ECO100661	MTU406545	27%	58.6%	83.3%
ECO100661	PMU100875	76%	100%	99.6%
ECO100661	PRT101157	75%	94.0%	97.3%
ECO100661	SPA101691	95%	67.7%	100%
ECO100661	STY101831	95%	100%	100%
ECO100661	SAU800569	35%	77.1%	81.3%
ECO100661	SEP200118	31%	90.6%	97.1%
ECO100661	SHA102516	37%	82.0%	90.5%
ECO100661	SMU100790	38%	77.1%	84.5%
ECO100661	SPN401271	32%	90.2%	94.2%
ECO100661	SPY201070	35%	79.3%	86.8%
ECO100661	VCH103743	79%	99.6%	99.6%
ECO100661	YPS001237	85%	100%	100%
ECO100662	BAN102604	46%	71.6%	100%
ECO100662	BAN102323	52%	71.6%	100%
ECO100662	BCE100659	55%	65.6%	98.9%
ECO100662	BFU102702	55%	74.1%	81.8%
ECO100662	BMA108578	54%	73.1%	98.5%
ECO100662	CTR200280	35%	10.6%	18.4%
ECO100662	CAC100601	48%	71.9%	98.8%
ECO100662	CBO100356	42%	18.8%	63.9%
ECO100662	CBO102223	38%	99.2%	99.1%
ECO100662	EBC101577	45%	70.7%	100%
ECO100662	EFA201939	40%	95.4%	95.6%
ECO100662	EFM200960	40%	96.6%	96.8%
ECO100662	ECO100662	100%	100%	100%
ECO100662	KPN301181	88%	99.8%	99.7%
ECO100662	MGE100071	32%	2.9%	20.9%
ECO100662	MPN100624	32%	2.9%	21.1%
ECO100662	PMU100876	43%	71.9%	99.8%
ECO100662	PRT101158	48%	100%	100%
ECO100662	PAE203758	50%	71.1%	98.4%
ECO100662	SPA101338	90%	99.8%	99.7%
ECO100662	STY101832	92%	99.8%	99.7%
ECO100662	STM101571	92%	99.8%	99.7%
ECO100662	SAU800189	39%	95.1%	95.2%
ECO100662	SEP201169	39%	96.0%	96.0%
ECO100662	SHA102201	38%	96.0%	98.9%
ECO100662	SMU100648	30%	95.8%	98.3%
ECO100662	SPY201526	31%	97.1%	96.6%
ECO100662	VCH100978	47%	71.8%	97.7%
ECO100662	YPS001239	52%	99.8%	99.7%
ECO100663	ABA100614	54%	70.2%	98.7%
ECO100663	BFR11594	52%	99.3%	98.3%
ECO100663	BPT101559	50%	99.1%	99.5%
ECO100663	BCE112007	56%	98.0%	97.7%
ECO100663	BFU109691	56%	98.0%	97.7%
ECO100663	BMA101111	57%	98.2%	93.5%
ECO100663	CDF100047	54%	98.4%	98.7%
ECO100663	EBC101578	94%	100%	100%
ECO100663	ECO100663	100%	100%	100%
ECO100663	HIN101320	76%	97.7%	97.1%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100663	KPN300629	92%	79.2%	100%
ECO100663	LPN102284	55%	7.2%	20.1%
ECO100663	LPN100517	56%	99.6%	99.8%
ECO100663	MCA100651	51%	99.1%	99.5%
ECO100663	NGO101291	60%	97.5%	97.7%
ECO100663	NME201607	60%	97.5%	95.8%
ECO100663	PMU100528	77%	98.0%	97.1%
ECO100663	PRT105627	85%	100%	99.6%
ECO100663	PAE201793	60%	99.1%	99.1%
ECO100663	PPU108911	62%	98.6%	96.8%
ECO100663	PSY100233	62%	98.2%	97.0%
ECO100663	SPA101340	95%	98.9%	100%
ECO100663	STY101833	95%	100%	100%
ECO100663	STM101572	96%	100%	100%
ECO100663	VCH100980	80%	100%	99.8%
ECO100663	YPS001246	87%	99.3%	99.1%
ECO100668	BCE111918	35%	49.2%	54.6%
ECO100668	BFU104827	30%	45.8%	59.8%
ECO100668	CBO100905	27%	70.8%	11.1%
ECO100668	EBC100041	81%	54.2%	100%
ECO100668	ECO100668	100%	100%	100%
ECO100668	KPN202849	81%	100%	100%
ECO100668	PMU100354	65%	70%	89.4%
ECO100668	PRT103333	83%	74.2%	91.8%
ECO100668	SPA102662	89%	80.8%	100%
ECO100668	STY101854	90%	80.8%	100%
ECO100668	YPS001261	86%	74.2%	93.7%
ECO100669	BAN106734	28%	46.5%	44.8%
ECO100669	BAN100793	32%	37.8%	33.3%
ECO100669	BAN108978	32%	37.8%	60.1%
ECO100669	BPT102964	23%	84.6%	68.9%
ECO100669	BFU101564	23%	92.1%	73.2%
ECO100669	EBC100042	68%	31.1%	97.5%
ECO100669	EFM201132	22%	53.1%	57.0%
ECO100669	ECO100669	100%	100%	100%
ECO100669	HIN100182	42%	98.8%	88.2%
ECO100669	KPN300270	85%	98.0%	100%
ECO100669	LPN102659	22%	95.3%	91.9%
ECO100669	LPN103657	28%	39.0%	36.2%
ECO100669	LMO100596	31%	41.7%	43.5%
ECO100669	MAV103780	24%	81.9%	72.4%
ECO100669	MBV106260	23%	81.9%	73.8%
ECO100669	MLP101364	22%	83.9%	75.3%
ECO100669	MTU200045	23%	81.9%	73.8%
ECO100669	MPN100323	42%	19.3%	17.6%
ECO100669	PMU100355	45%	94.5%	92.7%
ECO100669	PRT100195	58%	93.7%	89.8%
ECO100669	SPA102660	89%	100%	100%
ECO100669	STY101855	89%	100%	99.2%
ECO100669	STM104159	32%	45.3%	39.8%
ECO100669	SAU800615	22%	96.1%	93.9%
ECO100669	SHA101552	27%	37.4%	33.6%
ECO100669	UUR100019	23%	43.3%	38.4%
ECO100669	VCH102065	48%	92.5%	93.0%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100669	YPS001274	65%	99.6%	99.2%
ECO100672	CAC102879	34%	25%	8.6%
ECO100672	ECO100672	100%	100%	100%
ECO100683	ABA100225	26%	67.7%	56.8%
ECO100683	ABA100477	27%	24.1%	97.4%
ECO100683	BAN104847	19%	15.4%	26.9%
ECO100683	BAN109223	29%	7.2%	47.8%
ECO100683	BAN101440	29%	7.6%	42.7%
ECO100683	BAN110288	24%	23.0%	18.6%
ECO100683	BFR104422	62%	1.9%	27%
ECO100683	BCE104951	24%	86.2%	67.5%
ECO100683	BCE108121	27%	52.8%	59.9%
ECO100683	BFU100092	47%	6.3%	98.9%
ECO100683	BFU107935	31%	21.7%	7.3%
ECO100683	BFU100109	28%	14.8%	59.1%
ECO100683	BFU102581	29%	54.0%	49.1%
ECO100683	BMA107682	24%	50.1%	25.9%
ECO100683	CAC100404	29%	6.3%	31.6%
ECO100683	EBC107494	28%	9.8%	85%
ECO100683	EBC103412	28%	9.0%	59.2%
ECO100683	EBC104888	25%	64.4%	82.5%
ECO100683	ECO100686	96%	23.3%	68.1%
ECO100683	ECO101427	76%	37.7%	78.2%
ECO100683	ECO100488	77%	89.3%	88.2%
ECO100683	ECO103405	96%	89.3%	88.4%
ECO100683	ECO103515	96%	89.9%	91.2%
ECO100683	ECO100683	100%	100%	100%
ECO100683	PRT103688	31%	7.4%	73.6%
ECO100683	PRT103361	33%	8.1%	78.0%
ECO100683	PRT103421	25%	54.0%	66.8%
ECO100683	PAE202682	32%	90.6%	89.7%
ECO100683	PPU107712	33%	7.7%	93.1%
ECO100683	PPU110484	26%	21.5%	52.2%
ECO100683	PPU109654	25%	9.2%	55.3%
ECO100683	PPU107101	42%	3.9%	5.5%
ECO100683	PPU109653	28%	41.4%	38.3%
ECO100683	PPU109652	26%	55.8%	54.6%
ECO100683	PPU110482	26%	11.1%	5.4%
ECO100683	PSY108533	33%	5.0%	83.6%
ECO100683	PSY101322	59%	4.2%	24.3%
ECO100683	PSY105816	46%	7.4%	46.2%
ECO100683	PSY102083	24%	13.7%	11.8%
ECO100683	SPA106438	45%	6.1%	5.5%
ECO100683	SPA100247	27%	53.8%	67.7%
ECO100683	STY104094	25%	87.3%	77.3%
ECO100683	STY104095	30%	53.2%	39.6%
ECO100683	STM103807	45%	8.0%	46.3%
ECO100683	STM103806	25%	87.3%	76.6%
ECO100683	YPS002860	24%	86.3%	75.9%
ECO100702	ECO102977	37%	97.9%	97.8%
ECO100702	ECO100702	100%	100%	100%
ECO100702	PRT100741	24%	96.3%	94.1%
ECO100702	PRT100538	22%	95.7%	94.0%
ECO100702	PRT104405	27%	95.7%	98.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100702	PRT100936	26%	96.3%	98.9%
ECO100702	PRT105615	27%	95.7%	96.2%
ECO100702	PRT104834	26%	88.3%	87.4%
ECO100702	PRT104207	28%	88.3%	87.4%
ECO100702	PRT101358	32%	96.3%	97.3%
ECO100702	SPA102695	31%	95.7%	97.4%
ECO100702	STY104107	32%	95.7%	96.4%
ECO100702	YPS002768	38%	96.3%	94.6%
ECO100703	ABA104184	67%	97.9%	98.1%
ECO100703	BPT101628	62%	100%	99.5%
ECO100703	BCE109200	66%	98.6%	98.2%
ECO100703	BFU112530	65%	97.7%	97.2%
ECO100703	BFU100597	66%	99.8%	99.3%
ECO100703	BMA100455	66%	98.6%	98.2%
ECO100703	CJU101587	50%	93.4%	95.0%
ECO100703	CDP100042	50%	93.4%	93.9%
ECO100703	EBC101675	96%	100%	100%
ECO100703	ECO100703	100%	100%	100%
ECO100703	HPY100025	43%	93.4%	96.5%
ECO100703	KPN302561	95%	99.5%	100%
ECO100703	LPN103215	64%	98.8%	100%
ECO100703	MCA103218	62%	99.1%	99.1%
ECO100703	MAV104827	54%	98.6%	98.6%
ECO100703	MBV101665	52%	98.6%	98.6%
ECO100703	MLP101277	52%	98.6%	98.6%
ECO100703	MTU200887	52%	98.6%	98.6%
ECO100703	NGO101276	66%	97.2%	97.4%
ECO100703	NME201060	66%	97.2%	97.4%
ECO100703	PMU100276	71%	99.1%	99.1%
ECO100703	PRT102070	85%	99.8%	99.5%
ECO100703	PAE201579	70%	98.6%	98.4%
ECO100703	PPU107315	72%	98.4%	98.1%
ECO100703	PSY108243	72%	98.4%	98.1%
ECO100703	SPA100177	91%	78.0%	100%
ECO100703	STY101915	96%	100%	100%
ECO100703	VCH102060	77%	98.6%	97.9%
ECO100703	YPS002059	86%	100%	100%
ECO100706	ABA105020	52%	98.8%	97.2%
ECO100706	BPT101632	57%	99.7%	99.5%
ECO100706	BCE112329	55%	99.7%	98.8%
ECO100706	BFU100599	55%	99.7%	98.8%
ECO100706	BMA107039	55%	99.7%	98.8%
ECO100706	CTR100036	31%	92.2%	98.6%
ECO100706	EBC101678	96%	60.9%	100%
ECO100706	ECO100706	100%	100%	100%
ECO100706	HPY100189	35%	93.5%	82.1%
ECO100706	KPN301276	98%	100%	99.3%
ECO100706	LPN103357	69%	100%	100%
ECO100706	MCA101639	51%	99.7%	97.1%
ECO100706	MAV101732	48%	98.8%	99.0%
ECO100706	MBV103459	48%	98.8%	99.0%
ECO100706	MLP100428	47%	98.8%	99.0%
ECO100706	MTU203275	48%	98.8%	99.0%
ECO100706	NGO101280	56%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100706	NME201057	56%	100%	100%
ECO100706	PRT102073	92%	100%	100%
ECO100706	PAE201582	70%	98.8%	98.6%
ECO100706	PPU103107	69%	99.7%	99.5%
ECO100706	PSY104872	70%	96.8%	100%
ECO100706	SPA103275	78%	48.8%	100%
ECO100706	STY101918	97%	100%	100%
ECO100706	STM101667	97%	100%	100%
ECO100706	SHA100620	34%	59.5%	95.4%
ECO100706	VCH102057	82%	100%	100%
ECO100706	YPS002062	92%	100%	100%
ECO100712	ABA101768	71%	100%	98.3%
ECO100712	BAN108859	56%	100%	96.3%
ECO100712	BAN107819	65%	100%	96.3%
ECO100712	BFR12149	58%	98.6%	99.0%
ECO100712	BPT102810	54%	99.7%	100%
ECO100712	BCE103851	54%	99.7%	100%
ECO100712	BFU103478	52%	99.7%	100%
ECO100712	BMA108528	54%	99.7%	100%
ECO100712	CJU100496	58%	99.7%	99.7%
ECO100712	CPN200869	62%	98.6%	97.3%
ECO100712	CTR200204	61%	98.6%	97.9%
ECO100712	EBC102737	95%	100%	100%
ECO100712	ECO100712	100%	100%	100%
ECO100712	HIN101170	83%	100%	98.6%
ECO100712	KPN300770	94%	100%	100%
ECO100712	LPN101597	78%	99.3%	99.0%
ECO100712	LMO100662	25%	48.1%	38.4%
ECO100712	MAV101285	54%	100%	99.3%
ECO100712	MBV101961	54%	94.1%	92.7%
ECO100712	MLP100114	50%	99.7%	99%
ECO100712	MTU200943	54%	94.1%	92.7%
ECO100712	NGO101261	72%	100%	98.3%
ECO100712	NME201066	72%	100%	98.3%
ECO100712	PMU100281	86%	100%	100%
ECO100712	PRT102068	94%	99.7%	99.3%
ECO100712	PAE201588	88%	98.3%	96.3%
ECO100712	PPU101203	88%	98.3%	96.6%
ECO100712	PSY104865	88%	98.3%	96.9%
ECO100712	SPA103281	88%	99.3%	100%
ECO100712	STY101933	94%	100%	100%
ECO100712	STM101672	95%	100%	100%
ECO100712	SAU801246	65%	98.3%	94.0%
ECO100712	SEP201540	62%	98.3%	94.0%
ECO100712	SHA100180	64%	84.8%	93.9%
ECO100712	VCH102052	87%	99.3%	99.0%
ECO100712	YPS002067	90%	99.7%	99.3%
ECO100713	BAN101120	29%	80.8%	100%
ECO100713	BAN103767	30%	94.2%	95.0%
ECO100713	BPT101634	28%	94.2%	80.4%
ECO100713	BCE103528	36%	40%	66.2%
ECO100713	BCE107050	30%	82.5%	85.3%
ECO100713	BMA102686	30%	82.5%	85.3%
ECO100713	CAC103158	29%	95.4%	95.1%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100713	CBO100441	31%	96.2%	92.5%
ECO100713	CDF102412	32%	95.4%	96.2%
ECO100713	CDP100674	29%	93.3%	89.1%
ECO100713	EFA202447	32%	95%	97.0%
ECO100713	EFM201744	26%	95.4%	94.3%
ECO100713	ECO100713	100%	100%	100%
ECO100713	MCA101187	25%	86.2%	89.1%
ECO100713	MAV103447	30%	79.6%	70.4%
ECO100713	PPU107953	29%	95%	74.7%
ECO100713	SPA103556	29%	97.5%	95.5%
ECO100713	STY104116	29%	97.5%	95.5%
ECO100713	STM102067	24%	93.8%	92.5%
ECO100713	SEP200626	35%	28.3%	54.4%
ECO100713	SHA102044	28%	94.6%	95.4%
ECO100713	SMU100634	25%	95.8%	97.5%
ECO100713	SPN401698	31%	96.2%	98.3%
ECO100713	SPY200917	30%	96.2%	95.4%
ECO100716	ABA102257	69%	97.5%	96.6%
ECO100716	BAN108041	38%	96.6%	97.3%
ECO100716	BFR104147	43%	92.9%	99.4%
ECO100716	BPT102256	61%	95.6%	92.8%
ECO100716	BCE114299	55%	52.4%	99.6%
ECO100716	BFU102708	57%	53.9%	94.7%
ECO100716	BFU103213	77%	39.2%	98.1%
ECO100716	BFU102694	66%	98.1%	95.7%
ECO100716	BMA100835	62%	83.7%	97.6%
ECO100716	BMA109632	64%	99.2%	98.1%
ECO100716	CJU100072	45%	95.4%	96.3%
ECO100716	CPN200660	35%	95.6%	97.3%
ECO100716	CTR100525	30%	94.6%	96.6%
ECO100716	CDP100460	35%	92.0%	84.0%
ECO100716	EBC102736	94%	63.3%	100%
ECO100716	ECO100716	100%	100%	100%
ECO100716	HIN101051	64%	98.5%	99.8%
ECO100716	KPN300984	94%	96.0%	100%
ECO100716	LPN101998	59%	96.0%	98.4%
ECO100716	MCA100290	59%	97.7%	96.6%
ECO100716	PMU100974	68%	98.5%	99.8%
ECO100716	PRT103085	81%	95.4%	99.8%
ECO100716	PPU108559	31%	94.5%	91.6%
ECO100716	PSY107712	30%	89.7%	91.0%
ECO100716	SPA103282	95%	96.7%	100%
ECO100716	STY101934	95%	99.8%	100%
ECO100716	STM101673	96%	99.8%	100%
ECO100716	SAU801086	30%	95.8%	96.2%
ECO100716	SHA101846	29%	95.8%	96.9%
ECO100716	VCH103592	70%	98.3%	97.0%
ECO100716	VCH101814	74%	99.2%	95.9%
ECO100716	YPS002068	86%	99.8%	100%
ECO100725	ABA105807	25%	94.7%	97.3%
ECO100725	BFR102268	27%	43.0%	25.9%
ECO100725	BPT102433	25%	98.1%	99.1%
ECO100725	BBU100541	23%	43.0%	55.7%
ECO100725	BCE106489	25%	92.8%	92.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100725	BFU105257	24%	99.2%	98.8%
ECO100725	BMA107737	26%	100%	99.6%
ECO100725	CJU100103	20%	84.4%	78.7%
ECO100725	CDF103562	24%	39.2%	22.0%
ECO100725	EBC100263	85%	91.6%	97.6%
ECO100725	ECO100725	100%	100%	100%
ECO100725	HPY101257	25%	38.4%	17.4%
ECO100725	KPN300548	85%	100%	99.6%
ECO100725	LPN101284	31%	85.6%	72.7%
ECO100725	MBV103820	48%	12.5%	37.5%
ECO100725	NGO100180	25%	25.9%	30.0%
ECO100725	NME201512	20%	76.4%	74.8%
ECO100725	PRT100140	58%	99.6%	99.2%
ECO100725	PAE200973	36%	80.6%	77.0%
ECO100725	PPU108643	31%	94.7%	96.6%
ECO100725	PSY105481	41%	39.5%	93.7%
ECO100725	SPA100202	84%	74.5%	100%
ECO100725	STY101953	90%	100%	100%
ECO100725	STM101682	90%	100%	100%
ECO100725	TPA100980	24%	35.0%	9.4%
ECO100725	VCH101804	34%	98.9%	99.6%
ECO100725	YPS002077	69%	100%	100%
ECO100741	BPT100548	42%	96.0%	93.5%
ECO100741	BFU102456	40%	51.1%	80.7%
ECO100741	BFU115706	40%	51.7%	72.2%
ECO100741	EBC103505	88%	100%	100%
ECO100741	ECO100741	100%	100%	100%
ECO100741	HIN101656	53%	99.4%	99.7%
ECO100741	KPN305280	78%	100%	99.7%
ECO100741	MCA102353	44%	57.4%	91.9%
ECO100741	PMU100742	50%	99.4%	99.7%
ECO100741	PRT105509	62%	99.7%	99.2%
ECO100741	PAE201860	43%	99.7%	99.2%
ECO100741	PPU112554	42%	95.5%	94.8%
ECO100741	PSY105309	43%	94.3%	96.3%
ECO100741	SPA101804	91%	100%	100%
ECO100741	STY102291	91%	100%	100%
ECO100741	STM102051	91%	100%	100%
ECO100741	SAU802277	38%	57.4%	99.5%
ECO100741	SEP200346	37%	58.0%	98.1%
ECO100741	SHA102072	42%	56.8%	98.5%
ECO100741	VCH103445	49%	98.6%	96.2%
ECO100741	YPS002116	70%	99.1%	97.2%
ECO100748	CAC102362	27%	28.8%	40.8%
ECO100748	EBC103508	79%	100%	100%
ECO100748	EFM202173	28%	31.4%	45.6%
ECO100748	ECO100748	100%	100%	100%
ECO100748	KPN307027	77%	100%	100%
ECO100748	MLP100102	30%	14.1%	25.8%
ECO100748	SPA100494	59%	58.3%	99.2%
ECO100748	STY102294	86%	100%	100%
ECO100748	YPS000085	25%	28.6%	34.6%
ECO100757	ABA104944	30%	78.1%	83.9%
ECO100757	BAN113702	42%	45.9%	72.6%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100757	BAN111016	36%	86.3%	86.7%
ECO100757	BAN102075	36%	88.1%	87.0%
ECO100757	BAN106548	34%	100%	99.4%
ECO100757	BAN111025	34%	100%	100%
ECO100757	BFR100859	26%	46.2%	35.5%
ECO100757	BFR102551	21%	79.3%	60.3%
ECO100757	BPT101117	36%	98.2%	91.8%
ECO100757	BCE102679	33%	98.8%	92.7%
ECO100757	BFU105518	35%	91.8%	83.2%
ECO100757	BMA107904	35%	98.8%	100%
ECO100757	CJU100150	32%	92.7%	93.1%
ECO100757	CAC101752	31%	98.8%	100%
ECO100757	CBO102636	33%	98.8%	99.7%
ECO100757	CDF101204	29%	98.8%	100%
ECO100757	CDP101688	31%	86.0%	98.0%
ECO100757	EBC102210	89%	100%	100%
ECO100757	EFA202347	33%	98.8%	100%
ECO100757	ECO100757	100%	100%	100%
ECO100757	HIN101641	61%	99.4%	96.7%
ECO100757	HPY100755	27%	98.8%	99.7%
ECO100757	KPN303579	87%	100%	100%
ECO100757	LMO102857	31%	98.8%	99.1%
ECO100757	MCA103672	43%	99.1%	89.5%
ECO100757	MAV105594	35%	95.1%	87.4%
ECO100757	MBV102851	33%	92.4%	83.4%
ECO100757	MTU203069	33%	92.4%	85.5%
ECO100757	PMU100625	61%	98.8%	96.1%
ECO100757	PRT104379	73%	99.1%	99.4%
ECO100757	PAE201504	35%	99.4%	99.1%
ECO100757	PPU106301	36%	93.3%	92.2%
ECO100757	PSY105427	35%	98.2%	99.7%
ECO100757	SPA102732	91%	100%	100%
ECO100757	STY102330	92%	100%	100%
ECO100757	STM102089	92%	100%	100%
ECO100757	SAU802268	33%	100%	100%
ECO100757	SEP200319	32%	100%	100%
ECO100757	SHA101565	32%	100%	100%
ECO100757	SMU100479	23%	57.1%	50.4%
ECO100757	VCH101005	63%	100%	98.5%
ECO100757	YPS002149	78%	99.1%	99.4%
ECO100777	BPT102988	35%	92.2%	95.2%
ECO100777	BCE112934	54%	97.8%	95.4%
ECO100777	CAC102641	28%	89.2%	90.0%
ECO100777	ECO100777	100%	100%	100%
ECO100777	KPN303263	70%	99.7%	100%
ECO100777	PAE201251	32%	65.9%	69.8%
ECO100777	PPU110335	35%	67.0%	69.8%
ECO100784	BAN110623	55%	5.5%	81.1%
ECO100784	BAN108902	30%	31.7%	84.3%
ECO100784	BCE100234	33%	41.2%	84.5%
ECO100784	BFU111584	27%	72.5%	65.4%
ECO100784	CAC100165	28%	33.0%	88.1%
ECO100784	CBO103029	25%	28.4%	75.8%
ECO100784	CDP101252	28%	27.1%	60.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100784	EBC100646	89%	49.1%	100%
ECO100784	EFA201399	30%	32.6%	82.4%
ECO100784	ECO100784	100%	100%	100%
ECO100784	KPN306689	80%	92.6%	99.2%
ECO100784	LMO100404	28%	34.0%	92.2%
ECO100784	MAV104987	26%	33.8%	85.6%
ECO100784	MBV105868	27%	33.6%	89.3%
ECO100784	MTU203064	27%	33.6%	89.3%
ECO100784	PAE205116	23%	93.9%	97.8%
ECO100784	PPU108041	24%	92.6%	98.6%
ECO100784	PSY102229	25%	60.8%	77.4%
ECO100784	SPA100728	92%	34.9%	100%
ECO100784	STY102372	85%	94.3%	100%
ECO100784	SAU800361	30%	32.1%	87.7%
ECO100784	SEP201337	28%	32.1%	88.3%
ECO100784	SHA102218	31%	32.6%	89.1%
ECO100784	SMU101383	28%	29.4%	79.6%
ECO100784	SPN401595	29%	19.8%	79.6%
ECO100784	SPY201460	30%	28.2%	77.9%
ECO100785	BPT102642	71%	100%	99.2%
ECO100785	BCE104102	70%	100%	99.2%
ECO100785	BFU108289	57%	99.6%	86.0%
ECO100785	BMA103265	70%	100%	99.2%
ECO100785	CJU100833	51%	99.6%	98.8%
ECO100785	CAC102217	57%	99.2%	97.1%
ECO100785	CBO101000	56%	99.6%	92.3%
ECO100785	EBC100550	93%	61.2%	100%
ECO100785	EFA200968	56%	97.9%	95.9%
ECO100785	ECO100785	100%	100%	100%
ECO100785	KPN303595	93%	100%	100%
ECO100785	LPN103564	38%	98.8%	98.2%
ECO100785	SPA101969	91%	100%	100%
ECO100785	STY102373	95%	100%	100%
ECO100785	SHA100687	54%	93.3%	99.6%
ECO100785	SMU100131	57%	99.2%	96.7%
ECO100785	SPN400728	56%	99.6%	98.0%
ECO100785	YPS000346	83%	100%	100%
ECO100786	BAN105137	37%	93.2%	98.5%
ECO100786	BAN106432	38%	93.6%	87.8%
ECO100786	BCE107126	60%	100%	92.8%
ECO100786	BMA105276	60%	100%	100%
ECO100786	CJU100870	37%	97.3%	80.8%
ECO100786	EBC100624	93%	100%	100%
ECO100786	EFA201954	37%	97.3%	42.3%
ECO100786	EFM202037	33%	94.1%	94.9%
ECO100786	ECO100786	100%	100%	100%
ECO100786	HPY101152	27%	99.1%	98.2%
ECO100786	KPN303596	94%	100%	100%
ECO100786	LMO100160	38%	95.4%	42.7%
ECO100786	NGO100237	38%	98.2%	97.6%
ECO100786	NME201568	38%	98.2%	97.6%
ECO100786	PRT102830	34%	91.8%	79.1%
ECO100786	PAE205070	43%	95.0%	63.8%
ECO100786	PPU106787	45%	95.0%	63.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100786	PSY102557	39%	99.1%	97.7%
ECO100786	SPA101970	95%	99.5%	100%
ECO100786	STY102374	96%	100%	100%
ECO100786	SMU101490	38%	92.2%	40.8%
ECO100786	SPN400409	39%	92.2%	67.8%
ECO100786	SPY200205	37%	91.3%	40.0%
ECO100786	VCH103754	36%	92.2%	74.8%
ECO100786	YPS000343	83%	100%	100%
ECO100791	EBC102171	80%	99.8%	99.6%
ECO100791	ECO100791	100%	100%	100%
ECO100791	HIN101041	29%	77.6%	82.7%
ECO100791	HIN100985	31%	91.8%	92.5%
ECO100791	KPN301162	77%	98.7%	100%
ECO100791	LPN101642	24%	33.8%	27.8%
ECO100791	NGO100602	42%	24.3%	72.7%
ECO100791	NME101282	34%	86.1%	83.6%
ECO100791	PRT100704	35%	93.7%	95.3%
ECO100791	SPA102068	80%	74.6%	100%
ECO100791	STY102390	83%	99.8%	100%
ECO100798	ABA103859	41%	99.3%	99.6%
ECO100798	CBO103381	29%	94.8%	97.0%
ECO100798	CDF100774	31%	96.3%	98.5%
ECO100798	CDP100194	28%	97.0%	98.5%
ECO100798	EBC101153	80%	99.6%	100%
ECO100798	ECO100798	100%	100%	100%
ECO100798	KPN302749	81%	100%	100%
ECO100798	LMO102831	36%	98.5%	99.6%
ECO100798	MGE100271	23%	93.7%	96.0%
ECO100798	SPA100708	88%	99.3%	100%
ECO100798	STY102396	88%	99.3%	100%
ECO100798	STM102169	88%	99.3%	100%
ECO100798	SAU802525	36%	95.2%	97.4%
ECO100798	SEP201092	35%	96.3%	97.4%
ECO100798	SMU100886	36%	97.0%	98.5%
ECO100798	SPN401305	33%	97.4%	98.9%
ECO100798	SPY200407	29%	96.3%	99.6%
ECO100799	EBC101152	92%	94.0%	100%
ECO100799	ECO100799	100%	100%	100%
ECO100799	KPN302752	92%	100%	100%
ECO100799	SPA100176	95%	39.5%	99.1%
ECO100799	STY102397	95%	100%	100%
ECO100799	SMU101536	50%	99.0%	97.1%
ECO100799	SPN400232	50%	99.9%	98.7%
ECO100799	SPY201569	53%	99.0%	98.6%
ECO100808	BAN100561	50%	91.1%	100%
ECO100808	BAN104237	51%	91.1%	92.0%
ECO100808	BPT101723	71%	92.7%	94.0%
ECO100808	BCE106581	76%	93.4%	95.3%
ECO100808	BFU105826	76%	95.4%	96.3%
ECO100808	BMA100352	76%	93.4%	93.7%
ECO100808	CDP100606	41%	87.8%	98.2%
ECO100808	EBC102792	87%	100%	100%
ECO100808	ECO100808	100%	100%	100%
ECO100808	KPN302758	87%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100808	LPN102009	30%	71.9%	53.3%
ECO100808	MAV102744	36%	90.1%	93.8%
ECO100808	MBV101586	35%	90.1%	95.1%
ECO100808	MTU203610	36%	85.5%	97.4%
ECO100808	SPA101182	90%	100%	100%
ECO100808	STY102416	91%	100%	100%
ECO100808	STM102205	91%	100%	100%
ECO100808	SAU800207	37%	90.8%	70.8%
ECO100808	SPY201539	33%	74.6%	83.2%
ECO100809	ECO100809	100%	100%	100%
ECO100809	MCA102378	23%	13.9%	50.8%
ECO100809	SAU802073	32%	6.0%	9.9%
ECO100810	CAC100997	29%	36.0%	63.8%
ECO100810	CAC102604	28%	51.8%	91.3%
ECO100810	ECO100810	100%	100%	100%
ECO100811	ABA101330	68%	98.4%	98.2%
ECO100811	BFR102640	38%	97.3%	98.1%
ECO100811	BPT100744	73%	98.4%	99.1%
ECO100811	BCE106919	64%	98.6%	99.6%
ECO100811	BFU100161	64%	97.7%	100%
ECO100811	BMA105812	62%	97.7%	97.4%
ECO100811	CJU101372	34%	95.2%	95.2%
ECO100811	CPN200500	37%	99.1%	87.9%
ECO100811	CAC101960	36%	97.5%	97.3%
ECO100811	CBO102372	38%	97.5%	97.3%
ECO100811	CDF100866	39%	97.5%	98.0%
ECO100811	EBC102793	96%	100%	100%
ECO100811	ECO100811	100%	100%	100%
ECO100811	HPY100722	30%	95.0%	94.8%
ECO100811	KPN302759	94%	100%	100%
ECO100811	LPN100817	60%	42.0%	100%
ECO100811	MCA100109	62%	99.3%	86.8%
ECO100811	PMU101571	75%	98.4%	98.7%
ECO100811	PRT105016	87%	100%	99.5%
ECO100811	PAE200915	73%	99.1%	99.5%
ECO100811	PPU104571	71%	100%	100%
ECO100811	PSY104389	70%	91.6%	98.8%
ECO100811	SPA101181	97%	100%	100%
ECO100811	STY102418	97%	100%	100%
ECO100811	SPY200723	31%	16.8%	28.5%
ECO100811	VCH102583	77%	97.7%	91.7%
ECO100836	CPN200269	31%	88.5%	83.4%
ECO100836	CTR200650	29%	91.8%	86.1%
ECO100836	EBC100514	87%	100%	93.8%
ECO100836	ECO100836	100%	100%	100%
ECO100836	HPY101155	24%	84.4%	73.6%
ECO100836	KPN302146	87%	100%	98.0%
ECO100836	LPN100743	23%	99.2%	96.0%
ECO100836	LPN103487	27%	97.5%	98.3%
ECO100836	LPN102814	33%	94.7%	95.2%
ECO100836	LPN101937	26%	98.4%	97.6%
ECO100836	LPN103612	32%	97.5%	99.2%
ECO100836	MCA100559	35%	90.9%	84.4%
ECO100836	MCA102170	36%	95.5%	91.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100836	MCA100560	36%	92.6%	83.1%
ECO100836	PAE205148	42%	99.2%	96.4%
ECO100836	PPU109095	43%	89.3%	97.7%
ECO100836	SPA102374	91%	97.5%	100%
ECO100836	STY102490	91%	100%	100%
ECO100836	SEP100077	33%	90.1%	79.3%
ECO100836	SMU100993	32%	91.8%	82.7%
ECO100838	EBC104449	92%	75.2%	100%
ECO100838	ECO100838	100%	100%	100%
ECO100838	HIN101151	55%	95.4%	94.1%
ECO100838	KPN301800	91%	99.6%	99.6%
ECO100838	PMU100125	55%	95.4%	94.2%
ECO100838	PRT100750	67%	100%	100%
ECO100838	SPA100500	91%	45.4%	100%
ECO100838	STY102492	94%	99.6%	99.6%
ECO100838	VCH103478	53%	92.9%	89.1%
ECO100838	YPS001173	79%	100%	100%
ECO100844	BAN111580	48%	8.9%	77.5%
ECO100844	BAN100129	33%	66.2%	83.3%
ECO100844	BAN113145	35%	94.0%	98.8%
ECO100844	BFR13634	23%	95.4%	99.1%
ECO100844	EBC102012	88%	96.0%	100%
ECO100844	ECO100844	100%	100%	100%
ECO100844	KPN300042	88%	43.6%	96.2%
ECO100844	KPN301813	89%	96.6%	100%
ECO100844	LPN103633	35%	93.1%	97.6%
ECO100844	MAV100805	25%	92.6%	89.6%
ECO100844	MBV104384	23%	92.0%	88.1%
ECO100844	MTU201091	23%	92.0%	88.1%
ECO100844	PAE204359	31%	95.4%	99.7%
ECO100844	PPU101560	29%	94.0%	97.9%
ECO100844	PSY101773	30%	94.0%	97.9%
ECO100844	SPA100744	84%	100%	100%
ECO100844	STY102502	93%	96.6%	100%
ECO100844	SMU100712	25%	94.8%	95.1%
ECO100844	YPS002695	44%	94.3%	97.3%
ECO100844	YPS001180	73%	95.7%	99.1%
ECO100848	BCE111932	31%	95.0%	89.3%
ECO100848	BFU111768	29%	94.7%	88.1%
ECO100848	BMA108604	31%	95.0%	89.2%
ECO100848	CAC101222	26%	58.7%	70.5%
ECO100848	CBO101327	21%	65.5%	79.2%
ECO100848	CDF103953	36%	19.9%	9.8%
ECO100848	CDP100938	27%	88.5%	76.3%
ECO100848	EBC102313	86%	100%	100%
ECO100848	ECO100848	100%	100%	100%
ECO100848	KPN301808	89%	100%	100%
ECO100848	LPN100990	29%	96.6%	53.9%
ECO100848	MBV101709	28%	78.9%	68.7%
ECO100848	MTU203187	28%	78.9%	68.7%
ECO100848	PRT102449	55%	100%	100%
ECO100848	PAE205406	30%	94.7%	92.6%
ECO100848	PPU107514	27%	94.1%	91.6%
ECO100848	PSY102789	27%	95.7%	93.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100848	SPA100209	87%	95.7%	100%
ECO100848	STY102872	89%	100%	99.7%
ECO100848	YPS001188	59%	99.1%	97.4%
ECO100850	ABA101625	29%	92.7%	97.4%
ECO100850	BFR105073	28%	60.3%	97.1%
ECO100850	BFR10379	34%	60.3%	97%
ECO100850	CBO100922	37%	54.0%	86.9%
ECO100850	EBC102315	84%	94.9%	100%
ECO100850	ECO100850	100%	100%	100%
ECO100850	HIN101420	47%	60.3%	97.4%
ECO100850	KPN301812	82%	94.9%	100%
ECO100850	MCA102941	38%	93.7%	97.4%
ECO100850	NGO101297	39%	93.3%	97%
ECO100850	NME201609	39%	93.7%	97.3%
ECO100850	PMU100465	45%	94.9%	99.0%
ECO100850	PRT103160	59%	94.9%	100%
ECO100850	SPA100944	88%	94.9%	100%
ECO100850	STY102874	88%	94.9%	100%
ECO100850	VCH101132	52%	94.3%	98.3%
ECO100850	YPS001192	71%	94.6%	100%
ECO100851	ABA105899	66%	98.7%	99.1%
ECO100851	BAN110789	36%	95.2%	98.6%
ECO100851	BAN100809	43%	98.7%	46.2%
ECO100851	BCE113237	66%	99.1%	93.1%
ECO100851	BFU108967	66%	99.1%	89.6%
ECO100851	BMA109080	70%	95.7%	94.4%
ECO100851	CDF103952	26%	60.2%	46.6%
ECO100851	EBC102316	89%	100%	100%
ECO100851	EFA200743	45%	99.1%	99.5%
ECO100851	ECO100851	100%	100%	100%
ECO100851	KPN301409	90%	72.7%	94.4%
ECO100851	PAE204031	71%	99.1%	99.6%
ECO100851	PPU107265	69%	98.3%	97.0%
ECO100851	SPN401602	37%	97.4%	97.7%
ECO100852	BFU100163	23%	79.7%	75.4%
ECO100852	CBO101403	24%	31.7%	26.2%
ECO100852	EBC102317	84%	92.9%	100%
ECO100852	ECO100852	100%	100%	100%
ECO100852	KPN301415	86%	100%	100%
ECO100852	PMU100466	38%	99.3%	99.8%
ECO100852	PRT101841	55%	100%	100%
ECO100852	PPU100582	20%	79.7%	70.3%
ECO100852	PSY101212	22%	79.7%	72.5%
ECO100852	SPA101097	82%	61.6%	100%
ECO100852	STY102875	89%	100%	100%
ECO100852	STM102673	89%	100%	100%
ECO100852	VCH103268	43%	99.5%	97.7%
ECO100852	YPS001193	64%	100%	99.8%
ECO100867	ABA105367	43%	95.5%	99.5%
ECO100867	BAN106540	36%	80.5%	98.4%
ECO100867	BAN103047	39%	95.7%	97.9%
ECO100867	BFR11901	44%	95.5%	99.5%
ECO100867	BPT102656	54%	98.0%	98.2%
ECO100867	BCE114975	54%	95.7%	96.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100867	BFU101858	54%	93.1%	99.5%
ECO100867	BMA110026	54%	95.7%	96.8%
ECO100867	CJU100186	32%	84.8%	89.3%
ECO100867	CAC102995	47%	94.6%	94.8%
ECO100867	CBO100306	35%	91.9%	96.4%
ECO100867	CDF100879	35%	94.0%	96.5%
ECO100867	CDP100385	44%	95.5%	92.9%
ECO100867	EBC101259	94%	100%	100%
ECO100867	EFA202198	38%	91.5%	94.8%
ECO100867	EFM200319	38%	96.0%	92.4%
ECO100867	ECO100867	100%	100%	100%
ECO100867	HIN101557	73%	100%	100%
ECO100867	HPY101009	31%	84.8%	90.0%
ECO100867	KPN301123	95%	99.8%	100%
ECO100867	LPN101679	50%	87.5%	97.7%
ECO100867	LMO100087	37%	93.7%	99.1%
ECO100867	MCA101668	45%	90.2%	94.9%
ECO100867	MAV102138	44%	93.3%	90.4%
ECO100867	MBV100989	42%	95.1%	92.7%
ECO100867	MLP100308	42%	94.2%	87.5%
ECO100867	MTU202522	42%	95.1%	92.7%
ECO100867	NGO101204	54%	95.5%	96.6%
ECO100867	NME201305	54%	96.6%	97.7%
ECO100867	PMU100257	73%	99.8%	100%
ECO100867	PRT102616	85%	100%	97.8%
ECO100867	PAE202611	60%	97.8%	98.2%
ECO100867	PPU100863	59%	97.8%	98.2%
ECO100867	PSY104188	60%	96.6%	97.3%
ECO100867	SPA103469	95%	99.8%	100%
ECO100867	STY102895	97%	100%	100%
ECO100867	STM102717	97%	100%	100%
ECO100867	SAU801627	36%	90.6%	94.1%
ECO100867	SEP201572	35%	90.6%	94.3%
ECO100867	SHA100667	39%	38.0%	76.4%
ECO100867	SMU100656	36%	91.1%	95.0%
ECO100867	SPN401614	36%	91.1%	94.6%
ECO100867	SPY201532	37%	91.1%	94.8%
ECO100867	UUR100196	31%	91.3%	95.1%
ECO100867	VCH101089	73%	99.8%	99.6%
ECO100867	YPS001228	86%	100%	100%
ECO100868	ABA101808	66%	99.8%	99.8%
ECO100868	BAN101821	48%	96.0%	96.7%
ECO100868	BAN102446	52%	98.8%	98.8%
ECO100868	BFR104902	40%	98.1%	98.3%
ECO100868	BPT102654	55%	99.1%	98.9%
ECO100868	BBU100225	33%	99.8%	99.1%
ECO100868	BCE111542	55%	50.7%	98.2%
ECO100868	BFU101860	62%	99.3%	98.4%
ECO100868	BMA100713	62%	99.8%	98.4%
ECO100868	CJU100357	47%	98.1%	99.8%
ECO100868	CPN200980	40%	99.8%	98.8%
ECO100868	CTR200102	40%	99.8%	98.6%
ECO100868	CAC102168	46%	98.4%	98.6%
ECO100868	CBO103963	48%	99.8%	99.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100868	CDF100043	49%	24.0%	90.6%
ECO100868	CDF100480	48%	98.4%	98.6%
ECO100868	CDF100128	47%	98.4%	98.6%
ECO100868	CDP100672	38%	98.4%	97.9%
ECO100868	EBC101260	92%	100%	100%
ECO100868	EFA202450	52%	99.8%	99.8%
ECO100868	EFA200752	53%	99.8%	99.8%
ECO100868	EFM202627	51%	99.8%	99.8%
ECO100868	ECO100868	100%	100%	100%
ECO100868	HIN100109	77%	100%	99.8%
ECO100868	HPY101459	47%	98.4%	100%
ECO100868	KPN301832	95%	74.4%	100%
ECO100868	LPN101085	58%	99.8%	99.3%
ECO100868	LMO102194	51%	99.8%	99.1%
ECO100868	MCA100776	60%	99.8%	99.8%
ECO100868	MAV103250	37%	98.4%	97.2%
ECO100868	MBV105246	36%	99.8%	99.0%
ECO100868	MLP100058	34%	98.4%	97.8%
ECO100868	MTU203779	36%	99.8%	99.0%
ECO100868	MGE100005	38%	98.6%	98.8%
ECO100868	MPN100149	38%	98.6%	98.1%
ECO100868	NGO100535	64%	99.1%	98.6%
ECO100868	NME201792	64%	99.1%	98.6%
ECO100868	PMU100258	77%	100%	100%
ECO100868	PRT102618	81%	100%	100%
ECO100868	PAE202610	65%	100%	100%
ECO100868	PPU100866	67%	99.8%	99.8%
ECO100868	PSY104164	66%	100%	100%
ECO100868	SPA103470	95%	100%	100%
ECO100868	STY102896	97%	100%	100%
ECO100868	STM102719	97%	100%	100%
ECO100868	SAU800009	51%	98.8%	97.9%
ECO100868	SEP201273	53%	98.8%	97.9%
ECO100868	SHA102263	52%	98.8%	97.9%
ECO100868	SMU101313	55%	99.8%	99.1%
ECO100868	SPN400372	55%	99.8%	94.8%
ECO100868	SPY201341	56%	98.8%	98.4%
ECO100868	TPA100639	33%	99.8%	98.8%
ECO100868	UUR100105	47%	98.4%	99.8%
ECO100868	VCH101091	71%	100%	100%
ECO100868	YPS001230	84%	100%	100%
ECO100869	BCE108240	28%	92.4%	98.1%
ECO100869	BFU105642	27%	96.1%	98.7%
ECO100869	EBC101397	90%	96.3%	100%
ECO100869	ECO100869	100%	100%	100%
ECO100869	HIN101025	74%	100%	97.4%
ECO100869	KPN301830	89%	100%	96.4%
ECO100869	PMU101754	74%	100%	93.5%
ECO100869	PRT105822	80%	99.6%	100%
ECO100869	SPA103471	90%	99.9%	97.9%
ECO100869	STY102898	92%	99.9%	96.3%
ECO100869	STM103286	93%	99.9%	96.3%
ECO100869	YPS000005	82%	99.9%	96.3%
ECO100875	BCE105376	36%	99.7%	96.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100875	BFU114870	41%	95.7%	96.7%
ECO100875	BMA101338	35%	95.4%	96.4%
ECO100875	EBC103818	40%	94.4%	96.6%
ECO100875	ECO100875	100%	100%	100%
ECO100875	KPN301597	38%	95.4%	99.7%
ECO100875	PMU101945	47%	32.1%	66.0%
ECO100875	PAE201737	42%	94.7%	95.4%
ECO100875	PSY108744	39%	95.4%	95.7%
ECO100875	SPA101562	37%	94.4%	98.3%
ECO100875	STY103217	37%	97.4%	95.2%
ECO100876	BAN112918	36%	58.2%	58.6%
ECO100876	BAN107114	36%	58.2%	58.6%
ECO100876	BFR102217	24%	37.8%	52.9%
ECO100876	BFR104285	27%	36.7%	49.7%
ECO100876	BPT103683	29%	46.9%	40.4%
ECO100876	BFU103218	36%	63.8%	59.6%
ECO100876	CAC100905	30%	53.6%	51.5%
ECO100876	CBO103246	33%	56.6%	58.2%
ECO100876	EBC102970	30%	81.1%	83.4%
ECO100876	ECO100876	100%	100%	100%
ECO100876	HIN101513	33%	79.1%	79.2%
ECO100876	LMO101606	33%	30.1%	30.3%
ECO100876	PMU100887	29%	87.8%	86.8%
ECO100876	PSY103215	26%	55.1%	50.5%
ECO100876	SAU800601	27%	47.4%	51.7%
ECO100876	SEP201386	27%	47.4%	58.8%
ECO100876	SHA102380	24%	95.4%	90.1%
ECO100876	SHA102445	33%	56.6%	62.5%
ECO100876	SMU102024	33%	55.1%	55.9%
ECO100885	ABA100088	49%	95.6%	96.5%
ECO100885	BAN107282	44%	15.9%	83.7%
ECO100885	BAN109524	43%	83.3%	95.0%
ECO100885	BAN105277	47%	92.5%	93.3%
ECO100885	BFR11517	38%	84.1%	92.9%
ECO100885	BPT100195	57%	94.7%	94.6%
ECO100885	BBU100127	29%	90.7%	92.3%
ECO100885	BCE104244	52%	95.2%	93.0%
ECO100885	BFU102075	52%	94.3%	86.8%
ECO100885	BMA105406	52%	95.6%	90.3%
ECO100885	CPN200178	42%	93.0%	95.8%
ECO100885	CTR200727	42%	96.5%	99.5%
ECO100885	CAC100619	37%	95.6%	98.2%
ECO100885	CBO103038	40%	91.6%	89.1%
ECO100885	CDF100096	40%	93.0%	95.8%
ECO100885	CDP101063	43%	91.6%	86.7%
ECO100885	EBC100426	94%	95.2%	100%
ECO100885	EFA201887	41%	95.2%	95.6%
ECO100885	ECO100885	100%	100%	100%
ECO100885	HIN101612	63%	89.0%	77.0%
ECO100885	HIN101191	64%	95.2%	93.5%
ECO100885	KPN300479	91%	78.0%	100%
ECO100885	LPN101006	50%	96.5%	95.7%
ECO100885	LMO100736	42%	95.6%	96.4%
ECO100885	MCA101968	46%	96.5%	92.2%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100885	MAV102017	41%	97.4%	97.4%
ECO100885	MBV105382	40%	96.5%	95.7%
ECO100885	MLP100851	43%	95.6%	96.0%
ECO100885	MTU201690	40%	96.5%	95.7%
ECO100885	MGE100338	35%	96.5%	98.2%
ECO100885	MPN100365	38%	94.3%	95.9%
ECO100885	NGO100241	47%	95.2%	97.2%
ECO100885	NME201374	46%	95.2%	97.2%
ECO100885	PMU100802	67%	96.0%	96.0%
ECO100885	PRT100288	78%	97.8%	98.7%
ECO100885	PAE203161	60%	98.2%	98.3%
ECO100885	PPU108319	62%	94.7%	89.7%
ECO100885	PSY100434	62%	93.8%	88.5%
ECO100885	SPA102110	94%	75.8%	100%
ECO100885	STY102912	97%	100%	100%
ECO100885	STM103300	97%	100%	100%
ECO100885	SAU801478	38%	94.7%	96.8%
ECO100885	SEP200463	36%	92.5%	96.3%
ECO100885	SHA101407	34%	92.5%	95.0%
ECO100885	SMU100904	43%	90.7%	84.6%
ECO100885	SPN401455	38%	95.6%	97.8%
ECO100885	SPY200595	43%	91.2%	92.0%
ECO100885	UUR100344	29%	95.6%	95.1%
ECO100885	VCH101886	70%	98.7%	97.8%
ECO100885	YPS001262	84%	99.6%	98.3%
ECO100886	ABA101621	72%	6.5%	93.4%
ECO100886	BAN102603	35%	97.5%	94.8%
ECO100886	BAN106697	35%	97.5%	95.0%
ECO100886	BFR12241	37%	95.9%	89.1%
ECO100886	BPT100197	63%	97.5%	94.3%
ECO100886	BBU100126	28%	95.3%	95.5%
ECO100886	BCE109984	64%	99.5%	93.0%
ECO100886	BFU102076	65%	95.2%	91.9%
ECO100886	BMA105447	63%	99.5%	97.2%
ECO100886	CJU100824	32%	65.5%	94.8%
ECO100886	CPN200436	44%	93.5%	89.3%
ECO100886	CTR200367	45%	92.1%	46.6%
ECO100886	CAC100711	33%	93.2%	27.3%
ECO100886	CBO101243	35%	96.9%	93.8%
ECO100886	CDF100938	28%	93.9%	21.2%
ECO100886	CDP100313	46%	92.1%	17.9%
ECO100886	EBC100136	98%	94.1%	83.3%
ECO100886	EFA201885	35%	77.9%	87.6%
ECO100886	ECO100886	100%	100%	100%
ECO100886	HIN101192	78%	100%	100%
ECO100886	HPY100395	29%	96.4%	95.3%
ECO100886	KPN302625	98%	96.2%	83.5%
ECO100886	LPN102947	66%	100%	100%
ECO100886	LMO101312	36%	91.7%	66.9%
ECO100886	MCA101969	68%	94.8%	91.5%
ECO100886	MAV106579	45%	93.9%	72.7%
ECO100886	MBV101279	45%	93.9%	65.2%
ECO100886	MLP100855	44%	93.9%	72.6%
ECO100886	MTU201609	45%	93.9%	72.6%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100886	NGO100236	65%	98.9%	98.6%
ECO100886	NME201375	65%	98.9%	98.2%
ECO100886	PMU100801	81%	100%	100%
ECO100886	PRT100600	94%	100%	100%
ECO100886	PAE203160	75%	99.3%	98.9%
ECO100886	PPU100844	75%	96.9%	96.8%
ECO100886	PSY103125	74%	96.8%	96.1%
ECO100886	SPA102059	95%	98.7%	100%
ECO100886	STY102913	99%	100%	100%
ECO100886	STM103301	99%	100%	100%
ECO100886	SAU801476	35%	99.6%	99.7%
ECO100886	SEP200462	33%	97.1%	94.9%
ECO100886	SHA101408	34%	98.9%	97.7%
ECO100886	SMU101029	36%	88.7%	16.5%
ECO100886	SPN400764	34%	92.1%	85.8%
ECO100886	SPY200684	35%	88.7%	16.5%
ECO100886	TPA100276	36%	92.1%	59.9%
ECO100886	VCH101885	84%	100%	100%
ECO100886	YPS001263	94%	100%	100%
ECO100905	BAN103960	46%	95.1%	94.6%
ECO100905	BAN109694	59%	95.9%	95.7%
ECO100905	BFR11425	57%	95.9%	95.5%
ECO100905	BBU100101	53%	98.9%	98.3%
ECO100905	CAC102921	55%	96.1%	95.9%
ECO100905	CBO101487	56%	96.8%	96.5%
ECO100905	CDF103661	53%	98.3%	98.3%
ECO100905	EBC100631	93%	51.5%	100%
ECO100905	EFA200462	35%	96.8%	97.3%
ECO100905	EFM202427	35%	96.8%	97.2%
ECO100905	ECO100905	100%	100%	100%
ECO100905	HIN101268	80%	99.6%	97.3%
ECO100905	KPN303312	95%	96.8%	99.6%
ECO100905	LPN101111	69%	99.6%	99.4%
ECO100905	LMO102390	38%	95.3%	95.8%
ECO100905	MGE100115	39%	100%	100%
ECO100905	MPN100580	40%	98.5%	98.5%
ECO100905	PMU100643	82%	99.6%	98.5%
ECO100905	PRT101955	84%	100%	100%
ECO100905	SPA102566	86%	72.1%	100%
ECO100905	STY102938	94%	100%	100%
ECO100905	SAU801454	37%	96.8%	97.4%
ECO100905	SEP200424	36%	96.8%	97.4%
ECO100905	SHA101874	37%	96.8%	97.4%
ECO100905	SMU100320	34%	95.3%	95.3%
ECO100905	SPN401396	34%	95.3%	95.5%
ECO100905	SPY200469	35%	98.5%	97.3%
ECO100905	TPA100602	49%	95.5%	95.8%
ECO100905	UUR100367	43%	96.1%	95.8%
ECO100905	VCH101278	77%	100%	96.9%
ECO100905	YPS002091	87%	100%	100%
ECO100906	ABA104064	44%	98.5%	99.5%
ECO100906	BAN100917	21%	58.5%	49.3%
ECO100906	BAN111422	23%	79.5%	60.8%
ECO100906	BFR12483	34%	92.5%	95.6%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100906	BPT100765	41%	96.8%	99.2%
ECO100906	BCE108701	31%	21.8%	91.5%
ECO100906	BCE100481	43%	96.5%	97.2%
ECO100906	BFU104396	42%	96.5%	94.2%
ECO100906	BMA102366	43%	96.5%	87.6%
ECO100906	CDF101027	22%	90.2%	72.3%
ECO100906	CDP101373	24%	79.2%	65.4%
ECO100906	EBC100632	89%	74.8%	99.3%
ECO100906	EFA201594	22%	94.5%	73.1%
ECO100906	ECO100906	100%	100%	100%
ECO100906	KPN301496	87%	100%	100%
ECO100906	LPN101555	24%	93.8%	75.6%
ECO100906	LMO102099	22%	82.5%	62.1%
ECO100906	MCA100938	43%	96.5%	100%
ECO100906	MAV103522	23%	78.2%	64.2%
ECO100906	MBV100308	26%	91.2%	73.0%
ECO100906	MTU200570	26%	91.2%	73.0%
ECO100906	NGO100225	43%	96.8%	98.0%
ECO100906	NME201565	43%	98.2%	95.5%
ECO100906	PRT101956	66%	98.8%	98.8%
ECO100906	PAE204914	52%	97.8%	98.5%
ECO100906	PPU107582	52%	97.8%	98.0%
ECO100906	PSY101887	50%	98.2%	97.1%
ECO100906	SPA102570	90%	100%	100%
ECO100906	STY102950	90%	100%	100%
ECO100906	SAU801913	20%	87%	66.3%
ECO100906	SHA101008	21%	91%	81.4%
ECO100906	SPN401276	23%	86.8%	66.5%
ECO100906	SPY201274	21%	90.8%	71.1%
ECO100906	TPA100621	24%	76.8%	58.2%
ECO100906	VCH102834	42%	97.5%	93.1%
ECO100906	YPS002092	73%	100%	100%
ECO100907	ABA100602	41%	97.7%	96.9%
ECO100907	BFR11621	22%	49.4%	50.4%
ECO100907	BPT100086	46%	99.8%	99.3%
ECO100907	BCE114396	48%	99.0%	98.8%
ECO100907	BFU115907	47%	99.9%	99.7%
ECO100907	BMA106412	49%	81.6%	98.4%
ECO100907	CDF100790	24%	23.4%	39.0%
ECO100907	CDP101250	24%	56.0%	57.7%
ECO100907	EBC102285	90%	68.4%	100%
ECO100907	ECO100907	100%	100%	100%
ECO100907	HIN101581	60%	99.3%	99.5%
ECO100907	KPN301497	89%	100%	100%
ECO100907	LPN103383	48%	99.0%	98.7%
ECO100907	MCA101178	38%	97.6%	96.8%
ECO100907	MAV100155	25%	55.2%	56.1%
ECO100907	MBV101526	26%	51.4%	51.2%
ECO100907	MLP100917	26%	54.9%	55.2%
ECO100907	MTU202431	26%	51.4%	51.3%
ECO100907	NGO101948	47%	99.3%	98.7%
ECO100907	NME201487	48%	99.0%	99.2%
ECO100907	PMU100618	62%	99.5%	99.8%
ECO100907	PRT101957	74%	100%	99.9%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100907	PAE203081	49%	99.9%	99.8%
ECO100907	PPU101735	50%	99.9%	99.8%
ECO100907	PSY100727	49%	99.9%	100%
ECO100907	SPA102571	87%	89.0%	99.2%
ECO100907	STY103588	93%	100%	100%
ECO100907	STM103420	94%	100%	100%
ECO100907	SMU100931	25%	47.1%	49.1%
ECO100907	SPN400706	24%	54.1%	58.1%
ECO100907	SPY200949	23%	49.2%	51.4%
ECO100907	VCH101471	64%	99.9%	99.8%
ECO100907	YPS002093	77%	100%	99.9%
ECO100915	BFR101304	28%	12.9%	23.1%
ECO100915	ECO100915	100%	100%	100%
ECO100915	SPA104864	52%	96.0%	100%
ECO100915	STM100755	53%	96.0%	96.0%
ECO100954	ECO100954	100%	100%	100%
ECO100954	KPN108215	29%	23.1%	93.9%
ECO100954	PAE203677	29%	24.1%	23.3%
ECO100954	YPS000350	45%	99.1%	97.3%
ECO100956	ABA105111	37%	91.4%	97.2%
ECO100956	BPT100529	36%	86.8%	87.7%
ECO100956	BCE113904	34%	91.4%	86.4%
ECO100956	CAC100153	26%	91.4%	95.3%
ECO100956	EBC101811	60%	71.7%	100%
ECO100956	EFA202033	29%	91.4%	94.9%
ECO100956	ECO100956	100%	100%	100%
ECO100956	KPN206660	62%	92.8%	95.9%
ECO100956	MCA100619	25%	73.7%	83.8%
ECO100956	MAV105287	31%	85.5%	85.3%
ECO100956	MBV104448	27%	75.7%	84.7%
ECO100956	MTU202200	30%	92.1%	93.9%
ECO100956	NGO102044	25%	95.4%	81.6%
ECO100956	NME201339	25%	95.4%	100%
ECO100956	PAE202976	32%	85.5%	90.9%
ECO100956	PPU104816	34%	86.8%	92.2%
ECO100956	SAU801881	26%	83.6%	85.1%
ECO100956	SEP200520	28%	84.2%	85.7%
ECO100956	SHA100516	31%	84.2%	85.7%
ECO100956	SMU101303	22%	90.8%	97.2%
ECO100956	SPN401837	21%	92.1%	96.5%
ECO100956	VCH100900	34%	88.2%	84.9%
ECO100956	VCH101022	35%	92.1%	95.5%
ECO100967	ECO100967	100%	100%	100%
ECO100967	MGE100217	20%	18.6%	36.9%
ECO100967	PAE204977	31%	61.9%	57.0%
ECO100967	SPA101999	62%	60.6%	100%
ECO100967	STY103986	62%	99.1%	98.1%
ECO100967	STM100492	62%	99.1%	98.1%
ECO100967	VCH103430	32%	96.3%	91.7%
ECO100968	ECO100968	100%	100%	100%
ECO100968	SPA102000	66%	98.5%	99.4%
ECO100968	STY103988	66%	100%	100%
ECO100968	VCH103431	45%	86.0%	87.1%
ECO100974	ABA100027	42%	50.3%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100974	ABA102434	39%	97.1%	98.4%
ECO100974	BPT100939	41%	99.3%	99.7%
ECO100974	BBU100654	29%	95.4%	99.3%
ECO100974	BFU108703	44%	98.0%	94.2%
ECO100974	CJU101154	32%	89.5%	93.9%
ECO100974	ECO100974	100%	100%	100%
ECO100974	HPY101007	32%	89.2%	93.4%
ECO100974	KPN302023	81%	100%	100%
ECO100974	LPN101460	46%	98.4%	99.0%
ECO100974	PRT105958	73%	99.0%	99.0%
ECO100974	PPU107631	54%	99.7%	100%
ECO100974	PSY100875	53%	99.0%	97.8%
ECO100974	SPA102643	88%	100%	100%
ECO100974	STY103659	88%	100%	100%
ECO100975	CDF102870	27%	23.4%	35.0%
ECO100975	ECO100975	100%	100%	100%
ECO100975	MTU405812	24%	23.4%	38.1%
ECO100975	YPS002734	31%	12.2%	8.3%
ECO100980	ABA103609	64%	91.2%	98.4%
ECO100980	BPT100698	67%	90.5%	97.5%
ECO100980	BCE105957	69%	91.2%	97.2%
ECO100980	BFU100525	70%	93.3%	99.5%
ECO100980	BMA102208	71%	92.2%	98.4%
ECO100980	CDP100387	45%	88.8%	93.0%
ECO100980	EBC100227	84%	62.1%	100%
ECO100980	ECO100980	100%	100%	100%
ECO100980	KPN303632	88%	92.0%	97.0%
ECO100980	MCA101163	62%	91.4%	97.7%
ECO100996	ABA104763	51%	92.5%	96.9%
ECO100996	BAN108047	29%	38.1%	56.2%
ECO100996	BAN103651	30%	60.5%	42.0%
ECO100996	BPT101490	46%	93.0%	96.7%
ECO100996	BCE102619	53%	64.6%	96.9%
ECO100996	BFU112189	23%	56.5%	52.9%
ECO100996	CAC100112	22%	71.9%	74.5%
ECO100996	CAC102682	23%	85.3%	86.6%
ECO100996	CAC101653	27%	51.9%	53.9%
ECO100996	CBO103276	24%	82.1%	86.8%
ECO100996	CDF100916	23%	83.2%	89.0%
ECO100996	CDP101026	36%	20.4%	35.3%
ECO100996	EBC103183	65%	99.1%	99.1%
ECO100996	EFA200404	23%	91.4%	96.7%
ECO100996	ECO100996	100%	100%	100%
ECO100996	KPN302028	65%	99.1%	99.1%
ECO100996	LMO101233	26%	89.8%	95.0%
ECO100996	MAV104430	38%	10.9%	53.3%
ECO100996	MAV105180	31%	24.7%	30.2%
ECO100996	MAV108796	32%	24.9%	85.2%
ECO100996	MBV103262	25%	47.4%	43.2%
ECO100996	MTU301610	25%	30.6%	35.1%
ECO100996	MTU301614	37%	22.0%	27.7%
ECO100996	PMU101140	35%	26.5%	34.7%
ECO100996	PAE201013	27%	45.4%	59.4%
ECO100996	PAE200704	26%	45.8%	65.6%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO100996	PSY104248	35%	27.0%	39.8%
ECO100996	SAU802666	39%	91.8%	97.8%
ECO100996	SEP202130	38%	92.5%	98.5%
ECO100996	SMU100325	23%	89.8%	95.0%
ECO100996	SPY201683	22%	56.0%	62.1%
ECO100996	YPS002586	65%	99.8%	99.3%
ECO100997	ABA105171	39%	88.8%	90.4%
ECO100997	BAN105856	32%	7.7%	20.4%
ECO100997	BPT101492	39%	95.1%	91.3%
ECO100997	BCE107987	41%	88.8%	77.3%
ECO100997	CPN200056	26%	11.3%	35.3%
ECO100997	CTR200756	27%	28.7%	74.5%
ECO100997	EBC103182	53%	72.2%	100%
ECO100997	ECO100997	100%	100%	100%
ECO100997	KPN302029	52%	99.9%	99.3%
ECO100997	SPA106070	27%	34.1%	78.8%
ECO100997	STY104122	27%	34.1%	78.8%
ECO100997	STM103813	27%	34.1%	78.8%
ECO100997	YPS002580	48%	98.5%	98.4%
ECO101026	BAN109424	40%	92.9%	44.6%
ECO101026	BAN109023	47%	48.5%	99.3%
ECO101026	BCE102281	25%	47.1%	46.7%
ECO101026	BCE111625	25%	95.6%	47.5%
ECO101026	BFU103468	41%	94.1%	90.8%
ECO101026	CJU101182	35%	96.3%	47.7%
ECO101026	CAC102708	24%	93.4%	95.1%
ECO101026	EBC101388	87%	99.0%	44.9%
ECO101026	EFA201804	51%	97.3%	46.6%
ECO101026	EFM100140	50%	91.2%	64.3%
ECO101026	ECO101026	100%	100%	100%
ECO101026	KPN302511	86%	97.5%	47.3%
ECO101026	LPN100304	25%	94.9%	95.5%
ECO101026	LMO101440	62%	45.3%	97.0%
ECO101026	MAV102451	23%	93.9%	40.5%
ECO101026	PRT100222	71%	95.3%	100%
ECO101026	PSY109052	42%	44.1%	89.5%
ECO101026	SPA101126	90%	99.0%	48.8%
ECO101026	STY102475	90%	99.0%	48.8%
ECO101026	STM104345	60%	96.8%	98.3%
ECO101026	SAU800119	28%	93.6%	42.3%
ECO101026	SEP200736	22%	95.6%	98.7%
ECO101026	SHA102365	24%	95.6%	98.7%
ECO101026	SMU101114	45%	94.1%	98.2%
ECO101026	SPN400875	45%	94.9%	96.5%
ECO101026	SPY200356	44%	45.6%	98.0%
ECO101031	EBC105567	56%	80.4%	100%
ECO101031	ECO101031	100%	100%	100%
ECO101031	KPN306295	59%	80.4%	100%
ECO101031	SPA101094	57%	97.8%	100%
ECO101031	STY102485	64%	80.4%	100%
ECO101032	BCE107994	25%	99.2%	94.0%
ECO101032	EBC101043	75%	99.7%	98.9%
ECO101032	ECO101032	100%	100%	100%
ECO101032	KPN300314	73%	46.0%	95.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101032	KPN302520	76%	99.7%	99.5%
ECO101032	MAV101116	24%	56.2%	61.2%
ECO101032	PPU110237	28%	99.2%	97.7%
ECO101032	PSY104175	30%	98.9%	97.7%
ECO101032	SPA101093	83%	99.7%	100%
ECO101032	STY102486	84%	99.7%	99.5%
ECO101032	YPS003112	64%	100%	100%
ECO101034	EBC101041	82%	100%	100%
ECO101034	ECO101034	100%	100%	100%
ECO101034	KPN302510	70%	100%	97.6%
ECO101034	PRT101047	29%	95.1%	92.6%
ECO101034	SPA103953	37%	95.1%	76.5%
ECO101034	STY102488	83%	100%	100%
ECO101034	STM104609	47%	96.3%	98.7%
ECO101034	SAU801646	30%	56.8%	41.1%
ECO101034	YPS003073	62%	100%	100%
ECO101035	ABA100839	52%	96.8%	98.3%
ECO101035	BPT103038	56%	96.8%	96.6%
ECO101035	BCE114261	56%	97.4%	94.0%
ECO101035	BMA105687	55%	96.8%	96.9%
ECO101035	CJU100231	38%	97.7%	99.7%
ECO101035	EBC101229	93%	54.6%	100%
ECO101035	ECO101035	100%	100%	100%
ECO101035	HPY100574	30%	96.6%	97.3%
ECO101035	KPN302512	89%	100%	100%
ECO101035	MCA101086	52%	98.3%	98.9%
ECO101035	NGO100980	55%	98.3%	99.4%
ECO101035	NME200819	54%	98.3%	99.4%
ECO101035	PRT103497	75%	38.2%	100%
ECO101035	PAE203525	56%	98.3%	98.3%
ECO101035	PPU101541	57%	97.7%	97.7%
ECO101035	PSY105203	55%	98.9%	99.1%
ECO101035	SPA100686	86%	100%	100%
ECO101035	STY102489	88%	100%	100%
ECO101035	VCH103644	55%	97.7%	96.9%
ECO101035	YPS003083	72%	100%	100%
ECO101036	CAC100319	25%	83.3%	81.8%
ECO101036	EBC101230	82%	100%	100%
ECO101036	ECO101036	100%	100%	100%
ECO101036	KPN302515	78%	100%	100%
ECO101036	PRT103115	42%	97.8%	98.9%
ECO101036	PAE200954	42%	26.3%	15.4%
ECO101036	SPA100687	88%	100%	100%
ECO101036	STY102495	88%	98.9%	88.5%
ECO101036	YPS003344	64%	100%	100%
ECO101041	BAN106223	42%	98.7%	93.8%
ECO101041	BMA100330	30%	56.7%	54.8%
ECO101041	CDF101870	40%	97.7%	98.4%
ECO101041	EBC101201	79%	100%	100%
ECO101041	EFA200828	30%	97.4%	97.7%
ECO101041	EFM200723	28%	85.7%	85.3%
ECO101041	ECO101041	100%	100%	100%
ECO101041	KPN302526	75%	99.3%	99.0%
ECO101041	LMO100839	33%	97.4%	98.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101041	SPA100606	75%	96.1%	57.8%
ECO101041	STY102505	80%	100%	100%
ECO101041	STM102670	81%	100%	100%
ECO101041	SPY201609	30%	96.1%	94.9%
ECO101041	VCH103764	29%	96.7%	96.5%
ECO101041	YPS003368	62%	97.7%	56.0%
ECO101048	ABA102849	28%	64.5%	86.0%
ECO101048	BAN107248	24%	35.1%	69.6%
ECO101048	BAN108027	25%	45.0%	50.5%
ECO101048	BFR102099	23%	82.3%	71.5%
ECO101048	BPT101052	44%	98.3%	97.4%
ECO101048	BBU100283	29%	38.1%	63.9%
ECO101048	BCE104352	42%	97.0%	87.9%
ECO101048	BFU115968	42%	94.4%	90%
ECO101048	BMA102063	41%	91.3%	73.3%
ECO101048	CJU100042	26%	87.0%	71.4%
ECO101048	CAC100829	26%	93.5%	87.0%
ECO101048	CDF102709	34%	38.1%	45.5%
ECO101048	EBC100895	82%	100%	100%
ECO101048	ECO101048	100%	100%	100%
ECO101048	HPY100891	25%	68.4%	64.5%
ECO101048	LPN102505	32%	95.2%	98.7%
ECO101048	LMO101524	29%	56.7%	95%
ECO101048	PRT102170	38%	99.6%	99.6%
ECO101048	PAE201078	35%	95.2%	87.8%
ECO101048	PPU100759	32%	99.6%	99.1%
ECO101048	PSY104584	30%	83.5%	98.9%
ECO101048	SPA101329	79%	100%	100%
ECO101048	STY102512	84%	100%	100%
ECO101048	STM102682	84%	100%	100%
ECO101048	TPA100720	34%	26.4%	39.9%
ECO101048	VCH102165	34%	79.2%	75.3%
ECO101048	YPS001380	68%	97.4%	98.7%
ECO101060	ABA100920	45%	89.4%	95.4%
ECO101060	BPT102625	46%	93.2%	96.0%
ECO101060	BCE114484	48%	90.3%	90.5%
ECO101060	BFU100680	46%	93.2%	95.1%
ECO101060	BMA107485	48%	93.2%	82.3%
ECO101060	CDP100836	33%	77.8%	93.1%
ECO101060	EBC101771	79%	99.0%	100%
ECO101060	ECO101060	100%	100%	100%
ECO101060	KPN302522	81%	100%	100%
ECO101060	LPN101285	32%	81.2%	92.7%
ECO101060	MLP100441	30%	90.8%	93.9%
ECO101060	NGO101420	41%	91.3%	96.9%
ECO101060	NME200506	42%	91.3%	96.9%
ECO101060	PRT105698	57%	93.2%	97.0%
ECO101060	PAE202970	59%	90.8%	97.9%
ECO101060	PPU101763	51%	90.8%	97.9%
ECO101060	PSY101701	56%	90.8%	97.9%
ECO101060	SPA100594	84%	99.0%	100%
ECO101060	STY102526	86%	92.8%	99.0%
ECO101060	VCH101997	57%	90.8%	96.9%
ECO101060	YPS003109	67%	92.8%	97.0%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101066	ABA100557	58%	99.6%	99.6%
ECO101066	BAN107352	43%	96.7%	97.6%
ECO101066	BAN101218	56%	98.4%	99.2%
ECO101066	BFR10719	45%	98.4%	98.4%
ECO101066	BPT102619	65%	98.4%	96.4%
ECO101066	BCE112767	62%	97.5%	96.8%
ECO101066	BFU100684	63%	97.5%	95.8%
ECO101066	BMA106290	60%	97.5%	96.8%
ECO101066	CJU100403	45%	99.6%	100%
ECO101066	CPN200456	45%	97.1%	96.8%
ECO101066	CTR200501	50%	96.7%	96.8%
ECO101066	CAC102747	34%	97.5%	90.8%
ECO101066	CAC100570	51%	98.0%	97.6%
ECO101066	CBO102327	49%	97.5%	96.0%
ECO101066	CDF101772	49%	99.6%	99.2%
ECO101066	EBC100251	92%	67.6%	100%
ECO101066	EFA200243	42%	99.6%	99.2%
ECO101066	EFM201914	41%	99.6%	99.2%
ECO101066	ECO101066	100%	100%	100%
ECO101066	HIN100148	74%	98.4%	99.2%
ECO101066	HPY100554	45%	99.6%	100%
ECO101066	KPN300814	93%	100%	100%
ECO101066	LPN103118	60%	99.6%	99.2%
ECO101066	LMO102009	52%	99.6%	100%
ECO101066	MCA101812	58%	82.8%	94.0%
ECO101066	MAV103641	47%	98.8%	91.4%
ECO101066	MBV100667	44%	98.8%	94.3%
ECO101066	MLP101100	47%	98.8%	92.1%
ECO101066	MTU201462	44%	98.8%	94.3%
ECO101066	NGO101381	68%	99.2%	98.0%
ECO101066	NME200494	69%	99.2%	98.0%
ECO101066	PMU101916	78%	98.0%	98.8%
ECO101066	PRT100071	84%	100%	100%
ECO101066	PAE202965	64%	99.6%	99.6%
ECO101066	PPU101751	65%	99.6%	100%
ECO101066	PSY108154	64%	99.6%	99.6%
ECO101066	SPA100959	94%	100%	100%
ECO101066	STY102532	95%	100%	100%
ECO101066	STM102721	95%	100%	100%
ECO101066	SAU801231	55%	97.5%	98.4%
ECO101066	SEP200094	31%	97.5%	98.8%
ECO101066	SEP201523	55%	97.5%	99.2%
ECO101066	SHA101738	54%	97.5%	98.8%
ECO101066	SMU100541	40%	99.6%	99.6%
ECO101066	SPN400381	44%	99.6%	100%
ECO101066	SPY201348	42%	99.6%	99.6%
ECO101066	VCH101991	81%	100%	98.4%
ECO101066	YPS003130	86%	100%	100%
ECO101067	ABA100149	65%	56.4%	89.8%
ECO101067	BAN107311	61%	97.4%	95%
ECO101067	BFR100793	61%	97.4%	97.4%
ECO101067	BPT104633	75%	97.4%	96.2%
ECO101067	BBU100703	48%	89.7%	87.5%
ECO101067	BCE109854	77%	92.3%	91.1%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101067	BFU104450	77%	92.3%	91.1%
ECO101067	BMA104399	77%	92.3%	91.1%
ECO101067	CJU100409	47%	94.9%	94.8%
ECO101067	CPN200457	53%	97.4%	96.2%
ECO101067	CTR200500	50%	96.2%	97.4%
ECO101067	CAC100280	59%	91.0%	92.2%
ECO101067	CBO102204	61%	93.6%	70.2%
ECO101067	CDF104494	49%	91.0%	95.9%
ECO101067	CDF102560	55%	87.2%	92%
ECO101067	CDP102441	31%	78.2%	63.2%
ECO101067	EBC107855	26%	91.0%	85.5%
ECO101067	EFA204896	48%	87.2%	86.1%
ECO101067	EFM201177	56%	59.0%	88.5%
ECO101067	ECO101067	100%	100%	100%
ECO101067	HIN100147	82%	96.2%	98.7%
ECO101067	HPY100946	57%	87.2%	43.8%
ECO101067	HPY100552	55%	92.3%	92.3%
ECO101067	KPN301296	98%	100%	100%
ECO101067	LPN100598	78%	97.4%	92.7%
ECO101067	LMO102315	56%	97.4%	98.7%
ECO101067	MCA100571	58%	94.9%	94.9%
ECO101067	MAV103068	39%	84.6%	57.4%
ECO101067	MBV100652	37%	84.6%	57.4%
ECO101067	MLP101007	37%	84.6%	57.4%
ECO101067	MTU202210	37%	84.6%	57.4%
ECO101067	MPN100432	33%	50%	46.4%
ECO101067	NGO100692	75%	97.4%	97.4%
ECO101067	NME200041	73%	97.4%	97.4%
ECO101067	PMU101917	82%	96.2%	98.7%
ECO101067	PRT100070	89%	82.1%	100%
ECO101067	PAE202964	88%	98.7%	98.7%
ECO101067	PPU104838	85%	100%	100%
ECO101067	PSY106594	89%	100%	100%
ECO101067	SPA100630	100%	100%	100%
ECO101067	STY107110	100%	100%	100%
ECO101067	STM102722	100%	100%	100%
ECO101067	SAU801232	63%	88.5%	89.6%
ECO101067	SEP201525	65%	88.5%	89.6%
ECO101067	SHA101739	65%	88.5%	89.6%
ECO101067	SMU102800	40%	91.0%	86.6%
ECO101067	SPN400038	38%	92.3%	92.2%
ECO101067	SPY201351	41%	87.2%	87.8%
ECO101067	TPA100800	47%	85.9%	85.9%
ECO101067	UUR100511	33%	53.8%	54.5%
ECO101067	VCH101990	84%	97.4%	69.1%
ECO101067	YPS004652	89%	98.7%	98.7%
ECO101068	ABA102541	38%	99.3%	99.3%
ECO101068	BAN112689	47%	99.3%	100%
ECO101068	BAN107953	50%	99.5%	99.3%
ECO101068	BFR12010	50%	99.8%	99.3%
ECO101068	BPT102618	58%	99.5%	99.8%
ECO101068	BCE113298	63%	75.3%	100%
ECO101068	BFU100675	62%	99.8%	96.0%
ECO101068	BMA102164	62%	99.8%	99.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101068	CJU100410	51%	99.3%	99.5%
ECO101068	CPN200933	44%	99.8%	99.3%
ECO101068	CTR200146	45%	99.8%	98.8%
ECO101068	CAC100013	48%	99.0%	99.0%
ECO101068	CBO102384	46%	99.0%	98.1%
ECO101068	CDF101773	49%	99.0%	99.0%
ECO101068	CDP100587	27%	97.8%	27.4%
ECO101068	EBC100090	96%	64.6%	100%
ECO101068	EFA201888	50%	99.0%	98.8%
ECO101068	EFM201378	48%	98.8%	98.8%
ECO101068	ECO101068	100%	100%	100%
ECO101068	HPY100551	49%	99.0%	99.5%
ECO101068	KPN301302	95%	100%	100%
ECO101068	LPN100053	62%	100%	100%
ECO101068	LMO100394	49%	100%	99.5%
ECO101068	MCA101479	54%	98.8%	99.8%
ECO101068	MAV103067	40%	97.8%	99.3%
ECO101068	MBV100653	42%	98.1%	96.2%
ECO101068	MLP101008	41%	98.1%	96.2%
ECO101068	MTU202211	42%	98.1%	96.2%
ECO101068	NGO100696	60%	99.8%	92.2%
ECO101068	NME200042	60%	99.8%	99.3%
ECO101068	PRT104423	82%	100%	100%
ECO101068	PAE202963	66%	99.8%	99.3%
ECO101068	PPU104840	67%	99.8%	99.3%
ECO101068	PSY101697	65%	99.8%	99.3%
ECO101068	SPA100629	89%	100%	100%
ECO101068	STY102533	94%	100%	100%
ECO101068	STM102723	94%	100%	100%
ECO101068	SAU800984	51%	99.0%	98.3%
ECO101068	SEP200206	53%	98.8%	98.1%
ECO101068	SHA101847	52%	99.0%	98.3%
ECO101068	SMU100539	43%	99.8%	99.3%
ECO101068	SPN400382	43%	99.8%	98.3%
ECO101068	SPY201347	45%	99.5%	99.0%
ECO101068	VCH101989	75%	100%	100%
ECO101068	YPS003134	89%	100%	100%
ECO101069	ABA102122	36%	89.2%	88.5%
ECO101069	CDF103263	25%	87.4%	89.9%
ECO101069	EBC100872	64%	99.3%	99.3%
ECO101069	ECO101069	100%	100%	100%
ECO101069	HIN101143	30%	34.6%	45.7%
ECO101069	KPN301301	63%	98.9%	98.9%
ECO101069	LPN100258	25%	91.1%	96.0%
ECO101069	MCA100346	28%	70.3%	73.6%
ECO101069	MAV100375	26%	60.2%	56.3%
ECO101069	MBV101892	25%	60.2%	56.3%
ECO101069	MTU200806	25%	60.2%	57.4%
ECO101069	PMU101465	28%	37.2%	48.2%
ECO101069	PRT106034	49%	96.7%	93.8%
ECO101069	PAE202962	35%	90.3%	89.3%
ECO101069	PPU104805	34%	94.4%	93.4%
ECO101069	PSY101696	35%	90.0%	88.9%
ECO101069	SPA100628	69%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101069	STY102534	69%	100%	100%
ECO101069	STM102724	69%	100%	100%
ECO101069	VCH101988	38%	92.2%	89.5%
ECO101069	YPS003142	56%	98.5%	98.9%
ECO101084	ABA102335	34%	83.5%	92.0%
ECO101084	BAN111797	31%	66.9%	92.9%
ECO101084	BAN111738	31%	66.9%	81.7%
ECO101084	BFR104010	29%	34.3%	38.3%
ECO101084	BPT102076	38%	83.1%	94.7%
ECO101084	BCE113954	36%	83.5%	94.7%
ECO101084	BFU108190	35%	81.8%	95.5%
ECO101084	CJU100336	32%	28.8%	30.5%
ECO101084	CAC101145	26%	56.4%	64.1%
ECO101084	EBC101033	76%	95.3%	100%
ECO101084	ECO101084	100%	100%	100%
ECO101084	KPN302583	76%	81.4%	99.0%
ECO101084	MAV105209	33%	36.9%	49.5%
ECO101084	PAE202929	32%	82.6%	99.0%
ECO101084	PSY102126	30%	82.6%	86.8%
ECO101084	SPA102806	80%	89.0%	99.5%
ECO101084	STY102549	80%	89.0%	99.5%
ECO101084	VCH103717	27%	69.1%	84.3%
ECO101086	EBC101581	84%	97.8%	97.5%
ECO101086	ECO101086	100%	100%	100%
ECO101086	KPN302588	81%	100%	100%
ECO101086	LPN100159	41%	69.7%	89.3%
ECO101086	PRT102313	54%	94.4%	98.4%
ECO101086	PPU106532	39%	91.6%	89.2%
ECO101086	SPA102803	76%	100%	100%
ECO101086	STY102551	87%	82.2%	100%
ECO101086	VCH102794	48%	94.1%	96.4%
ECO101088	BFR100953	23%	55.2%	53.1%
ECO101088	BCE105922	22%	65.0%	65.2%
ECO101088	EBC100965	68%	97.5%	97.5%
ECO101088	EFM200997	25%	32.8%	17.9%
ECO101088	ECO101088	100%	100%	100%
ECO101088	LMO102112	20%	90.8%	88.0%
ECO101088	PAE202240	23%	55.2%	51.0%
ECO101088	SPN300353	24%	34.5%	29.8%
ECO101089	CJU100871	21%	100%	100%
ECO101089	CTR200422	25%	45.9%	39.9%
ECO101089	EBC100964	90%	67.2%	94.7%
ECO101089	ECO101089	100%	100%	100%
ECO101089	HIN101524	45%	99.2%	99.2%
ECO101089	HPY100774	24%	98.2%	98.0%
ECO101089	KPN302592	90%	100%	99.3%
ECO101089	MAV108493	26%	80.2%	76.9%
ECO101089	MBV103715	22%	92.5%	86.3%
ECO101089	MTU200976	22%	93.0%	96.7%
ECO101089	MGE100066	25%	17.3%	5.3%
ECO101089	PMU100560	44%	99.0%	99.0%
ECO101089	PRT100169	60%	100%	100%
ECO101089	SPA102801	91%	100%	100%
ECO101089	STY102553	93%	100%	91.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101089	STM102743	93%	100%	91.5%
ECO101089	SAU802360	20%	41.4%	44.7%
ECO101089	VCH101854	52%	100%	99.0%
ECO101089	YPS003223	78%	100%	100%
ECO101095	BCE110408	34%	46.8%	28.1%
ECO101095	BFU109811	35%	30.8%	15.0%
ECO101095	ECO101095	100%	100%	100%
ECO101096	ABA105535	24%	54.0%	52.8%
ECO101096	BAN107331	34%	86.8%	98.4%
ECO101096	BAN107811	36%	96.8%	97.1%
ECO101096	BFR11543	28%	87.6%	73.8%
ECO101096	BBU100638	34%	82.5%	82.5%
ECO101096	CAC100714	39%	92.5%	91.0%
ECO101096	CBO100586	40%	92.2%	52.0%
ECO101096	CDF100910	40%	92.8%	91.7%
ECO101096	EBC101881	91%	98.6%	100%
ECO101096	EFA201564	40%	96.0%	92.2%
ECO101096	EFM202059	39%	95.4%	91.6%
ECO101096	ECO101096	100%	100%	100%
ECO101096	HIN101310	54%	94.3%	86.8%
ECO101096	KPN300453	94%	58.3%	96.7%
ECO101096	KPN302593	91%	100%	100%
ECO101096	LPN101055	39%	95.7%	97.9%
ECO101096	LMO102691	38%	92.8%	90.5%
ECO101096	MPN100096	23%	69.0%	56.7%
ECO101096	PMU100260	50%	98.0%	98.3%
ECO101096	PMU100261	54%	100%	97.2%
ECO101096	PRT100582	78%	100%	100%
ECO101096	SPA102407	92%	95.7%	100%
ECO101096	STY102558	93%	100%	100%
ECO101096	SAU801102	38%	96.8%	97.2%
ECO101096	SEP200816	38%	99.1%	98.9%
ECO101096	SHA100355	40%	92.8%	91.1%
ECO101096	SMU100062	40%	92.8%	90.2%
ECO101096	SPN401242	41%	91.1%	90.2%
ECO101096	SPY200838	39%	98.0%	95.2%
ECO101096	TPA100647	32%	98.0%	97.4%
ECO101096	VCH103826	39%	99.1%	99.4%
ECO101096	VCH101404	58%	100%	93.7%
ECO101096	VCH101403	65%	95.7%	95.9%
ECO101102	EBC102866	81%	99.8%	99.8%
ECO101102	ECO101102	100%	100%	100%
ECO101102	KPN302587	82%	60.7%	100%
ECO101102	PRT103095	53%	96.7%	97.1%
ECO101102	PAE201179	33%	95.7%	98.7%
ECO101102	PPU108062	32%	95.7%	98.7%
ECO101102	PSY104543	30%	95.7%	98.7%
ECO101102	SPA104232	86%	96.9%	100%
ECO101102	STY102565	85%	100%	100%
ECO101102	VCH101612	32%	59.9%	61.7%
ECO101102	YPS003253	62%	97.9%	98.6%
ECO101104	ABA105711	64%	99.3%	98.5%
ECO101104	BAN108908	26%	67.5%	70.6%
ECO101104	BAN107339	26%	63.2%	65.1%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101104	BFR11423	50%	97.8%	97.6%
ECO101104	BPT102211	62%	98.0%	94.3%
ECO101104	BCE110636	61%	99.3%	98.1%
ECO101104	BFU103343	25%	62.1%	59.3%
ECO101104	BMA107095	62%	99.3%	93.8%
ECO101104	CJU100023	30%	58.6%	57.9%
ECO101104	CBO102979	22%	66.9%	60.8%
ECO101104	CDF100863	21%	85.1%	82.7%
ECO101104	CDP100537	25%	61.8%	58.0%
ECO101104	EBC102864	92%	100%	100%
ECO101104	EFA200867	27%	72.8%	75.4%
ECO101104	EFM201242	28%	73.9%	74.7%
ECO101104	ECO101104	100%	100%	100%
ECO101104	HIN100620	77%	99.8%	99.8%
ECO101104	HPY101095	27%	57.9%	57.5%
ECO101104	KPN300325	87%	19.3%	87.1%
ECO101104	KPN301141	93%	99.8%	100%
ECO101104	LPN100438	56%	99.1%	99.1%
ECO101104	LMO102395	28%	65.6%	67.9%
ECO101104	MCA100711	66%	98.2%	98.5%
ECO101104	MAV104228	24%	67.1%	62.7%
ECO101104	MBV105328	23%	67.1%	62.9%
ECO101104	MLP101330	24%	67.1%	62.9%
ECO101104	MTU200771	23%	67.1%	62.9%
ECO101104	NGO101832	62%	97.8%	98.2%
ECO101104	NME202038	62%	97.8%	98.2%
ECO101104	PMU101851	77%	99.8%	100%
ECO101104	PRT100590	84%	99.8%	99.8%
ECO101104	PAE202627	70%	98.2%	98.5%
ECO101104	PPU103014	68%	93.4%	98.4%
ECO101104	PSY104080	70%	98.2%	95.1%
ECO101104	SPA104234	90%	100%	100%
ECO101104	STY102567	94%	100%	100%
ECO101104	SAU801908	27%	71.5%	74.0%
ECO101104	SEP200567	25%	77.2%	81.7%
ECO101104	SHA100373	27%	67.5%	69.1%
ECO101104	SMU101297	28%	73.9%	74.5%
ECO101104	SPN400056	28%	73.9%	74.5%
ECO101104	SPY200028	27%	82.0%	86.7%
ECO101104	VCH101107	82%	99.8%	100%
ECO101104	YPS003261	88%	100%	100%
ECO101111	ECO101111	100%	100%	100%
ECO101111	KPN202195	62%	98.3%	99.6%
ECO101111	SAU600734	30%	26.9%	30.0%
ECO101111	SEP202424	30%	29.5%	18.7%
ECO101111	UUR100275	24%	40.2%	32.3%
ECO101111	VCH103209	28%	38.0%	34.2%
ECO101128	EBC102415	23%	85.4%	82.6%
ECO101128	ECO102311	60%	74.5%	65.8%
ECO101128	ECO101128	100%	100%	100%
ECO101128	NME201221	42%	25.5%	17.4%
ECO101128	SPA103143	28%	43.8%	17.8%
ECO101128	STY102590	56%	87.6%	82.9%
ECO101134	ECO100548	44%	96.3%	86%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101134	ECO101520	44%	100%	95.0%
ECO101134	ECO101134	100%	100%	100%
ECO101134	KPN304995	34%	93.3%	96.2%
ECO101134	SPA104168	39%	98.5%	99.3%
ECO101134	STY102095	40%	94.8%	96.9%
ECO101134	STM101947	40%	94.8%	96.9%
ECO101134	SAU800348	24%	37.3%	38.8%
ECO101136	EBC102244	60%	100%	100%
ECO101136	ECO101136	100%	100%	100%
ECO101136	KPN301814	65%	100%	100%
ECO101136	PAE203256	27%	53.6%	36.4%
ECO101136	PSY103058	31%	59.6%	91.3%
ECO101136	SMU101553	26%	23.8%	23.8%
ECO101136	VCH101614	31%	59.8%	94.6%
ECO101139	ECO101139	100%	100%	100%
ECO101139	KPN300326	56%	70.5%	98.4%
ECO101139	SPA109612	41%	75%	79.3%
ECO101139	STY105236	40%	75%	79.3%
ECO101152	ABA103728	35%	69.4%	83.2%
ECO101152	EBC100100	83%	84.3%	100%
ECO101152	ECO101152	100%	100%	100%
ECO101152	HIN101415	43%	75%	75.7%
ECO101152	KPN304811	79%	86.1%	100%
ECO101152	MCA101920	32%	87.0%	96.2%
ECO101152	PMU100444	45%	75.9%	98.8%
ECO101152	PRT106055	64%	86.1%	97.9%
ECO101152	PAE201294	39%	76.9%	84.5%
ECO101152	PPU108346	43%	75.9%	92.8%
ECO101152	PSY105502	42%	64.8%	95.1%
ECO101152	SPA103241	85%	89.8%	100%
ECO101152	STY101740	83%	95.4%	93.6%
ECO101152	VCH101927	48%	85.2%	89.2%
ECO101152	YPS003546	71%	78.7%	94.4%
ECO101153	ABA100124	44%	89.0%	91.5%
ECO101153	BAN101423	32%	83.1%	64.2%
ECO101153	BAN104355	33%	90.0%	67.9%
ECO101153	BFR11202	38%	92.2%	97.1%
ECO101153	BPT102787	40%	90.4%	87.0%
ECO101153	BCE110764	45%	90.4%	79.5%
ECO101153	BFU108950	42%	83.1%	62.6%
ECO101153	BMA106711	43%	92.7%	86.8%
ECO101153	CJU100021	25%	87.2%	68.8%
ECO101153	CDF103166	30%	83.1%	61.7%
ECO101153	CDF101613	30%	84.9%	63%
ECO101153	CDP100223	30%	89.0%	69.6%
ECO101153	EBC101919	37%	90.0%	5.4%
ECO101153	ECO101153	100%	100%	100%
ECO101153	KPN308845	86%	100%	100%
ECO101153	LPN100114	24%	77.6%	54.5%
ECO101153	LMO102616	33%	89.5%	71.3%
ECO101153	MCA102285	39%	93.6%	94.3%
ECO101153	MAV100179	41%	89.0%	72.4%
ECO101153	MBV101328	40%	89.0%	72.1%
ECO101153	MLP101033	38%	89.0%	80.2%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101153	MTU202955	40%	89.0%	79.9%
ECO101153	NGO100109	39%	89.5%	89.9%
ECO101153	NME201411	38%	89.5%	89.9%
ECO101153	PMU101529	32%	83.1%	70.5%
ECO101153	PRT105162	68%	100%	100%
ECO101153	PAE200317	51%	99.5%	99.1%
ECO101153	PPU102070	50%	99.5%	99.1%
ECO101153	PSY107523	45%	99.5%	98.6%
ECO101153	SPA103242	80%	100%	100%
ECO101153	STY101738	84%	100%	100%
ECO101153	STM102228	38%	86.8%	7.9%
ECO101153	SAU800968	31%	93.2%	69.3%
ECO101153	SEP200184	31%	93.2%	69.1%
ECO101153	SHA101674	30%	93.2%	69.1%
ECO101153	VCH103722	36%	85.8%	83.8%
ECO101153	YPS003552	72%	100%	100%
ECO101161	BAN104595	27%	90.4%	94.9%
ECO101161	BAN106003	30%	91.2%	93.6%
ECO101161	BPT101374	61%	94.9%	94.9%
ECO101161	BCE109277	65%	95.9%	88.0%
ECO101161	BFU100577	65%	95.1%	84.8%
ECO101161	CAC101054	35%	92.9%	94.8%
ECO101161	EBC101838	96%	100%	100%
ECO101161	ECO101161	100%	100%	100%
ECO101161	KPN304804	94%	99.2%	99.2%
ECO101161	LPN101390	65%	96.5%	97.0%
ECO101161	PAE200585	68%	96.7%	95.2%
ECO101161	PPU100633	68%	92.5%	95.9%
ECO101161	PSY103400	66%	96.7%	94.6%
ECO101161	SPA101758	97%	100%	100%
ECO101161	STY101724	96%	100%	100%
ECO101161	STM101822	96%	100%	100%
ECO101161	VCH101844	74%	97.5%	95.9%
ECO101161	YPS000678	84%	99.0%	99.4%
ECO101174	EBC105172	64%	6.1%	78%
ECO101174	EBC103524	71%	99.4%	99.5%
ECO101174	ECO101174	100%	100%	100%
ECO101174	KPN308982	74%	98.1%	98.3%
ECO101175	BFR104377	22%	14.6%	35.6%
ECO101175	CPN100014	25%	15.4%	15.0%
ECO101175	CPN100432	20%	32.1%	35.6%
ECO101175	CPN100430	18%	19.6%	50.5%
ECO101175	CPN100435	20%	40.9%	37.0%
ECO101175	CAC102963	23%	32.0%	48.4%
ECO101175	ECO101175	100%	100%	100%
ECO101175	NGO103389	27%	28.4%	90.8%
ECO101175	YPS002558	24%	57.1%	31.5%
ECO101179	ABA100211	24%	87.1%	91.3%
ECO101179	ABA104416	24%	93.6%	95.8%
ECO101179	BAN100939	22%	74.9%	78.8%
ECO101179	BAN109556	30%	88.5%	91.1%
ECO101179	BFR11789	37%	95.5%	98.1%
ECO101179	BPT103036	41%	96.5%	93.4%
ECO101179	BCE112681	27%	92%	95.9%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101179	BFU113350	28%	84.2%	88.0%
ECO101179	BMA103833	27%	88.7%	91.5%
ECO101179	CPN200824	35%	97.5%	93.5%
ECO101179	CTR200240	35%	97.8%	88.4%
ECO101179	CBO103098	38%	94.7%	93.3%
ECO101179	CDP103271	30%	14.7%	71.9%
ECO101179	EBC101346	91%	58.5%	96.7%
ECO101179	EFA202070	32%	94.7%	93.1%
ECO101179	ECO101179	100%	100%	100%
ECO101179	HPY100224	26%	75.5%	95.4%
ECO101179	KPN305984	89%	100%	98.4%
ECO101179	LPN103014	25%	74.4%	85.1%
ECO101179	LPN101097	28%	75.3%	81.8%
ECO101179	LMO100913	37%	96.9%	96.3%
ECO101179	MCA100381	25%	81.6%	80.5%
ECO101179	MAV101853	30%	75.1%	83.5%
ECO101179	MBV105373	31%	88.2%	90.7%
ECO101179	MLP101357	29%	75.1%	78.0%
ECO101179	MTU201685	31%	88.2%	90.7%
ECO101179	PMU100948	58%	95.8%	93.8%
ECO101179	PRT104187	71%	99.8%	97.5%
ECO101179	PAE202561	29%	87.6%	90.5%
ECO101179	PPU103595	29%	90.2%	91.0%
ECO101179	PSY101243	29%	92%	91.6%
ECO101179	SPA100376	87%	69.3%	100%
ECO101179	STY101680	92%	100%	98.0%
ECO101179	STM101479	93%	100%	99.5%
ECO101179	SEP200020	37%	23.8%	72.8%
ECO101179	SEP200018	28%	88.5%	90.9%
ECO101179	SHA102089	22%	74.4%	93.3%
ECO101179	SHA102439	28%	88.5%	90.9%
ECO101179	VCH102813	39%	96.4%	94.9%
ECO101180	ABA100157	66%	98.4%	100%
ECO101180	BAN112499	57%	45.1%	92.2%
ECO101180	BAN106136	39%	89.5%	87.8%
ECO101180	BAN101660	51%	98.7%	97.2%
ECO101180	BFR10407	44%	97.8%	96.8%
ECO101180	BPT100617	64%	97.8%	97.2%
ECO101180	BBU100543	28%	89.2%	75.9%
ECO101180	BCE112713	63%	98.4%	96.6%
ECO101180	BFU100079	62%	98.4%	97.2%
ECO101180	BMA100055	63%	98.4%	97.2%
ECO101180	CJU100848	56%	99.4%	99.7%
ECO101180	CAC100050	53%	99.0%	97.5%
ECO101180	CBO100851	55%	98.7%	97.5%
ECO101180	CDF100459	53%	98.7%	98.1%
ECO101180	CDP100215	42%	99.0%	95.7%
ECO101180	EBC101345	99%	100%	100%
ECO101180	EFA201512	50%	99.4%	96.6%
ECO101180	EFM200023	50%	99.4%	96.6%
ECO101180	ECO101180	100%	100%	100%
ECO101180	HIN101576	85%	99.4%	99.7%
ECO101180	HPY100730	53%	99.4%	96.9%
ECO101180	KPN303464	96%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101180	LPN101587	63%	99.4%	99.4%
ECO101180	LMO100583	47%	99.4%	97.8%
ECO101180	MCA100701	65%	100%	100%
ECO101180	MAV105952	43%	99.0%	96.0%
ECO101180	MBV105572	43%	98.1%	98.7%
ECO101180	MLP100179	43%	99.0%	95.7%
ECO101180	MTU201006	43%	99.0%	96.0%
ECO101180	MGE100060	43%	88.9%	94.9%
ECO101180	MPN100082	43%	97.8%	79.9%
ECO101180	NGO101084	66%	98.4%	94.5%
ECO101180	NME201007	66%	98.4%	94.5%
ECO101180	PMU100244	87%	99.4%	99.7%
ECO101180	PRT101362	94%	100%	100%
ECO101180	PAE204667	67%	99.4%	99.7%
ECO101180	PPU104089	67%	78.1%	99.6%
ECO101180	PSY102431	67%	99.4%	99.7%
ECO101180	SPA100616	97%	99.7%	100%
ECO101180	STY101673	99%	100%	100%
ECO101180	STM101478	99%	100%	100%
ECO101180	SAU800500	49%	98.7%	96.9%
ECO101180	SEP201833	48%	98.7%	96.9%
ECO101180	SHA100895	49%	69.2%	95.6%
ECO101180	SMU101229	50%	99.0%	97.2%
ECO101180	SPN400028	50%	99.0%	92.3%
ECO101180	SPY200014	51%	99.0%	97.8%
ECO101180	TPA100291	29%	90.8%	74.8%
ECO101180	UUR100193	41%	99.4%	94.5%
ECO101180	VCH102150	82%	99.4%	99.7%
ECO101180	YPS003242	97%	100%	100%
ECO101183	ABA100136	45%	95.9%	93.9%
ECO101183	BAN108277	32%	99.5%	99.5%
ECO101183	BAN105102	33%	100%	94.6%
ECO101183	BPT101741	45%	97.4%	95.5%
ECO101183	BCE101777	43%	53.8%	93.8%
ECO101183	BFU107323	44%	98.3%	97.2%
ECO101183	BMA107107	44%	98.6%	86.7%
ECO101183	CJU100504	31%	93.8%	88.9%
ECO101183	CPN200031	28%	52.4%	62.2%
ECO101183	CTR200033	29%	53.8%	65.2%
ECO101183	CAC100929	29%	81.6%	81.3%
ECO101183	CDF100797	23%	46.9%	30.1%
ECO101183	CDP100770	28%	99.8%	92.1%
ECO101183	EBC101342	94%	100%	100%
ECO101183	ECO101183	100%	100%	100%
ECO101183	HPY100235	27%	96.4%	90.4%
ECO101183	KPN303475	92%	100%	100%
ECO101183	LPN100434	41%	98.6%	88.7%
ECO101183	LMO102359	34%	85.4%	81.8%
ECO101183	MCA100694	41%	99.3%	98.2%
ECO101183	MBV102365	32%	100%	91.2%
ECO101183	MLP101439	31%	100%	91.4%
ECO101183	MTU200507	32%	100%	91.2%
ECO101183	NGO101400	44%	96.2%	96.1%
ECO101183	NME200701	44%	96.2%	96.1%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101183	PMU100684	50%	99.3%	98.8%
ECO101183	PRT101365	74%	99.8%	99.3%
ECO101183	PAE204663	50%	100%	98.6%
ECO101183	PPU109698	51%	99.8%	97.6%
ECO101183	PSY102425	50%	85.9%	96.8%
ECO101183	SPA100011	74%	65.6%	100%
ECO101183	STY101664	94%	100%	100%
ECO101183	SAU801672	33%	100%	93.8%
ECO101183	SEP201646	32%	100%	93.8%
ECO101183	SHA100381	33%	100%	93.8%
ECO101183	VCH102147	60%	100%	99.3%
ECO101183	YPS003254	79%	100%	99.5%
ECO101184	ABA105579	61%	99.7%	99.2%
ECO101184	BAN113068	47%	94.2%	99.4%
ECO101184	BAN100929	51%	96.7%	98.6%
ECO101184	BFR11151	47%	97.2%	97.3%
ECO101184	BPT101750	65%	98.9%	98.9%
ECO101184	BBU100195	49%	98.1%	99.4%
ECO101184	BCE108751	61%	100%	100%
ECO101184	BFU107325	61%	100%	100%
ECO101184	BMA103540	60%	100%	100%
ECO101184	CJU101518	53%	98.6%	99.2%
ECO101184	CPN200648	52%	94.2%	95.8%
ECO101184	CTR200287	54%	94.4%	95.5%
ECO101184	CAC101625	50%	96.9%	97.8%
ECO101184	CBO100481	50%	97.8%	98.9%
ECO101184	CDF101347	51%	97.8%	100%
ECO101184	CDP100071	45%	97.8%	99.4%
ECO101184	EBC100920	95%	68.9%	100%
ECO101184	EFA201655	51%	96.1%	97.5%
ECO101184	EFM200375	50%	96.9%	98.3%
ECO101184	ECO101184	100%	100%	100%
ECO101184	HIN101530	73%	99.7%	99.4%
ECO101184	HPY100075	53%	96.1%	98.3%
ECO101184	KPN303478	92%	100%	100%
ECO101184	LPN101572	61%	100%	100%
ECO101184	LMO101439	50%	97.5%	98.6%
ECO101184	MCA100127	61%	99.7%	100%
ECO101184	MAV106507	46%	96.7%	98.0%
ECO101184	MBV105506	45%	94.2%	95.5%
ECO101184	MLP100700	43%	94.2%	95.6%
ECO101184	MTU201282	45%	94.2%	95.5%
ECO101184	MGE100263	42%	89.2%	89.7%
ECO101184	MPN100475	41%	89.2%	89.7%
ECO101184	NGO100540	62%	99.4%	100%
ECO101184	NME201794	63%	99.4%	100%
ECO101184	PMU100555	74%	99.7%	99.7%
ECO101184	PRT101055	82%	100%	100%
ECO101184	PAE204662	65%	99.4%	100%
ECO101184	PPU109700	66%	99.4%	100%
ECO101184	PSY102423	66%	99.4%	100%
ECO101184	SPA100352	87%	100%	100%
ECO101184	STY101661	96%	100%	100%
ECO101184	SAU802118	50%	98.1%	98.9%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101184	SEP201909	50%	98.1%	98.9%
ECO101184	SHA100601	50%	98.1%	98.9%
ECO101184	SMU100318	49%	98.6%	99.7%
ECO101184	SPN400924	49%	98.6%	99.7%
ECO101184	SPY200868	48%	98.3%	99.4%
ECO101184	TPA100050	49%	94.4%	97.4%
ECO101184	UUR100003	43%	95.8%	97.8%
ECO101184	VCH102146	72%	99.7%	99.7%
ECO101184	YPS003258	85%	100%	100%
ECO101185	ABA104460	46%	91.0%	92.3%
ECO101185	BAN105078	28%	87.0%	87.9%
ECO101185	BAN103528	30%	95.3%	95.8%
ECO101185	BFR102113	29%	97.1%	97.5%
ECO101185	BPT101752	42%	91.7%	94.4%
ECO101185	BCE115118	45%	94.2%	95.7%
ECO101185	BFU107327	45%	94.2%	93.7%
ECO101185	BMA107849	44%	95.7%	95.4%
ECO101185	CJU100672	28%	89.5%	87.5%
ECO101185	CAC100499	31%	90.3%	89.5%
ECO101185	CBO100136	30%	91.7%	88.7%
ECO101185	CDF100750	35%	92.8%	92.9%
ECO101185	CDP100074	29%	94.2%	93.8%
ECO101185	EBC100919	69%	99.3%	100%
ECO101185	EFA201657	34%	86.6%	87.0%
ECO101185	EFM201604	36%	90.3%	86.2%
ECO101185	ECO101185	100%	100%	100%
ECO101185	HIN101528	57%	98.6%	98.6%
ECO101185	HPY100377	30%	90.6%	89.1%
ECO101185	KPN300226	89%	23.8%	100%
ECO101185	KPN300540	71%	51.3%	80.7%
ECO101185	KPN303481	75%	98.9%	97.2%
ECO101185	LPN101502	43%	96.8%	94.1%
ECO101185	LMO101395	32%	81.9%	81.3%
ECO101185	MCA100943	41%	97.1%	93.2%
ECO101185	MAV106509	31%	96.8%	90.1%
ECO101185	MBV105507	32%	79.8%	68.6%
ECO101185	MLP100701	34%	82.7%	80.9%
ECO101185	MTU201283	32%	79.8%	68.6%
ECO101185	NGO101039	43%	94.6%	91.0%
ECO101185	NME200343	43%	94.6%	96.0%
ECO101185	PMU100556	51%	98.6%	99.0%
ECO101185	PRT105490	65%	99.3%	97.5%
ECO101185	PAE204661	53%	95.3%	95.7%
ECO101185	PPU109702	49%	94.9%	95.3%
ECO101185	PSY102421	48%	94.6%	94.9%
ECO101185	SPA100351	74%	59.9%	100%
ECO101185	STY101658	76%	99.3%	99.3%
ECO101185	SAU802117	32%	97.5%	97.8%
ECO101185	SEP201908	31%	94.6%	94.2%
ECO101185	SHA100602	27%	97.5%	97.8%
ECO101185	SMU100315	33%	90.3%	89.9%
ECO101185	SPN400925	36%	76.9%	76.0%
ECO101185	SPY200869	33%	89.2%	88.2%
ECO101185	TPA100051	28%	93.9%	86.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101185	VCH102145	53%	97.1%	95.1%
ECO101185	YPS003269	62%	99.3%	99.3%
ECO101186	BCE103057	28%	93.8%	29.6%
ECO101186	BMA105726	26%	74.6%	18.9%
ECO101186	EBC100918	63%	95.4%	99.2%
ECO101186	ECO101186	100%	100%	100%
ECO101186	HIN101225	27%	85.4%	87.4%
ECO101186	KPN303484	58%	100%	100%
ECO101186	NGO101989	28%	89.2%	90.3%
ECO101186	NME200882	29%	89.2%	90.3%
ECO101186	PMU100842	25%	91.5%	96.7%
ECO101186	PAE110961	31%	91.5%	94.1%
ECO101186	SPA103126	72%	98.5%	99.2%
ECO101186	STY101655	73%	98.5%	99.2%
ECO101186	VCH102144	38%	96.9%	97.6%
ECO101186	YPS003272	50%	92.3%	89.5%
ECO101188	ABA105640	66%	98.6%	97.5%
ECO101188	BAN100484	28%	68.0%	52.1%
ECO101188	BAN110262	28%	72.5%	54.5%
ECO101188	BFR11555	46%	90.1%	95.1%
ECO101188	BPT101704	45%	94.4%	96.5%
ECO101188	BCE113835	43%	93.7%	95.1%
ECO101188	BFU102357	43%	95.1%	96.5%
ECO101188	BMA104317	42%	95.1%	96.5%
ECO101188	CJU100352	45%	90.1%	97.4%
ECO101188	CPN200024	42%	91.2%	95.6%
ECO101188	CTR200025	41%	92.6%	96.3%
ECO101188	CAC100242	30%	74.3%	59.3%
ECO101188	CBO100238	23%	94.7%	94.4%
ECO101188	CDF102295	28%	74.6%	59.6%
ECO101188	EBC100731	93%	99.6%	100%
ECO101188	EFA201864	28%	77.1%	60.1%
ECO101188	EFM101476	27%	77.1%	62.5%
ECO101188	ECO101188	100%	100%	100%
ECO101188	HIN101526	81%	99.6%	99.6%
ECO101188	HPY100003	42%	89.4%	95.7%
ECO101188	KPN303462	95%	100%	100%
ECO101188	LPN101508	44%	66.9%	91.7%
ECO101188	LMO100466	27%	91.2%	66.8%
ECO101188	MCA101098	64%	98.6%	96.9%
ECO101188	NGO101001	71%	95.1%	96.4%
ECO101188	NME201359	71%	95.1%	96.4%
ECO101188	PMU100558	80%	99.6%	99.6%
ECO101188	PRT101058	89%	100%	100%
ECO101188	PAE203634	68%	99.6%	100%
ECO101188	PPU107961	73%	95.1%	96.4%
ECO101188	PSY104331	66%	99.6%	100%
ECO101188	SPA103128	93%	99.3%	100%
ECO101188	STY101650	93%	99.3%	99.3%
ECO101188	SAU801737	26%	74.3%	55.1%
ECO101188	SEP202083	26%	74.3%	55.1%
ECO101188	SHA100400	26%	74.3%	74.6%
ECO101188	SPY201217	26%	76.1%	81.2%
ECO101188	VCH102142	80%	98.9%	99.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101188	YPS003280	90%	100%	100%
ECO101196	BMA100869	53%	97.4%	3.7%
ECO101196	CTR200330	21%	73.9%	66.2%
ECO101196	EBC100127	84%	47.5%	100%
ECO101196	ECO101196	100%	100%	100%
ECO101196	KPN303485	86%	99.1%	99.4%
ECO101196	MCA101703	51%	95.7%	4.4%
ECO101196	MBV104795	41%	96.5%	93.3%
ECO101196	MLP100509	35%	95.7%	85.7%
ECO101196	MTU200266	41%	96.5%	93.3%
ECO101196	PRT102088	77%	100%	100%
ECO101196	PAE203873	60%	97.2%	96.2%
ECO101196	SPA103125	79%	99.8%	100%
ECO101196	STY102957	94%	99.8%	99.4%
ECO101197	BAN101011	41%	97.4%	98.8%
ECO101197	BAN102461	51%	99.0%	99.5%
ECO101197	BMA109820	66%	99.8%	94.4%
ECO101197	EBC101930	94%	56.9%	100%
ECO101197	ECO101197	100%	100%	100%
ECO101197	KPN200831	93%	100%	100%
ECO101197	MCA101683	69%	99.6%	99.3%
ECO101197	MAV100250	46%	98.4%	95.9%
ECO101197	PRT105206	79%	99.4%	99.0%
ECO101197	PAE203872	70%	99.0%	98.4%
ECO101197	STY102963	95%	100%	100%
ECO101197	SAU802397	49%	98.2%	99.3%
ECO101197	SEP202550	49%	98.2%	99.3%
ECO101197	SHA101605	50%	98.2%	99.3%
ECO101203	ABA105151	41%	95.4%	94.8%
ECO101203	BPT101640	39%	97.1%	97.2%
ECO101203	BCE105517	38%	97.1%	95.3%
ECO101203	BFU103387	41%	97.1%	82.8%
ECO101203	BMA109464	39%	97.1%	96.9%
ECO101203	CJU100729	52%	97.1%	98.5%
ECO101203	EBC100441	91%	85%	99.6%
ECO101203	ECO101203	100%	100%	100%
ECO101203	HIN101555	72%	98.9%	99.6%
ECO101203	HPY101413	44%	97.1%	98.3%
ECO101203	KPN300907	95%	100%	100%
ECO101203	MBV102042	40%	95.4%	88.1%
ECO101203	MTU202926	40%	95.4%	88.1%
ECO101203	PMU100873	73%	98.9%	99.6%
ECO101203	PRT105372	83%	98.6%	97.9%
ECO101203	PAE204312	43%	95.4%	96.1%
ECO101203	PPU103326	42%	95.4%	96.1%
ECO101203	PSY106080	42%	95.4%	96.1%
ECO101203	SPA100447	95%	100%	100%
ECO101203	STY102981	96%	100%	100%
ECO101203	STM101443	96%	100%	100%
ECO101203	VCH101962	72%	98.9%	100%
ECO101204	ABA103927	36%	98.7%	96.8%
ECO101204	BPT102324	44%	61.8%	96.7%
ECO101204	BCE100650	40%	78.3%	95.2%
ECO101204	BFU112636	38%	80.9%	88.6%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101204	BMA106301	40%	80.9%	88%
ECO101204	CDP102030	35%	34.9%	93.1%
ECO101204	EBC100442	76%	100%	100%
ECO101204	ECO101204	100%	100%	100%
ECO101204	HIN100264	37%	96.7%	90.7%
ECO101204	KPN300906	77%	78.3%	100%
ECO101204	LPN100121	40%	96.1%	96.9%
ECO101204	MCA100478	40%	78.9%	98.4%
ECO101204	NGO103687	43%	97.4%	91.3%
ECO101204	NME301805	40%	79.6%	94.5%
ECO101204	PMU101617	35%	99.3%	95.5%
ECO101204	PRT105076	55%	98.7%	93.3%
ECO101204	PAE201038	42%	96.7%	94.3%
ECO101204	PPU109585	43%	96.7%	92.5%
ECO101204	PSY105223	44%	98.0%	95.5%
ECO101204	SPA100448	78%	73.0%	100%
ECO101204	STM101441	78%	100%	100%
ECO101204	VCH101822	45%	96.7%	98.7%
ECO101204	YPS000756	53%	100%	100%
ECO101207	ABA100162	55%	95.7%	98.6%
ECO101207	BAN111872	47%	96.4%	99.3%
ECO101207	BAN109040	47%	96.4%	97.6%
ECO101207	BPT102489	47%	92.4%	97.8%
ECO101207	BBU100206	32%	88.7%	92.1%
ECO101207	BCE105937	51%	95.4%	95.6%
ECO101207	BFU111093	50%	88.7%	98.9%
ECO101207	BFU109685	53%	95.4%	96.2%
ECO101207	BFU101657	53%	97.4%	98.3%
ECO101207	BMA104769	54%	95.4%	96.2%
ECO101207	CJU101445	41%	88.7%	96.0%
ECO101207	CAC100976	43%	95.0%	97.6%
ECO101207	CAC101984	45%	95.4%	92.7%
ECO101207	CBO100817	46%	96.0%	87.3%
ECO101207	CDF100364	42%	97.4%	91.4%
ECO101207	CDF100059	45%	97.0%	87.7%
ECO101207	CDP100145	35%	79.1%	94.8%
ECO101207	EBC100908	92%	100%	100%
ECO101207	EFA201011	45%	91.7%	90.6%
ECO101207	EFM201430	44%	95.4%	95.9%
ECO101207	ECO101207	100%	100%	100%
ECO101207	HIN100792	73%	94.7%	97.6%
ECO101207	HPY100638	41%	90.1%	97.8%
ECO101207	KPN300622	94%	97.7%	100%
ECO101207	LMO100023	42%	91.7%	93.1%
ECO101207	MCA101061	49%	92.4%	97.3%
ECO101207	MAV101486	38%	97.4%	96.7%
ECO101207	MBV100622	38%	96.0%	95.4%
ECO101207	MLP100129	38%	96.0%	94.4%
ECO101207	MTU200982	38%	96.0%	95.4%
ECO101207	MGE100462	40%	90.1%	91.4%
ECO101207	MPN100175	43%	89.1%	91.1%
ECO101207	NGO100830	50%	95.7%	97.6%
ECO101207	NME200784	49%	95.7%	97.6%
ECO101207	PMU101289	73%	95.0%	98.0%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101207	PRT105513	76%	97.7%	98.7%
ECO101207	PAE202021	43%	88.7%	94.3%
ECO101207	PPU110452	42%	88.7%	94.3%
ECO101207	PSY105455	44%	88.7%	94.3%
ECO101207	SPA100524	89%	82.5%	100%
ECO101207	STY102987	97%	100%	100%
ECO101207	SAU802500	44%	95.7%	97.9%
ECO101207	SEP201007	46%	96.0%	98.3%
ECO101207	SHA101112	43%	96.0%	98.3%
ECO101207	SMU100644	45%	96.0%	93.8%
ECO101207	SPN401900	43%	96.4%	96.3%
ECO101207	SPY201685	43%	95.7%	94.1%
ECO101207	SPY200163	44%	95.7%	95.7%
ECO101207	TPA100106	35%	17.9%	10.3%
ECO101207	VCH100390	42%	88.7%	90.0%
ECO101207	YPS002957	73%	96.7%	99.3%
ECO101221	ABA100441	23%	38.6%	52.6%
ECO101221	BAN113211	22%	49.2%	66.3%
ECO101221	BAN103300	25%	53.5%	64.4%
ECO101221	BFR100072	27%	27.1%	40.1%
ECO101221	BPT100842	39%	88.2%	92.2%
ECO101221	BCE108130	36%	89.9%	94.6%
ECO101221	BFU104983	25%	19.7%	28.1%
ECO101221	BMA108356	24%	52.0%	67.2%
ECO101221	CTR100599	25%	31.7%	51.6%
ECO101221	CAC102036	32%	24.2%	38.7%
ECO101221	CDF102584	29%	28.5%	29.1%
ECO101221	CDP100971	24%	50.6%	58.3%
ECO101221	EBC101263	27%	42.0%	68.0%
ECO101221	EFA202691	27%	29.5%	82.7%
ECO101221	ECO101221	100%	100%	100%
ECO101221	HPY100485	21%	51.8%	57.9%
ECO101221	KPN301638	24%	46.3%	72.9%
ECO101221	LMO101830	34%	13.2%	23.5%
ECO101221	MCA101345	26%	47.2%	67.6%
ECO101221	MAV103284	28%	40.5%	28.4%
ECO101221	PRT102456	34%	89.0%	98.9%
ECO101221	PAE201495	26%	48.7%	72.8%
ECO101221	PPU107172	27%	25.2%	38.2%
ECO101221	PSY100737	24%	66.4%	79.5%
ECO101221	SPA103428	31%	24.2%	53.7%
ECO101221	STY103008	26%	48.0%	77.7%
ECO101221	STM105235	23%	39.8%	47.2%
ECO101221	UUR100580	23%	38.1%	34.3%
ECO101221	VCH102929	33%	24.0%	36.8%
ECO101221	YPS001416	37%	89.7%	94.6%
ECO101224	ABA100364	47%	100%	92.1%
ECO101224	BAN102628	31%	84.1%	69.2%
ECO101224	BAN101664	31%	87.1%	65.3%
ECO101224	BAN103900	32%	84.1%	64.3%
ECO101224	BPT102004	43%	94.7%	91.2%
ECO101224	BCE115180	43%	97.0%	92.6%
ECO101224	BFU110989	42%	98.5%	97.7%
ECO101224	BMA108472	44%	93.9%	89.1%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101224	CJU100845	41%	93.2%	89.8%
ECO101224	CPN200091	30%	81.1%	67.1%
ECO101224	CTR200811	30%	84.1%	67.9%
ECO101224	EBC101093	89%	90.2%	96.7%
ECO101224	EFA200335	29%	82.6%	59.6%
ECO101224	ECO101224	100%	100%	100%
ECO101224	HEN100807	69%	93.9%	80.5%
ECO101224	HPY100877	27%	90.2%	66.1%
ECO101224	KPN302777	84%	100%	100%
ECO101224	LPN100109	53%	93.2%	95.2%
ECO101224	LMO100599	30%	90.9%	68.6%
ECO101224	MCA103553	31%	96.2%	67.8%
ECO101224	NGO100300	60%	94.7%	85.1%
ECO101224	NME201034	60%	94.7%	85.1%
ECO101224	PMU100328	73%	93.9%	84.4%
ECO101224	PRT100747	74%	98.5%	90.9%
ECO101224	PAE205366	43%	93.9%	90.3%
ECO101224	PPU102253	44%	93.9%	91.7%
ECO101224	PSY103255	46%	93.2%	90.2%
ECO101224	SPA103418	90%	100%	100%
ECO101224	STY103013	90%	100%	99.2%
ECO101224	STM101403	90%	100%	99.2%
ECO101224	SAU801878	32%	84.1%	61.4%
ECO101224	SEP200517	34%	84.1%	61.4%
ECO101224	SHA100418	33%	84.1%	61.0%
ECO101224	VCH101673	63%	97.7%	88.4%
ECO101224	YPS000842	82%	94.7%	83.9%
ECO101225	ABA100372	31%	98.9%	99.5%
ECO101225	BPT100713	43%	98.9%	95.2%
ECO101225	BCE113703	45%	70.9%	100%
ECO101225	BFU101346	44%	98.3%	100%
ECO101225	BMA103282	42%	98.3%	84.6%
ECO101225	CAC101842	33%	38.0%	22.6%
ECO101225	CDF100727	35%	21.8%	11.5%
ECO101225	EBC101094	93%	99.4%	99.4%
ECO101225	ECO101225	100%	100%	100%
ECO101225	HIN100806	46%	98.3%	95.1%
ECO101225	KPN301102	93%	98.9%	98.9%
ECO101225	LPN103351	42%	98.3%	97.2%
ECO101225	MCA100772	30%	89.9%	87.7%
ECO101225	NGO101561	35%	98.9%	100%
ECO101225	NME201982	37%	98.9%	100%
ECO101225	PMU100329	51%	97.8%	96.2%
ECO101225	PRT100746	56%	98.9%	82.0%
ECO101225	PAB203199	44%	98.9%	96.4%
ECO101225	PPU112224	43%	96.6%	94.4%
ECO101225	PSY107398	44%	96.6%	93.9%
ECO101225	SPA103416	92%	100%	100%
ECO101225	STY103014	93%	100%	100%
ECO101225	STM101401	93%	100%	100%
ECO101225	SEP202595	22%	63.1%	59.1%
ECO101225	VCH101672	60%	99.4%	97.8%
ECO101225	YPS000845	75%	99.4%	98.9%
ECO101227	ABA104132	26%	95.3%	90.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101227	BPT102085	46%	97.2%	93.9%
ECO101227	BCE113475	27%	98.6%	93.7%
ECO101227	BFU105556	34%	97.2%	95.4%
ECO101227	BMA104685	37%	97.2%	92.5%
ECO101227	EBC101097	78%	100%	100%
ECO101227	ECO101227	100%	100%	100%
ECO101227	KPN301099	80%	100%	100%
ECO101227	PMU100331	46%	100%	100%
ECO101227	PRT100743	56%	100%	100%
ECO101227	PAE204064	44%	98.6%	97.8%
ECO101227	PPU108105	44%	99.5%	99.1%
ECO101227	PSY102225	46%	99.1%	97.4%
ECO101227	SPA103429	88%	100%	100%
ECO101227	STY103017	88%	100%	100%
ECO101227	VCH103587	53%	99.1%	99.5%
ECO101227	YPS000864	58%	100%	100%
ECO101232	ABA101674	31%	49.1%	97.1%
ECO101232	ABA101271	54%	96.2%	93.4%
ECO101232	BAN112775	46%	95.7%	96.2%
ECO101232	BAN112641	55%	95.7%	95.7%
ECO101232	BFR12098	50%	95.5%	96.7%
ECO101232	BPT100787	52%	95.7%	95.2%
ECO101232	BCE106968	55%	95.7%	95.7%
ECO101232	BFU106334	56%	95.7%	95.7%
ECO101232	BMA105225	56%	95.7%	90.0%
ECO101232	CJU100317	51%	97.0%	97.7%
ECO101232	CTR100786	54%	94.0%	95.2%
ECO101232	CAC100088	55%	96.5%	97.2%
ECO101232	CDP101544	56%	98.0%	79.4%
ECO101232	CDP101563	65%	99.5%	90.7%
ECO101232	EBC101417	94%	98.0%	100%
ECO101232	ECO101232	100%	100%	100%
ECO101232	HIN101397	82%	98.0%	98.0%
ECO101232	HPY101261	66%	97.0%	97.7%
ECO101232	KPN301482	94%	100%	100%
ECO101232	LPN101519	55%	95.7%	95.2%
ECO101232	LMO100726	52%	98.0%	97.2%
ECO101232	MCA100829	55%	96.5%	94.8%
ECO101232	MAV106589	55%	95.5%	89.4%
ECO101232	MBV101736	55%	94.5%	91.5%
ECO101232	MLP100789	55%	94.0%	89.4%
ECO101232	MTU201591	55%	94.5%	91.5%
ECO101232	NGO101060	55%	95.7%	95.2%
ECO101232	NME200836	54%	95.7%	95.2%
ECO101232	PMU100578	78%	99.0%	97.8%
ECO101232	PRT101792	85%	99.0%	99.2%
ECO101232	PAE200036	55%	95.5%	94.3%
ECO101232	PPU102955	54%	98.0%	96.0%
ECO101232	PSY101235	54%	97.7%	94.9%
ECO101232	SPA103415	95%	99.0%	100%
ECO101232	STY103023	96%	100%	100%
ECO101232	STM101376	96%	100%	100%
ECO101232	SAU801372	49%	97.7%	95.8%
ECO101232	SEP202063	52%	98.0%	96.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101232	SHA101692	50%	98.0%	96.3%
ECO101232	SMU100051	53%	97.5%	96.3%
ECO101232	SPN401630	52%	97.2%	95.1%
ECO101232	SPY100159	56%	41.8%	94.9%
ECO101232	VCH101151	81%	99.0%	99.2%
ECO101232	YPS000868	90%	99.5%	99.7%
ECO101233	ABA100546	40%	53.2%	91.8%
ECO101233	BAN104627	30%	75.9%	85.2%
ECO101233	BAN101920	33%	85.7%	96.6%
ECO101233	BFR11333	37%	53.0%	90.4%
ECO101233	BPT101671	40%	55.8%	99.6%
ECO101233	BCE110367	38%	53.6%	95.8%
ECO101233	BFU102502	39%	53.9%	96.2%
ECO101233	BMA104977	38%	55.6%	99.2%
ECO101233	CJU100463	39%	44.8%	79.5%
ECO101233	CTR200595	28%	42.6%	95.2%
ECO101233	CAC101913	40%	53.4%	94.3%
ECO101233	CDP101556	40%	99.8%	97.7%
ECO101233	EBC101418	84%	99.8%	100%
ECO101233	ECO101233	100%	100%	100%
ECO101233	HIN101357	55%	98.7%	96.9%
ECO101233	HPY101262	46%	99.8%	100%
ECO101233	KPN300203	87%	22.5%	100%
ECO101233	KPN301483	81%	99.8%	100%
ECO101233	LPN102878	38%	55.8%	99.2%
ECO101233	LMO102173	36%	52.5%	93.3%
ECO101233	MCA102336	34%	55.4%	96.7%
ECO101233	MAV106588	39%	45.9%	77.2%
ECO101233	MBV101739	35%	54.5%	89.0%
ECO101233	MLP100788	39%	45.9%	77.2%
ECO101233	MTU201590	35%	54.5%	92.3%
ECO101233	NGO101889	41%	55.6%	99.6%
ECO101233	NME202047	41%	55.6%	99.6%
ECO101233	PMU100580	51%	98.9%	98.7%
ECO101233	PRT101793	60%	98.9%	98.0%
ECO101233	PAE200650	40%	56.1%	94.6%
ECO101233	PPU107434	38%	56.1%	94.9%
ECO101233	PSY107999	40%	41.7%	95.0%
ECO101233	SPA102154	86%	99.1%	100%
ECO101233	STY103024	87%	99.8%	100%
ECO101233	STM101373	87%	99.8%	100%
ECO101233	SAU801370	36%	53.6%	94.2%
ECO101233	SEP202061	36%	56.3%	98.1%
ECO101233	SHA101691	34%	53.6%	94.2%
ECO101233	SMU100047	34%	52.1%	94.5%
ECO101233	SPN401632	37%	55.8%	98.0%
ECO101233	VCH101152	60%	99.8%	96.8%
ECO101233	YPS000870	72%	99.6%	94.9%
ECO101239	BCE115057	59%	3.5%	39.3%
ECO101239	ECO101239	100%	100%	100%
ECO101239	MBV101177	58%	4.4%	9.7%
ECO101239	YPS002265	27%	95.7%	93.4%
ECO101256	ABA105014	34%	63.7%	62.1%
ECO101256	BAN100800	32%	11.6%	92.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101256	BAN110296	30%	33.0%	51.7%
ECO101256	BAN110043	38%	30.9%	95.8%
ECO101256	BAN109795	27%	65.8%	53.1%
ECO101256	BAN104356	28%	65.2%	49.2%
ECO101256	BAN100401	30%	65.8%	93.8%
ECO101256	BAN101643	27%	90.6%	68.6%
ECO101256	BAN113748	33%	65.5%	62.7%
ECO101256	BAN106855	35%	56.9%	96.2%
ECO101256	BAN101846	30%	83.5%	62.4%
ECO101256	BAN106371	36%	64.1%	52.7%
ECO101256	BCE106179	53%	98.8%	98.4%
ECO101256	BFU111465	56%	98.8%	89.7%
ECO101256	BMA100349	37%	62.3%	52.9%
ECO101256	CAC102781	30%	63.8%	55.2%
ECO101256	CBO102943	34%	66.0%	48.8%
ECO101256	CDF103324	31%	6.2%	83.7%
ECO101256	CDF102742	27%	27.5%	21.6%
ECO101256	CDF101314	29%	28.3%	32.2%
ECO101256	CDF101143	27%	33.6%	73.6%
ECO101256	CDF103236	32%	23.3%	30.3%
ECO101256	CDF102708	23%	39.9%	48.0%
ECO101256	CDF102082	30%	28.3%	22.5%
ECO101256	CDF102872	31%	31.0%	18.2%
ECO101256	CDF103636	30%	32.7%	17.9%
ECO101256	CDF104338	27%	22.2%	18.3%
ECO101256	CDF104477	26%	63.5%	68.5%
ECO101256	CDF100533	26%	64.3%	69.8%
ECO101256	CDF101308	27%	63.7%	57.8%
ECO101256	CDF102441	27%	63.5%	82.5%
ECO101256	CDF101353	27%	64.1%	83.1%
ECO101256	CDF104196	28%	65.1%	57.3%
ECO101256	CDF101484	28%	64.6%	57.7%
ECO101256	CDF104553	28%	63.8%	57.8%
ECO101256	CDF104427	31%	63.7%	56.8%
ECO101256	CDF103374	28%	64.4%	56.5%
ECO101256	CDF102134	30%	63.5%	82.1%
ECO101256	CDF101213	28%	66.4%	45.3%
ECO101256	EBC101287	79%	99.1%	98.9%
ECO101256	ECO101256	100%	100%	100%
ECO101256	KPN303278	33%	81.1%	96.9%
ECO101256	LPN100768	45%	14.2%	87.9%
ECO101256	LPN101593	31%	28.4%	37.3%
ECO101256	LPN101435	25%	64.1%	80.3%
ECO101256	LPN102855	31%	83.4%	65.9%
ECO101256	LPN101338	34%	80.9%	70.3%
ECO101256	LPN101049	39%	63.4%	53.4%
ECO101256	LPN100036	37%	66.3%	80.8%
ECO101256	MAV105530	34%	64.0%	69.2%
ECO101256	MBV103119	32%	63.7%	68.2%
ECO101256	MLP101071	33%	64.0%	68.2%
ECO101256	MTU201337	32%	63.7%	68.2%
ECO101256	PAE204599	36%	83.7%	40.1%
ECO101256	PPU109748	37%	83.2%	44.5%
ECO101256	PSY104256	39%	44.9%	96.1%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101256	PSY105293	35%	91.2%	48.8%
ECO101256	SPA104345	84%	82.5%	97.5%
ECO101256	STY103069	79%	99.4%	98.9%
ECO101256	STM101295	79%	99.4%	98.9%
ECO101256	VCH100646	40%	63.4%	62.0%
ECO101256	YPS001063	36%	65.2%	54.8%
ECO101257	EBC100780	87%	75.2%	97.8%
ECO101257	ECO101257	100%	100%	100%
ECO101257	HIN101697	49%	99.2%	99.2%
ECO101257	KPN300505	87%	20.7%	86.9%
ECO101257	KPN301047	89%	76.7%	100%
ECO101257	PMU100181	47%	99.2%	99.4%
ECO101257	PRT101542	69%	99.8%	100%
ECO101257	SPA104347	64%	100%	100%
ECO101257	STY103071	90%	100%	100%
ECO101257	STM101292	90%	100%	100%
ECO101257	VCH103525	53%	99.7%	95.7%
ECO101257	YPS001621	74%	100%	100%
ECO101258	BCE111288	28%	24.7%	61.7%
ECO101258	BFU111198	28%	72.3%	57.1%
ECO101258	EBC101482	45%	97.5%	100%
ECO101258	ECO101258	100%	100%	100%
ECO101258	KPN301048	53%	94.0%	100%
ECO101258	PSY105711	29%	24.7%	63.0%
ECO101258	SPA104349	53%	94.3%	100%
ECO101258	STY103073	55%	70.3%	94.1%
ECO101258	STM101289	50%	80.8%	100%
ECO101258	YPS002921	37%	76.6%	73.7%
ECO101259	ABA105845	65%	98.1%	89.6%
ECO101259	BAN111495	32%	96.6%	98.1%
ECO101259	BAN110931	47%	96.6%	99.2%
ECO101259	BFR102480	27%	96.9%	87.1%
ECO101259	BPT101515	64%	96.2%	96.9%
ECO101259	BFU100534	65%	96.2%	95.8%
ECO101259	BMA108591	63%	96.2%	95.8%
ECO101259	CJU101319	47%	98.1%	93.4%
ECO101259	CPN200344	29%	95.4%	94.3%
ECO101259	CTR200374	32%	70.2%	61.4%
ECO101259	EBC101481	95%	100%	100%
ECO101259	EFA201890	47%	94.7%	98%
ECO101259	ECO101259	100%	100%	100%
ECO101259	HIN101698	75%	98.9%	87.8%
ECO101259	HPY100192	45%	100%	94.9%
ECO101259	KPN301049	89%	100%	100%
ECO101259	LPN103417	57%	98.9%	97.4%
ECO101259	LMO102350	45%	95.4%	97.3%
ECO101259	MCA100281	57%	97.3%	95.3%
ECO101259	MAV103640	33%	95.8%	97.8%
ECO101259	MBV101416	33%	95.0%	97.0%
ECO101259	MLP101099	32%	95.8%	97.8%
ECO101259	MTU201463	33%	95.0%	97.0%
ECO101259	NGO101585	60%	98.1%	98.9%
ECO101259	NME201989	61%	98.1%	98.9%
ECO101259	PMU100182	81%	99.2%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101259	PRT101421	86%	100%	100%
ECO101259	PAE201805	69%	99.2%	99.2%
ECO101259	PSY103929	70%	99.2%	99.6%
ECO101259	SPA104351	80%	100%	100%
ECO101259	STY103075	98%	100%	100%
ECO101259	STM101286	97%	100%	100%
ECO101259	SAU801011	44%	94.7%	97.3%
ECO101259	SEP200257	44%	94.7%	97.3%
ECO101259	SHA100265	56%	43.5%	94.2%
ECO101261	EBC101285	93%	100%	100%
ECO101261	ECO101261	100%	100%	100%
ECO101261	HIN101608	49%	98.5%	98.1%
ECO101261	KPN301207	92%	99.6%	99.3%
ECO101261	PMU100915	53%	97.0%	98.1%
ECO101261	PRT104263	71%	99.6%	99.3%
ECO101261	SPA104355	97%	100%	100%
ECO101261	STY103077	97%	100%	100%
ECO101261	STM101280	97%	100%	100%
ECO101261	VCH101656	58%	96.6%	98.9%
ECO101261	YPS002920	82%	99.6%	98.5%
ECO101298	ABA100361	28%	38.4%	38.9%
ECO101298	ABA100173	24%	69.7%	68.4%
ECO101298	BAN107308	40%	24.5%	90.9%
ECO101298	BFR11511	35%	91.6%	79.2%
ECO101298	BPT102123	26%	70.6%	74.7%
ECO101298	BCE113494	32%	18.7%	15.6%
ECO101298	BFU100516	38%	86.8%	100%
ECO101298	EBC101778	34%	92.6%	83.6%
ECO101298	EFM201682	32%	99.4%	94.1%
ECO101298	ECO101298	100%	100%	100%
ECO101298	KPN301258	34%	92.3%	93.4%
ECO101298	LPN102062	26%	26.8%	37.8%
ECO101298	LPN101639	29%	27.1%	38.2%
ECO101298	PMU101361	29%	42.9%	21.4%
ECO101298	PRT104467	29%	23.2%	21.5%
ECO101298	PAE202216	34%	98.1%	81.7%
ECO101298	PSY104382	34%	97.4%	88.6%
ECO101298	SMU100781	33%	32.3%	23.2%
ECO101298	YPS003214	36%	93.9%	80.4%
ECO101307	BFR12135	31%	93.3%	98.8%
ECO101307	CDF101113	36%	94.9%	97.8%
ECO101307	CDF103684	38%	94.9%	94.4%
ECO101307	CDP101707	34%	88.4%	98.3%
ECO101307	EBC100434	86%	77.3%	100%
ECO101307	ECO101307	100%	100%	100%
ECO101307	KPN304537	87%	99.6%	100%
ECO101307	MCA101881	38%	98.6%	94.7%
ECO101307	NGO100614	38%	96.5%	97.1%
ECO101307	NME201822	38%	96.9%	97.5%
ECO101307	PMU101104	39%	97.8%	98.3%
ECO101307	PRT100243	38%	94.9%	96.5%
ECO101307	SAU802473	35%	94.9%	95.3%
ECO101307	SHA101725	36%	98.4%	98.6%
ECO101307	VCH100864	38%	94.9%	93.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101307	YPS001074	33%	96.9%	96.9%
ECO101308	BAN111842	26%	16.6%	52.3%
ECO101308	BAN109593	38%	42.8%	90.5%
ECO101308	BAN105036	29%	95.2%	96.8%
ECO101308	CAC101783	26%	59.5%	68.9%
ECO101308	CBO102190	25%	62.0%	70.8%
ECO101308	CDF101708	37%	97.1%	98.3%
ECO101308	CDF101472	37%	96.0%	97.8%
ECO101308	CDF103674	42%	95.8%	98.5%
ECO101308	EBC100570	81%	90.9%	99.5%
ECO101308	EFM202575	30%	94.4%	95.1%
ECO101308	ECO101308	100%	100%	100%
ECO101308	KPN308729	85%	5.6%	67.5%
ECO101308	KPN300134	75%	28.3%	100%
ECO101308	KPN304546	75%	100%	100%
ECO101308	MAV100227	32%	57.0%	63.5%
ECO101308	MBV100846	28%	70.1%	79.2%
ECO101308	MTU203263	28%	70.1%	79.2%
ECO101308	SAU802133	33%	57.4%	66.0%
ECO101308	SEP201928	33%	57.4%	66.0%
ECO101308	SHA101910	33%	57.4%	66.0%
ECO101314	BPT102886	51%	99.8%	98.9%
ECO101314	BFU107954	52%	99.1%	97.2%
ECO101314	BMA103404	55%	99.6%	98.1%
ECO101314	EBC100501	90%	46.8%	100%
ECO101314	ECO101314	100%	100%	100%
ECO101314	KPN302014	86%	100%	100%
ECO101314	LPN103227	51%	96.3%	94.7%
ECO101314	PRT105211	73%	100%	100%
ECO101314	PAE200454	56%	99.6%	99.3%
ECO101314	PPU109266	54%	99.6%	92.3%
ECO101314	PSY100041	55%	99.6%	99.3%
ECO101314	SPA102108	87%	100%	100%
ECO101314	VCH102527	54%	99.6%	99.1%
ECO101314	YPS001287	68%	99.8%	99.3%
ECO101324	ECO101324	100%	100%	100%
ECO101328	ABA104605	34%	69.4%	83.1%
ECO101328	BPT102482	56%	52.0%	60.2%
ECO101328	ECO101328	100%	100%	100%
ECO101328	KPN307048	31%	64.3%	81.8%
ECO101328	MCA102180	29%	65.3%	84.2%
ECO101328	NGO102451	41%	64.3%	81.6%
ECO101328	PRT100612	67%	68.4%	84.8%
ECO101328	PPU112131	29%	63.3%	92.5%
ECO101328	SPA104405	40%	48.0%	74.2%
ECO101329	EBC100838	43%	47.1%	50.4%
ECO101329	ECO101329	100%	100%	100%
ECO101329	KPN200238	34%	67.9%	53.4%
ECO101329	STY102208	95%	100%	100%
ECO101333	BCE106664	33%	50.5%	17.1%
ECO101333	BMA103588	40%	50.5%	7.2%
ECO101333	ECO100546	93%	98.0%	64.7%
ECO101333	ECO101333	100%	100%	100%
ECO101333	KPN201795	50%	75.2%	88.2%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101333	PRT102245	37%	98.0%	64.1%
ECO101333	PRT104707	37%	99.0%	64.7%
ECO101333	PRT105949	38%	99.0%	64.7%
ECO101333	SPA104286	48%	100%	65.4%
ECO101333	STM103352	70%	98.0%	63.5%
ECO101333	STM102620	70%	100%	64.0%
ECO101333	YPS000024	47%	100%	67.1%
ECO101334	ABA105243	24%	82.1%	89.2%
ECO101334	BAN113435	21%	61.0%	70.9%
ECO101334	BAN113076	23%	83.7%	92.9%
ECO101334	BFR100347	33%	98.8%	95.8%
ECO101334	BFR102868	35%	86.4%	94.6%
ECO101334	BPT100811	36%	97.7%	98.2%
ECO101334	BBU100723	23%	83.9%	92.1%
ECO101334	CJU101207	22%	85.8%	95.3%
ECO101334	CBO100061	32%	97.3%	97.7%
ECO101334	CDF103152	19%	82.1%	88.4%
ECO101334	CDP100542	21%	80.2%	89.9%
ECO101334	EBC102781	70%	100%	97.4%
ECO101334	EFA201649	23%	87.0%	94.3%
ECO101334	EFM201563	22%	77.1%	38.4%
ECO101334	ECO101334	100%	100%	100%
ECO101334	LMO100586	22%	81.9%	92.1%
ECO101334	NGO100874	37%	98.1%	98.6%
ECO101334	NME200795	37%	98.1%	98.6%
ECO101334	PAE203208	31%	98.8%	98.8%
ECO101334	PPU101061	31%	98.8%	98.8%
ECO101334	PSY103115	32%	99.8%	99.8%
ECO101334	SAU801024	23%	83.5%	92.7%
ECO101334	SEP200277	24%	83.3%	92.7%
ECO101334	SHA101419	23%	83.3%	92.7%
ECO101334	SPN400426	31%	99.6%	99.4%
ECO101334	TPA100139	22%	87.8%	76.7%
ECO101343	ABA104282	20%	26.2%	80.9%
ECO101343	ABA104487	32%	28.0%	16.2%
ECO101343	ABA100799	29%	27.8%	45.6%
ECO101343	BAN107557	30%	10.8%	20.4%
ECO101343	BFR100872	29%	21.7%	28.0%
ECO101343	BPT103725	27%	32.9%	31.6%
ECO101343	BCE109890	24%	15.5%	43.7%
ECO101343	BCE107896	24%	89.1%	70.4%
ECO101343	BCE102461	25%	34.8%	100%
ECO101343	BCE112211	23%	93.2%	17.9%
ECO101343	BCE114917	26%	88.1%	18.9%
ECO101343	BFU105204	30%	3.6%	79.7%
ECO101343	BFU106847	34%	78.8%	43.2%
ECO101343	CPN201044	23%	19.0%	91.4%
ECO101343	CTR200857	24%	40.2%	75.5%
ECO101343	CAC102338	20%	82.9%	47.3%
ECO101343	CDP100418	27%	18.6%	64.0%
ECO101343	EFA203174	23%	79.6%	24.6%
ECO101343	EFM201322	22%	79.3%	24.4%
ECO101343	ECO101343	100%	100%	100%
ECO101343	HPY101160	19%	22.5%	39.2%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101343	HPY101140	23%	14.3%	46.6%
ECO101343	HPY100077	21%	32.4%	45.2%
ECO101343	KPN104916	21%	30.4%	49.9%
ECO101343	LPN101461	22%	13.4%	57.9%
ECO101343	LMO102167	22%	40.6%	56.8%
ECO101343	MAV103075	29%	13.0%	86.5%
ECO101343	MAV103280	27%	11.1%	42.6%
ECO101343	MAV103843	26%	25.7%	26.8%
ECO101343	MAV105169	23%	34.5%	27.8%
ECO101343	MAV103659	27%	29.5%	46.2%
ECO101343	MBV103797	23%	31.8%	82.7%
ECO101343	MTU201261	24%	35.9%	6.7%
ECO101343	MPN100430	22%	12.4%	18.9%
ECO101343	NGO102691	28%	31.4%	73.1%
ECO101343	NME102710	26%	25.9%	89.9%
ECO101343	PAE205248	29%	17.4%	88.4%
ECO101343	PSY101251	30%	11.1%	90.6%
ECO101343	STM102646	49%	50.4%	39.7%
ECO101343	STM103396	49%	95.6%	41.1%
ECO101343	SAU802654	20%	85.1%	14.3%
ECO101343	SEP201799	21%	35.7%	41.8%
ECO101343	SHA102148	25%	84.5%	31.9%
ECO101343	SHA103225	27%	86.2%	42.0%
ECO101343	SMU101323	21%	34.3%	24.9%
ECO101343	SPN301653	37%	41.4%	6.5%
ECO101343	SPY101502	29%	22.4%	59.1%
ECO101343	TPA100721	22%	31.0%	68.6%
ECO101346	ECO101515	98%	100%	100%
ECO101346	ECO101346	100%	100%	100%
ECO101347	BAN105621	28%	85.7%	94.7%
ECO101347	BCE100831	29%	86.9%	97.3%
ECO101347	BFU108387	28%	90.5%	92.1%
ECO101347	CBO102953	30%	44.6%	58.1%
ECO101347	CDF103746	27%	83.9%	96.3%
ECO101347	CDP100748	24%	82.7%	96.3%
ECO101347	EBC101954	62%	85.7%	100%
ECO101347	EFA201536	26%	82.1%	96.5%
ECO101347	ECO101347	100%	100%	100%
ECO101347	KPN302017	76%	85.7%	100%
ECO101347	LPN102113	32%	73.2%	87.9%
ECO101347	LPN100657	31%	85.7%	96.5%
ECO101347	MAV106572	26%	83.9%	94.6%
ECO101347	MLP100860	27%	83.9%	94.6%
ECO101347	PRT100566	42%	85.7%	100%
ECO101347	PRT101051	42%	85.7%	100%
ECO101347	SPA101820	80%	70.2%	100%
ECO101347	STY103689	90%	85.7%	100%
ECO101347	STM100915	90%	85.7%	100%
ECO101347	SPN401808	27%	94.6%	93.6%
ECO101347	VCH100423	29%	85.7%	97.9%
ECO101348	BPT102493	24%	67.9%	67.9%
ECO101348	BCE113692	23%	92.3%	91.1%
ECO101348	BMA103136	23%	92.3%	84.7%
ECO101348	EBC102812	65%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101348	EBC101129	83%	81.2%	100%
ECO101348	ECO101348	100%	100%	100%
ECO101348	KPN302018	76%	100%	100%
ECO101348	MCA101727	24%	91.2%	86.6%
ECO101348	NME301914	23%	76.4%	74.6%
ECO101348	PMU100389	22%	91.5%	91.7%
ECO101348	PMU100388	22%	100%	100%
ECO101348	PRT100163	57%	100%	100%
ECO101348	PAE202698	33%	26.5%	27.1%
ECO101348	SPA103439	79%	100%	100%
ECO101348	STY100529	80%	100%	100%
ECO101348	STM102581	68%	100%	100%
ECO101348	VCH103726	24%	100%	100%
ECO101348	VCH100621	26%	100%	97.4%
ECO101348	YPS002089	62%	100%	99.7%
ECO101355	ABA104145	25%	98.7%	98.4%
ECO101355	BCE111853	27%	89.0%	86.8%
ECO101355	BFU102407	26%	84.1%	84.4%
ECO101355	BMA105038	29%	78.1%	74.9%
ECO101355	EBC101162	64%	97.7%	97.4%
ECO101355	ECO101355	100%	100%	100%
ECO101355	KPN300181	59%	47.8%	100%
ECO101355	KPN304960	64%	97.3%	96.7%
ECO101355	LMO102225	28%	74.4%	30%
ECO101355	PAE204067	28%	96.7%	95.6%
ECO101355	PPU110142	24%	84.4%	81.8%
ECO101355	PSY108507	23%	68.4%	68.3%
ECO101365	ABA104344	60%	98.5%	98.1%
ECO101365	BPT100507	60%	98.5%	98.1%
ECO101365	BCE112553	58%	95.8%	94.7%
ECO101365	BFU102518	59%	95.4%	94.3%
ECO101365	BMA109462	58%	95.4%	94.3%
ECO101365	EBC100355	80%	51.1%	100%
ECO101365	ECO101365	100%	100%	100%
ECO101365	KPN306385	84%	100%	100%
ECO101365	MCA101046	31%	67.9%	72.5%
ECO101365	MAV100851	36%	98.5%	96.9%
ECO101365	MAV101794	37%	95.0%	95.2%
ECO101365	MAV101174	40%	96.6%	96.4%
ECO101365	MBV101674	35%	95.8%	92.2%
ECO101365	MTU201127	35%	95.8%	92.2%
ECO101365	PAE204975	37%	97.7%	97.0%
ECO101365	PPU111662	61%	99.2%	98.9%
ECO101365	SMU100553	34%	98.5%	98.1%
ECO101365	SPN400375	34%	99.6%	100%
ECO101365	SPY201354	30%	98.5%	98.1%
ECO101366	ABA103707	45%	96.4%	94.1%
ECO101366	BAN102785	35%	97.5%	93.7%
ECO101366	BAN107403	41%	97.5%	93.3%
ECO101366	BPT102322	45%	54.9%	95.6%
ECO101366	BCE107218	42%	97.1%	92.3%
ECO101366	BFU100415	49%	98.7%	70.3%
ECO101366	CAC103282	44%	97.1%	92.9%
ECO101366	CBO103696	41%	96%	91.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101366	CDF100453	41%	96%	91.5%
ECO101366	EBC100356	79%	98.5%	78.0%
ECO101366	ECO101366	100%	100%	100%
ECO101366	KPN305008	72%	99.8%	93.8%
ECO101366	MAV101275	41%	98.5%	90.6%
ECO101366	MBV104755	41%	98.5%	94.1%
ECO101366	MLP101467	42%	98.5%	93.7%
ECO101366	MTU200466	41%	98.5%	94.1%
ECO101366	PAE201627	38%	99.2%	53.2%
ECO101366	PAE203588	39%	98.1%	96.7%
ECO101366	PPU111663	47%	97.3%	96.8%
ECO101366	SEP200029	23%	64.2%	97.8%
ECO101369	ABA102526	65%	97.9%	97.5%
ECO101369	BFR101369	46%	95.4%	98.6%
ECO101369	BFR10873	50%	97.7%	99.1%
ECO101369	BPT100503	66%	97.5%	97.5%
ECO101369	BCE113086	65%	98.9%	99.5%
ECO101369	BFU102520	66%	98.9%	99.1%
ECO101369	BMA105289	64%	98.9%	99.5%
ECO101369	EBC101022	92%	87.9%	100%
ECO101369	EFM101677	21%	84.9%	79.3%
ECO101369	ECO101369	100%	100%	100%
ECO101369	KPN305001	94%	99.5%	99.3%
ECO101369	PPU111666	68%	97.5%	97.3%
ECO101369	PSY108977	24%	69.8%	75%
ECO101369	VCH100908	25%	71.4%	66.8%
ECO101370	ABA104199	38%	98.1%	97.2%
ECO101370	BPT101079	35%	95.6%	97.7%
ECO101370	EBC102965	87%	100%	100%
ECO101370	ECO101370	100%	100%	100%
ECO101370	KPN304998	81%	100%	100%
ECO101370	LMO101698	21%	58.2%	22.4%
ECO101370	MBV100825	29%	68.0%	77.9%
ECO101370	MTU200671	29%	68.0%	77.9%
ECO101370	PPU106601	43%	96.2%	98.7%
ECO101372	ABA104065	23%	45.1%	64.9%
ECO101372	BAN113185	26%	25.5%	92.0%
ECO101372	BAN100006	23%	49.1%	79.5%
ECO101372	BFR102947	26%	2.2%	14.3%
ECO101372	BFR100205	23%	30.0%	20.4%
ECO101372	BFR101444	24%	12.6%	36.8%
ECO101372	BMA107841	25%	16.8%	71.9%
ECO101372	CPN100435	21%	39.7%	46.7%
ECO101372	CPN100431	19%	46.5%	43.6%
ECO101372	CPN100014	21%	51.5%	32.6%
ECO101372	CPN100432	22%	39.8%	56.6%
ECO101372	CPN100430	22%	75.6%	18.2%
ECO101372	CTR200684	20%	53.8%	62.2%
ECO101372	CTR200685	20%	73.7%	49.5%
ECO101372	CAC102754	22%	56.1%	48.8%
ECO101372	CBO102489	20%	16.2%	56.1%
ECO101372	EBC101205	24%	72.5%	6.5%
ECO101372	EBC100399	24%	15.4%	93.9%
ECO101372	EBC100820	22%	57.5%	74.2%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101372	EBC100805	22%	41.5%	99.4%
ECO101372	EFM200844	25%	68.9%	21.2%
ECO101372	ECO101372	100%	100%	100%
ECO101372	HIN100251	24%	13.0%	54.1%
ECO101372	MCA100348	21%	87.1%	47.6%
ECO101372	MAV103822	28%	15.1%	32.3%
ECO101372	MBV100578	26%	52.3%	43.6%
ECO101372	MTU201447	23%	33.0%	65.1%
ECO101372	MTU201785	25%	19.7%	42.8%
ECO101372	MTU200277	24%	40.7%	36.1%
ECO101372	MTU200968	24%	51.5%	14.3%
ECO101372	MTU201737	22%	51.6%	39.2%
ECO101372	MTU202128	22%	52.6%	44.9%
ECO101372	MTU200529	25%	33.3%	52.2%
ECO101372	MTU200124	22%	32.0%	67.8%
ECO101372	MTU200296	24%	51.6%	11.3%
ECO101372	MTU200278	24%	52.5%	70.7%
ECO101372	MTU202704	26%	46.4%	75.8%
ECO101372	MTU201308	23%	68.8%	36.3%
ECO101372	MTU203538	23%	26.4%	54.6%
ECO101372	MTU203543	23%	15.4%	68.3%
ECO101372	MTU201807	24%	35.1%	70.1%
ECO101372	MTU202597	23%	46.4%	17.0%
ECO101372	MTU201422	25%	10.0%	67.6%
ECO101372	MTU201746	24%	48.6%	49.2%
ECO101372	MTU201377	26%	46.6%	39.8%
ECO101372	MTU201630	24%	11.0%	57.9%
ECO101372	MTU201226	25%	41.0%	71.4%
ECO101372	MTU202578	24%	45.0%	46.0%
ECO101372	MTU203301	27%	31.0%	89.3%
ECO101372	MTU201056	24%	14.9%	46.6%
ECO101372	MTU203322	23%	50.8%	24.7%
ECO101372	MTU202451	24%	48.6%	60.7%
ECO101372	MTU200863	26%	49.9%	43.4%
ECO101372	MTU201774	26%	51.2%	33.5%
ECO101372	MTU200575	25%	30.4%	38.7%
ECO101372	MTU203460	25%	24.9%	57.9%
ECO101372	MTU202815	26%	52.3%	35.8%
ECO101372	NGO101218	19%	52.9%	70.0%
ECO101372	NME101006	21%	34.4%	23.9%
ECO101372	NME103369	22%	46.0%	31.0%
ECO101372	NME102132	20%	68.8%	20.2%
ECO101372	PMU100714	23%	76.4%	18.8%
ECO101372	PAE204623	21%	80.0%	51.7%
ECO101372	SPA103182	34%	40.5%	96.6%
ECO101372	SMU101300	20%	77.0%	55.8%
ECO101372	SPN102747	26%	37.1%	31.4%
ECO101372	SPN103543	25%	51.2%	60%
ECO101372	SPY103363	27%	59.4%	26.6%
ECO101372	VCH103569	23%	43.4%	10.6%
ECO101376	BFR101740	26%	12.1%	13.1%
ECO101376	BMA108003	22%	23.8%	89.9%
ECO101376	CJU101583	20%	76.6%	45.8%
ECO101376	CJU100590	24%	24.7%	77.2%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101376	CDF102290	21%	49.7%	63.8%
ECO101376	ECO101376	100%	100%	100%
ECO101376	HPY101226	23%	30.2%	42.2%
ECO101376	HPY100602	22%	57.5%	14.7%
ECO101376	HPY100603	21%	26.6%	20.7%
ECO101376	HPY100285	20%	48.4%	29.7%
ECO101376	HPY100906	24%	36.1%	14.1%
ECO101376	KPN305340	21%	1.7%	95.3%
ECO101376	MBV101505	24%	32.6%	67.3%
ECO101376	NME301139	19%	20.1%	38.5%
ECO101376	NME300455	21%	61.8%	14.8%
ECO101376	NME301662	21%	67.6%	15.6%
ECO101376	PRT101929	20%	62.5%	52.5%
ECO101376	PSY108622	24%	4.9%	94.9%
ECO101376	PSY106453	22%	59.3%	55.8%
ECO101376	SPA103183	51%	74.2%	92.9%
ECO101376	STM102835	47%	37.9%	26.8%
ECO101376	SPY201103	21%	25.4%	41.8%
ECO101376	VCH101430	21%	76.2%	19.6%
ECO101378	ABA106017	25%	18.1%	55.6%
ECO101378	CAC102021	32%	10.3%	42.4%
ECO101378	ECO100384	43%	10.3%	84.9%
ECO101378	ECO101378	100%	100%	100%
ECO101381	ABA102855	26%	42.1%	72.8%
ECO101381	BCE109833	53%	61.0%	90.9%
ECO101381	BFU102061	26%	45.5%	88.4%
ECO101381	BMA109995	25%	43.6%	85.5%
ECO101381	EFA202448	22%	46.8%	98.7%
ECO101381	ECO101381	100%	100%	100%
ECO101381	MAV102145	24%	46.5%	97.5%
ECO101381	MBV102643	24%	46.5%	96.8%
ECO101381	MLP101539	25%	44.4%	92.5%
ECO101381	MTU200182	24%	46.5%	83.6%
ECO101381	PAE202538	56%	97.3%	97.8%
ECO101381	PSY103261	56%	97.6%	98.3%
ECO101381	SHA100260	20%	43.1%	91.3%
ECO101381	YPS002556	65%	99.3%	99.0%
ECO101382	BAN102413	28%	42.3%	81.4%
ECO101382	BCE107754	37%	80.7%	98.1%
ECO101382	CAC103685	25%	42.1%	82.2%
ECO101382	CBO103233	22%	38.4%	74.2%
ECO101382	ECO101382	100%	100%	100%
ECO101382	PAE202537	41%	97.2%	95.0%
ECO101382	PSY108146	39%	97.2%	89.7%
ECO101382	YPS002537	49%	96.5%	92.3%
ECO101393	BPT100171	27%	77.7%	85.1%
ECO101393	BCE100512	39%	77.1%	90.4%
ECO101393	BFU101107	41%	85.0%	89.6%
ECO101393	BMA103090	37%	46.0%	71.3%
ECO101393	BMA101500	39%	84.5%	91.2%
ECO101393	EBC103166	78%	96.3%	100%
ECO101393	ECO101393	100%	100%	100%
ECO101393	KPN307476	80%	96.0%	100%
ECO101393	PAE200152	36%	75.4%	97.1%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101393	PPU107994	41%	77.1%	88.1%
ECO101393	PSY102576	34%	82.8%	94.5%
ECO101393	SPA103480	26%	82.8%	92.7%
ECO101393	STY104247	28%	79.9%	94.0%
ECO101393	STM100853	83%	86.4%	99.7%
ECO101393	YPS001640	27%	85.6%	85.9%
ECO101400	ABA104283	22%	87.9%	84.6%
ECO101400	BFU107308	38%	93.0%	90.0%
ECO101400	CBO100793	18%	80%	84.8%
ECO101400	CDF101725	23%	67.9%	71.3%
ECO101400	CDP100861	21%	87.0%	93.4%
ECO101400	EFA201740	17%	64.2%	63.4%
ECO101400	ECO101400	100%	100%	100%
ECO101400	HIN100490	38%	96.1%	95.7%
ECO101400	KPN304048	77%	98.2%	100%
ECO101400	NME301505	42%	96.4%	100%
ECO101400	PMU101587	43%	95.8%	99.1%
ECO101400	PSY102817	23%	90%	88.1%
ECO101400	SPA103397	84%	99.4%	100%
ECO101400	STY103732	87%	99.4%	97.3%
ECO101400	SPY200689	21%	77.6%	81.1%
ECO101400	VCH103249	23%	90.6%	90.6%
ECO101400	VCH102289	20%	94.5%	96.9%
ECO101403	BAN110650	28%	67.7%	98.2%
ECO101403	BAN102654	29%	94.0%	98.9%
ECO101403	CDF104202	37%	19.9%	84.5%
ECO101403	CDF102535	35%	26.1%	85.8%
ECO101403	CDF103887	35%	52.5%	97.1%
ECO101403	CDF100871	34%	76.6%	95.2%
ECO101403	CDF103297	32%	92.0%	96.2%
ECO101403	CDF101218	33%	92.0%	96.2%
ECO101403	CDF103939	33%	92.0%	96.2%
ECO101403	CDF100573	33%	92.0%	96.2%
ECO101403	CDF101412	33%	92.0%	96.2%
ECO101403	CDF100312	33%	92.0%	96.2%
ECO101403	CDF103189	34%	92.0%	96.2%
ECO101403	EFA200364	25%	87.1%	96.6%
ECO101403	EFM201897	23%	80.1%	91.4%
ECO101403	EFM201232	32%	93.0%	96.9%
ECO101403	ECO101403	100%	100%	100%
ECO101403	HPY100981	30%	91.3%	83.4%
ECO101403	HPY100434	30%	91.3%	83.4%
ECO101403	HPY100973	30%	91.3%	83.4%
ECO101403	HPY101512	30%	91.3%	83.4%
ECO101403	HPY101078	30%	91.3%	83.4%
ECO101403	KPN204073	83%	99.5%	100%
ECO101403	MCA103372	28%	55.5%	97.5%
ECO101403	MBV101240	26%	97.3%	91.7%
ECO101403	MTU203772	25%	79.6%	85.3%
ECO101403	MTU202753	26%	97.3%	91.7%
ECO101403	NME102130	56%	56.0%	100%
ECO101403	PRT106097	80%	11.4%	100%
ECO101403	PRT104808	89%	31.6%	96.9%
ECO101403	PRT103046	80%	53.7%	99.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101403	PRT105185	83%	90.8%	100%
ECO101403	PRT102105	82%	94.8%	99.7%
ECO101403	PRT102853	82%	99.8%	97.8%
ECO101403	PRT105904	83%	99.3%	99.3%
ECO101403	PRT105312	82%	99.8%	97.8%
ECO101403	PRT101071	83%	99.8%	99.8%
ECO101403	SPA101059	64%	97.0%	100%
ECO101403	STY101241	64%	96.0%	97.3%
ECO101403	STM101920	35%	95.5%	88.5%
ECO101406	BFR11829	46%	92.4%	99.3%
ECO101406	CAC101457	32%	37.3%	96.6%
ECO101406	CBO101154	33%	73.8%	61.3%
ECO101406	CDF100070	37%	16.8%	97.5%
ECO101406	CDF103927	32%	38.4%	96.1%
ECO101406	EBC107301	89%	97.6%	99.5%
ECO101406	ECO101406	100%	100%	100%
ECO101406	KPN300274	91%	25.5%	92.9%
ECO101406	KPN308666	87%	97.3%	99.2%
ECO101406	KPN300541	93%	6.9%	63.0%
ECO101406	KPN300422	87%	16.3%	87.9%
ECO101406	KPN300254	71%	29.8%	100%
ECO101406	PPU102549	69%	97.6%	98.5%
ECO101406	PSY104961	69%	97.6%	99.6%
ECO101406	SPA103388	87%	100%	100%
ECO101406	STY103739	92%	97.2%	99.1%
ECO101421	ABA104573	24%	81.2%	88.2%
ECO101421	BPT102546	35%	68.8%	67.6%
ECO101421	BCE112411	28%	86.2%	82.3%
ECO101421	EBC100706	46%	89.2%	95.5%
ECO101421	EFA200682	25%	83.8%	86.1%
ECO101421	ECO101421	100%	100%	100%
ECO101421	KPN301120	28%	54.2%	54.6%
ECO101421	MAV108571	26%	80%	83.5%
ECO101421	MBV102645	25%	55%	49.8%
ECO101421	MTU200164	25%	55%	50%
ECO101421	PAE205520	29%	77.9%	75.2%
ECO101421	SPA101753	52%	70.4%	100%
ECO101421	STY103774	58%	91.2%	99.1%
ECO101421	YPS003104	25%	89.6%	96.8%
ECO101423	BCE102082	23%	69.7%	83.9%
ECO101423	BFU111349	23%	42.8%	58.5%
ECO101423	BMA105152	24%	65.7%	66.7%
ECO101423	CDF104423	19%	70.0%	94.4%
ECO101423	EBC100616	77%	100%	100%
ECO101423	ECO101423	100%	100%	100%
ECO101423	KPN304022	77%	100%	100%
ECO101423	MAV103258	30%	26.9%	83.5%
ECO101423	MBV100019	26%	31.4%	66.9%
ECO101423	MTU202185	23%	50.7%	73.2%
ECO101423	PAE200518	39%	12.2%	7.6%
ECO101423	PAE200515	20%	93.2%	86.2%
ECO101423	PPU105397	21%	95.8%	24.0%
ECO101423	PSY102870	32%	21.2%	22.1%
ECO101423	SPA101751	88%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101423	STY103776	89%	100%	100%
ECO101436	BAN103501	28%	60.6%	87.3%
ECO101436	BAN110205	34%	97.8%	96.5%
ECO101436	BMA101276	47%	99.6%	100%
ECO101436	CDP101662	29%	97.3%	86.1%
ECO101436	ECO101436	100%	100%	100%
ECO101436	KPN300233	87%	31.4%	100%
ECO101436	KPN305071	82%	100%	100%
ECO101436	MCA101686	48%	98.7%	95.7%
ECO101436	MAV100393	34%	98.2%	92.2%
ECO101436	MBV101203	34%	96.0%	52.8%
ECO101436	PAE203869	52%	97.8%	97.8%
ECO101436	SPA102906	95%	100%	100%
ECO101436	STY103788	96%	100%	100%
ECO101436	STM100371	96%	100%	100%
ECO101436	SAU802394	37%	98.2%	99.1%
ECO101436	SEP200989	39%	98.2%	99.1%
ECO101436	SHA103168	32%	84.5%	100%
ECO101438	BAN111998	37%	88.9%	99.1%
ECO101438	BAN110721	60%	94.0%	98.4%
ECO101438	CDP101667	55%	90.3%	87.6%
ECO101438	ECO101438	100%	100%	100%
ECO101438	KPN305069	88%	100%	100%
ECO101438	MCA101684	74%	94.9%	95.3%
ECO101438	MAV100251	60%	28.6%	100%
ECO101438	MAV100389	57%	94.4%	89.9%
ECO101438	MBV101453	56%	94.0%	87.5%
ECO101438	MTU201147	56%	94.0%	87.5%
ECO101438	PAE203871	73%	99.0%	100%
ECO101438	SPA102908	89%	98.2%	100%
ECO101438	STY103792	94%	100%	100%
ECO101438	STM100369	94%	100%	100%
ECO101444	ABA105622	35%	99.7%	96.0%
ECO101444	ABA100551	45%	99.0%	96.0%
ECO101444	BCE108394	51%	44.0%	99.2%
ECO101444	EBC101738	74%	93.2%	100%
ECO101444	EFM201176	24%	44.7%	37.9%
ECO101444	ECO101444	100%	100%	100%
ECO101444	HPY200933	32%	22.2%	15.0%
ECO101444	KPN305038	75%	99.7%	100%
ECO101444	PRT102506	51%	98.3%	99.3%
ECO101444	SPA102630	85%	99.7%	100%
ECO101444	STM100351	85%	93.2%	99.6%
ECO101444	VCH103555	44%	98.0%	87.5%
ECO101444	YPS000836	41%	97.3%	96.7%
ECO101452	EBC100834	77%	77.2%	100%
ECO101452	ECO101452	100%	100%	100%
ECO101452	SPA100470	88%	77.2%	100%
ECO101452	STY104204	88%	77.2%	100%
ECO101452	STM100342	88%	77.2%	100%
ECO101455	EBC100261	79%	84.8%	100%
ECO101455	ECO101455	100%	100%	100%
ECO101458	BPT100319	28%	92.4%	94.5%
ECO101458	BCE110600	29%	100%	93.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101458	BFU103600	29%	96.3%	96.1%
ECO101458	BMA103798	30%	98.4%	98.7%
ECO101458	EBC100975	85%	97.1%	99.6%
ECO101458	ECO101458	100%	100%	100%
ECO101458	KPN102930	31%	66.1%	97.8%
ECO101458	MLP100689	22%	87.4%	83.8%
ECO101459	BFR10990	32%	86.0%	72.3%
ECO101459	BCE111976	49%	87.6%	90.4%
ECO101459	BFU103598	50%	92.2%	87.7%
ECO101459	BFU113321	50%	91.2%	94.1%
ECO101459	BMA105422	50%	90.2%	92.1%
ECO101459	EBC100976	77%	95.3%	96.3%
ECO101459	EFA200947	34%	77.2%	84.2%
ECO101459	ECO101459	100%	100%	100%
ECO101459	LPN101358	36%	35.8%	32.3%
ECO101459	MAV100337	30%	85.0%	76.7%
ECO101459	MBV101864	34%	84.5%	86.3%
ECO101459	MTU200829	34%	85.5%	69.9%
ECO101459	PAE105948	31%	59.1%	56.5%
ECO101459	SPA103398	33%	35.2%	69.6%
ECO101459	STY103754	28%	84.5%	80.9%
ECO101467	BCE109104	32%	84.0%	92.9%
ECO101467	BFU111125	28%	94.5%	89.2%
ECO101467	BFU102927	33%	96.3%	88.9%
ECO101467	BMA106486	33%	96.3%	91.3%
ECO101467	ECO101467	100%	100%	100%
ECO101467	HIN101436	29%	94.7%	89.8%
ECO101467	HIN100035	31%	95.2%	91.2%
ECO101467	MAV102866	29%	91.8%	85.0%
ECO101467	MBV103266	27%	98.6%	94.2%
ECO101467	MLP101262	29%	91.8%	85.1%
ECO101467	MTU201786	27%	98.6%	91.4%
ECO101467	NGO102937	23%	37.4%	93.4%
ECO101467	NME100881	33%	31.7%	93.4%
ECO101467	PMU100041	35%	97.0%	96.6%
ECO101467	PRT105836	35%	97.3%	100%
ECO101467	PPU111319	33%	91.4%	94.6%
ECO101467	PSY104758	34%	91.1%	95.0%
ECO101468	BAN106302	22%	80.8%	84.9%
ECO101468	BFU107652	24%	43.6%	41.5%
ECO101468	BMA110009	25%	43.6%	39.6%
ECO101468	CAC100511	30%	43.1%	32.4%
ECO101468	CBO101042	24%	81.5%	68.4%
ECO101468	CDF100503	25%	82.6%	69.3%
ECO101468	EFM200472	30%	93.1%	95.0%
ECO101468	ECO101468	100%	100%	100%
ECO101468	PMU100600	45%	92.6%	95.0%
ECO101468	PAE200510	21%	81.0%	81.7%
ECO101468	YPS000797	65%	98.2%	97.7%
ECO101475	BFU103224	31%	89.8%	44.5%
ECO101475	ECO101475	100%	100%	100%
ECO101476	BFR100408	21%	45.0%	25.7%
ECO101476	EFM103220	44%	12.6%	28.7%
ECO101476	ECO101476	100%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101480	BAN100201	29%	21.5%	10.3%
ECO101480	CDF100113	68%	6.9%	100%
ECO101480	ECO101480	100%	100%	100%
ECO101480	NGO100287	28%	69.7%	99.0%
ECO101480	NME202012	31%	68.9%	48.6%
ECO101480	NME201584	28%	69.7%	48.4%
ECO101480	PMU101717	35%	96.6%	48.8%
ECO101480	SPA104198	46%	99.4%	65.4%
ECO101480	STM100045	46%	99.4%	52.8%
ECO101480	YPS001070	47%	99.8%	11.8%
ECO101482	BAN101903	43%	19.8%	100%
ECO101482	BAN103207	48%	90.4%	98.0%
ECO101482	BAN113148	53%	97.4%	100%
ECO101482	EBC102576	78%	87.4%	89.9%
ECO101482	ECO101482	100%	100%	100%
ECO101482	KPN303693	79%	84.7%	86.5%
ECO101482	PMU101272	71%	98.3%	99.8%
ECO101482	SPA102584	84%	66.6%	100%
ECO101482	STY103182	83%	100%	100%
ECO101482	TPA100292	30%	20.4%	25.8%
ECO101482	YPS000064	78%	100%	100%
ECO101485	BAN104164	43%	87.4%	97.4%
ECO101485	BAN100431	45%	87.4%	94.3%
ECO101485	BFU112884	35%	92.1%	90.9%
ECO101485	EBC103772	67%	90.4%	99.7%
ECO101485	ECO101485	100%	100%	100%
ECO101485	KPN305506	45%	12.3%	76.1%
ECO101485	KPN300172	56%	31.6%	93.5%
ECO101485	KPN300355	61%	38.9%	89.3%
ECO101485	KPN308245	67%	94.2%	100%
ECO101485	MCA101148	26%	59.9%	70.0%
ECO101485	MBV101598	24%	72.2%	26.0%
ECO101485	PMU101275	67%	94.7%	97.6%
ECO101485	SPA101836	83%	100%	100%
ECO101485	STY103163	83%	100%	100%
ECO101485	STM101620	83%	100%	100%
ECO101485	SPN200508	28%	73.4%	89.2%
ECO101485	SPY200769	23%	64.6%	78.2%
ECO101485	YPS000060	75%	99.7%	99.7%
ECO101498	ABA104052	34%	24.0%	34.5%
ECO101498	CPN300253	30%	18.3%	40.8%
ECO101498	ECO101498	100%	100%	100%
ECO101499	ABA103825	31%	93.7%	91.6%
ECO101499	CAC101460	25%	93.7%	95.2%
ECO101499	EBC100447	87%	70.2%	99.6%
ECO101499	ECO101499	100%	100%	100%
ECO101499	HIN100128	51%	91.9%	91.9%
ECO101499	HPY101168	50%	95.7%	96.9%
ECO101499	KPN302890	33%	90.7%	86.4%
ECO101499	KPN302908	81%	99.2%	98.5%
ECO101499	MAV104012	28%	91.4%	89.6%
ECO101499	MBV102693	28%	88.9%	91.4%
ECO101499	MTU200190	28%	88.9%	87.2%
ECO101499	NGO102033	50%	92.4%	98.9%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101499	PMU100949	53%	95.2%	93.3%
ECO101499	PRT105535	63%	98.0%	95.1%
ECO101499	PAE204110	58%	99.0%	99.0%
ECO101499	PPU103772	58%	95.2%	94.5%
ECO101499	PSY104435	60%	92.7%	90.2%
ECO101499	SPA103066	87%	99.5%	100%
ECO101499	STY104274	88%	99.5%	99.5%
ECO101499	SAU802452	26%	92.4%	94.9%
ECO101499	SPN203024	32%	23.2%	38.7%
ECO101500	BPT102646	29%	94.1%	82.5%
ECO101500	EBC101127	87%	100%	100%
ECO101500	ECO101500	100%	100%	100%
ECO101500	KPN300463	84%	62.4%	100%
ECO101500	KPN302911	84%	100%	99.5%
ECO101500	PRT103903	64%	96.4%	86.9%
ECO101500	PAE205200	51%	98.2%	94.0%
ECO101500	SPA103077	91%	100%	100%
ECO101500	STY104276	91%	100%	100%
ECO101500	STM100262	91%	100%	100%
ECO101500	YPS003072	74%	99.5%	96.5%
ECO101505	BAN103144	25%	89.9%	87.9%
ECO101505	EBC101122	67%	85.1%	100%
ECO101505	ECO101505	100%	100%	100%
ECO101505	KPN302924	71%	98.5%	97.7%
ECO101505	LPN102440	18%	94.9%	95.2%
ECO101505	LPN100524	19%	95.2%	92.8%
ECO101505	LMO101074	23%	92.9%	93.3%
ECO101505	PRT101718	60%	95.7%	96.2%
ECO101505	PAE201211	21%	95.2%	93.4%
ECO101505	PPU104566	32%	94.7%	95.9%
ECO101505	PSY104789	21%	85.1%	81.3%
ECO101505	SPA103073	68%	38.2%	100%
ECO101505	STY104286	76%	100%	100%
ECO101505	SAU800178	23%	92.9%	94.2%
ECO101505	SEP202208	19%	87.8%	90.1%
ECO101505	VCH103690	23%	92.2%	85.0%
ECO101505	YPS002313	38%	94.2%	96.2%
ECO101506	ABA100836	33%	53.4%	39.0%
ECO101506	ABA104797	34%	57.4%	55.3%
ECO101506	ECO101506	100%	100%	100%
ECO101506	MAV102284	33%	54.7%	45.4%
ECO101513	BMA101585	44%	85.6%	83.1%
ECO101513	EBC103255	80%	99.6%	99.4%
ECO101513	EFM201843	26%	93.0%	89.2%
ECO101513	ECO101513	100%	100%	100%
ECO101513	KPN304564	78%	99.2%	99.0%
ECO101513	MAV105552	38%	97.9%	92.0%
ECO101513	SPA102280	79%	99.6%	99.6%
ECO101513	STY104302	81%	99.6%	99.2%
ECO101513	STM100236	81%	99.6%	99.2%
ECO101515	ECO101346	98%	100%	100%
ECO101515	ECO101515	100%	100%	100%
ECO101524	BPT106030	31%	92.7%	92.4%
ECO101524	ECO101524	100%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101524	PPU111952	28%	77.6%	75.9%
ECO101524	PPU109160	30%	81.2%	76.1%
ECO101524	PSY103499	30%	90.9%	86.0%
ECO101524	PSY104398	29%	89.1%	88.8%
ECO101524	PSY108879	29%	92.7%	91.2%
ECO101524	STY102996	66%	92.7%	85.5%
ECO101525	ECO101525	100%	100%	100%
ECO101525	KPN300756	76%	95.5%	96.0%
ECO101526	ECO101526	100%	100%	100%
ECO101526	LPN102896	22%	84.5%	8.6%
ECO101528	ECO101528	100%	100%	100%
ECO101539	ECO101539	100%	100%	100%
ECO101539	MPN100067	29%	45.8%	43.6%
ECO101540	ECO101540	100%	100%	100%
ECO101567	ABA105948	30%	72.1%	66.7%
ECO101567	BCE110976	34%	70.3%	87.0%
ECO101567	EBC107569	51%	91.9%	100%
ECO101567	ECO101567	100%	100%	100%
ECO101567	KPN307669	63%	91.0%	83.5%
ECO101567	MCA102058	37%	53.2%	31.0%
ECO101567	MBV100531	32%	71.2%	24.2%
ECO101567	MTU202117	32%	71.2%	24.2%
ECO101567	SPA105667	55%	91.9%	100%
ECO101567	STY105056	56%	99.1%	97.8%
ECO101567	STM102133	30%	82.9%	12.5%
ECO101567	YPS004039	52%	91.9%	100%
ECO101568	EBC103462	78%	99.3%	99.3%
ECO101568	EFA200509	22%	79.5%	73.2%
ECO101568	ECO101568	100%	100%	100%
ECO101568	KPN306333	74%	99.3%	99.3%
ECO101568	NME201346	37%	12.8%	11.3%
ECO101568	PSY103969	33%	13.9%	9.4%
ECO101568	SPA101240	77%	99.6%	100%
ECO101568	STY104356	77%	99.6%	99.6%
ECO101568	YPS001910	62%	96.0%	93.5%
ECO101575	ABA103948	53%	94.3%	99.1%
ECO101575	BAN103387	39%	99.3%	98.7%
ECO101575	BAN103848	40%	99.8%	98.1%
ECO101575	BFU104892	47%	98.3%	98.1%
ECO101575	BMA104571	45%	98.9%	91.3%
ECO101575	CPN200806	40%	97.8%	96.3%
ECO101575	CTR200643	40%	98.5%	96.1%
ECO101575	CBO103715	34%	97.4%	96.6%
ECO101575	CDP100879	36%	96.1%	92.8%
ECO101575	EBC102507	85%	50.2%	100%
ECO101575	EFM202049	32%	99.8%	97.9%
ECO101575	EFM200706	34%	99.6%	98.1%
ECO101575	ECO101575	100%	100%	100%
ECO101575	KPN300202	86%	33.5%	85.6%
ECO101575	KPN305499	88%	100%	100%
ECO101575	PMU100162	52%	98.7%	97.4%
ECO101575	PRT103781	69%	99.8%	99.6%
ECO101575	PAE201193	45%	98.9%	97.0%
ECO101575	PPU109535	45%	99.1%	97.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101575	SPA103436	91%	99.6%	100%
ECO101575	STY100523	92%	100%	100%
ECO101575	SAU802633	42%	98.0%	96.0%
ECO101575	SEP201754	41%	93.3%	93.6%
ECO101575	SHA101613	42%	97.6%	95.6%
ECO101575	VCH100428	56%	99.6%	98.9%
ECO101575	YPS001880	75%	99.8%	99.8%
ECO101583	BFR11487	29%	29.7%	41.5%
ECO101583	BBU100406	32%	96.4%	94.9%
ECO101583	CAC102434	23%	34.8%	16.9%
ECO101583	CBO103509	29%	98.7%	93.6%
ECO101583	CDF100717	29%	26.6%	29.9%
ECO101583	CDP100913	37%	98.2%	98.7%
ECO101583	EBC102499	85%	90.8%	99.7%
ECO101583	EFA201620	34%	25.6%	31.0%
ECO101583	EFM200644	32%	25.6%	31.6%
ECO101583	ECO101583	100%	100%	100%
ECO101583	KPN304521	80%	100%	100%
ECO101583	LMO100517	29%	25.3%	29.6%
ECO101583	MAV101383	38%	97.4%	97.1%
ECO101583	MBV104868	37%	99.2%	98.5%
ECO101583	MLP100466	38%	96.2%	95.9%
ECO101583	MTU203212	37%	99.2%	98.5%
ECO101583	PMU100829	35%	95.1%	94.8%
ECO101583	SPA101151	84%	100%	100%
ECO101583	STY100543	86%	100%	100%
ECO101583	SAU802143	32%	22.8%	26.6%
ECO101583	SEP201764	34%	25.6%	31.3%
ECO101583	SHA101234	34%	18.4%	22.3%
ECO101583	SMU101180	33%	24.6%	30.4%
ECO101583	SPN400647	30%	25.8%	32.2%
ECO101583	SPY201392	29%	26.9%	33.1%
ECO101583	VCH100266	46%	98.2%	96.7%
ECO101583	VCH101797	48%	98.7%	99.7%
ECO101583	YPS001750	70%	99.5%	99.5%
ECO101591	BBU100644	40%	97.0%	98.8%
ECO101591	CBO103697	39%	97.7%	98.6%
ECO101591	CDF100635	46%	97.7%	99.4%
ECO101591	EBC102299	44%	87.2%	99.1%
ECO101591	EFA200635	57%	97.0%	97.9%
ECO101591	EFM201316	36%	96.4%	98.4%
ECO101591	ECO101591	100%	100%	100%
ECO101591	KPN304517	86%	19.4%	100%
ECO101591	KPN304985	89%	100%	100%
ECO101591	PMU101752	40%	87.5%	98.2%
ECO101591	PRT105483	34%	95.7%	97.1%
ECO101591	SAU800242	41%	97.4%	99.2%
ECO101591	SPN401527	40%	96.4%	97.5%
ECO101613	BCE110619	42%	78.2%	86.6%
ECO101613	EBC100663	66%	100%	100%
ECO101613	ECO101613	100%	100%	100%
ECO101613	KPN301024	76%	100%	100%
ECO101613	PAE201229	28%	73.1%	81.5%
ECO101613	SPA102319	76%	100%	97.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101613	STY100591	76%	100%	100%
ECO101614	ABA100405	33%	93.6%	97.0%
ECO101614	BCE101176	42%	93.6%	89.1%
ECO101614	BCE115062	45%	93.6%	95.9%
ECO101614	BFU107135	46%	94.6%	97.3%
ECO101614	BMA104937	45%	93.6%	95.2%
ECO101614	EBC100664	77%	85.3%	99.2%
ECO101614	ECO101614	100%	100%	100%
ECO101614	KPN301023	64%	94.3%	99.3%
ECO101614	PAE203302	43%	93.3%	97.9%
ECO101614	PPU103467	45%	93.0%	96.2%
ECO101614	PSY101352	56%	13.0%	88.6%
ECO101614	PSY101350	45%	93.6%	97.6%
ECO101614	SPA102318	84%	95.3%	86.4%
ECO101614	STY100593	84%	96.3%	99.7%
ECO101623	BCE100945	40%	41.9%	84.9%
ECO101623	BFU111464	31%	94.8%	95.2%
ECO101623	BMA100071	39%	57.7%	85.4%
ECO101623	CDP100089	46%	94.7%	99.3%
ECO101623	ECO101623	100%	100%	100%
ECO101623	KPN207289	39%	4.0%	68.8%
ECO101623	KPN201518	25%	38.0%	72.5%
ECO101623	MAV101236	55%	59.5%	99.3%
ECO101623	MBV104588	47%	94.8%	99.5%
ECO101623	MLP100829	21%	24.5%	42.2%
ECO101623	MTU203253	47%	98.9%	99.1%
ECO101623	PAE203270	32%	95.0%	97.3%
ECO101623	PPU101466	31%	93.2%	95.7%
ECO101623	PSY100837	27%	55.1%	94.6%
ECO101628	CAC102213	33%	96.5%	97.6%
ECO101628	EBC100562	93%	72.1%	99.6%
ECO101628	EFA202357	31%	90.6%	92.2%
ECO101628	EFM101435	33%	97.1%	99.1%
ECO101628	ECO101628	100%	100%	100%
ECO101628	HIN101601	55%	97.1%	98.8%
ECO101628	KPN300879	93%	60.7%	95.4%
ECO101628	MBV100614	26%	78.9%	90.9%
ECO101628	MTU203523	27%	89.4%	90.3%
ECO101628	PMU100547	57%	97.1%	98.8%
ECO101628	PRT100632	81%	100%	100%
ECO101628	PPU103881	44%	99.7%	100%
ECO101628	PSY102604	44%	97.4%	97.6%
ECO101628	SPA101415	94%	91.2%	100%
ECO101628	STY100617	95%	100%	100%
ECO101628	SMU101203	29%	97.1%	99.7%
ECO101628	VCH101693	51%	97.7%	98.8%
ECO101628	YPS002950	82%	100%	100%
ECO101635	BAN106226	47%	92.1%	85.3%
ECO101635	BAN102708	46%	96.0%	94.2%
ECO101635	ECO101635	100%	100%	100%
ECO101635	SPA100886	66%	97.0%	83.1%
ECO101635	STY101449	65%	97.0%	95.1%
ECO101635	YPS001944	50%	99.0%	100%
ECO101637	BFR10242	27%	32.2%	41.6%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101637	BPT104008	33%	25.2%	18.5%
ECO101637	CAC101067	23%	48.5%	10.2%
ECO101637	ECO101637	100%	100%	100%
ECO101637	PRT105079	34%	97.8%	93.2%
ECO101656	ABA104107	28%	93.2%	93.3%
ECO101656	BPT104814	27%	92.7%	95.3%
ECO101656	BCE104286	27%	91.4%	92.9%
ECO101656	BFU112633	31%	90.8%	91.6%
ECO101656	BMA103873	29%	90.3%	94.7%
ECO101656	EBC101891	83%	94.3%	99.4%
ECO101656	ECO101656	100%	100%	100%
ECO101656	KPN303003	78%	100%	100%
ECO101656	MCA101759	29%	91.4%	87.2%
ECO101656	PRT102242	56%	97.0%	97.6%
ECO101656	PAE201624	33%	92.7%	97.2%
ECO101656	PPU106275	35%	89.5%	95.1%
ECO101656	PSY105020	36%	90.3%	96.0%
ECO101656	SPA103730	90%	64.3%	99.2%
ECO101656	STY101075	88%	100%	99.5%
ECO101656	VCH100612	26%	91.9%	95.6%
ECO101656	YPS002998	63%	96.5%	97.5%
ECO101669	BFR10371	29%	92.6%	96.6%
ECO101669	BPT100702	28%	89.4%	96.6%
ECO101669	BCE100738	31%	86.7%	93.9%
ECO101669	BFU100216	32%	91.3%	93.4%
ECO101669	ECO101669	100%	100%	100%
ECO101669	MAV105805	27%	89.0%	97.0%
ECO101669	MAV100637	27%	90.3%	98.2%
ECO101669	MAV101497	33%	88.5%	97.6%
ECO101669	MAV101780	32%	93.1%	97.9%
ECO101669	MAV100482	33%	92.4%	96.1%
ECO101669	MAV102258	35%	92.4%	96.8%
ECO101669	MBV101174	32%	86.4%	89.6%
ECO101669	MLP101504	29%	90.5%	91.1%
ECO101669	MTU202468	32%	86.4%	89.6%
ECO101669	SPN400966	23%	59.4%	73.2%
ECO101671	ABA104295	46%	97.5%	96.8%
ECO101671	BAN100578	26%	96.0%	100%
ECO101671	BAN112243	27%	96.8%	97.0%
ECO101671	BPT101147	47%	97.5%	97.8%
ECO101671	BCE112791	46%	97.1%	69.7%
ECO101671	BFU105739	46%	97.1%	98.5%
ECO101671	BMA108973	45%	97.1%	98.5%
ECO101671	CBO100467	27%	93.9%	95.9%
ECO101671	CDF100604	28%	94.6%	92.9%
ECO101671	EBC100597	91%	100%	100%
ECO101671	EFA202131	28%	92.1%	93.7%
ECO101671	EFA200379	32%	97.1%	93.3%
ECO101671	ECO101671	100%	100%	100%
ECO101671	KPN303005	91%	100%	100%
ECO101671	LPN102482	49%	97.5%	99.3%
ECO101671	LMO101177	28%	94.9%	94.9%
ECO101671	MCA103646	47%	97.5%	93.4%
ECO101671	NGO100762	47%	97.1%	98.2%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101671	NME200764	47%	97.1%	98.2%
ECO101671	PRT102244	71%	98.6%	94.8%
ECO101671	PAE201768	49%	97.1%	97.8%
ECO101671	PPU101850	50%	97.1%	98.5%
ECO101671	PSY105558	51%	79.8%	97.8%
ECO101671	SPA101612	97%	100%	100%
ECO101671	STY101082	97%	100%	100%
ECO101671	SAU801563	24%	93.5%	94.9%
ECO101671	SEP201637	28%	94.6%	95.6%
ECO101671	SHA100874	26%	92.1%	91.7%
ECO101671	VCH103704	50%	97.8%	97.5%
ECO101671	YPS003004	80%	98.6%	100%
ECO101675	EBC102496	47%	100%	99.6%
ECO101675	ECO101675	100%	100%	100%
ECO101675	SPA100008	49%	94.1%	100%
ECO101675	STY101099	52%	98.3%	98.3%
ECO101675	STM103463	52%	98.3%	98.3%
ECO101679	BPT102451	41%	97.5%	96.2%
ECO101679	BCE104877	37%	82.8%	78.9%
ECO101679	BFU114351	35%	95.1%	89.1%
ECO101679	BMA102774	38%	96.6%	90.3%
ECO101679	CJU101521	31%	95.4%	95.7%
ECO101679	CPN200459	27%	22.1%	7.7%
ECO101679	CAC100433	32%	95.1%	95.0%
ECO101679	CBO103820	32%	83.7%	77.4%
ECO101679	CBO102965	30%	94.5%	97.0%
ECO101679	CBO103219	36%	84.4%	75.8%
ECO101679	CDF101617	34%	83.4%	81.5%
ECO101679	CDP100773	35%	95.7%	92.3%
ECO101679	EBC102490	75%	100%	100%
ECO101679	ECO101679	100%	100%	100%
ECO101679	HIN101440	33%	95.4%	95.8%
ECO101679	KPN301694	83%	99.4%	98.8%
ECO101679	NGO100092	31%	95.7%	95.7%
ECO101679	NME200420	33%	95.7%	95.7%
ECO101679	PMU101148	36%	86.8%	83.2%
ECO101679	PRT101302	53%	98.2%	93.3%
ECO101679	PAE204703	47%	85.0%	87.5%
ECO101679	PPU100241	41%	94.2%	95.9%
ECO101679	SPA101351	89%	100%	100%
ECO101679	STY101110	91%	100%	100%
ECO101679	STM103452	91%	100%	100%
ECO101679	VCH101225	47%	97.5%	96.1%
ECO101679	YPS003045	68%	99.1%	97.0%
ECO101684	ABA102501	81%	100%	99.2%
ECO101684	BAN104202	39%	96.6%	95.8%
ECO101684	BAN110178	57%	96.6%	96.6%
ECO101684	BFR104064	56%	98.3%	100%
ECO101684	BPT100292	67%	100%	99.2%
ECO101684	BBU100187	47%	93.2%	95.7%
ECO101684	BCE102715	70%	100%	99.2%
ECO101684	BFU102443	71%	100%	99.2%
ECO101684	BMA107401	70%	100%	99.2%
ECO101684	CJU100217	58%	99.2%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101684	CPN200847	43%	99.2%	96.7%
ECO101684	CTR200218	44%	99.2%	95.1%
ECO101684	CAC101951	59%	96.6%	95.8%
ECO101684	CDF102735	56%	100%	100%
ECO101684	CDP100976	58%	99.2%	92.1%
ECO101684	EBC102984	100%	100%	100%
ECO101684	EFA200358	60%	100%	99.2%
ECO101684	EFM201307	60%	100%	99.2%
ECO101684	ECO101684	100%	100%	100%
ECO101684	HIN101286	95%	99.2%	100%
ECO101684	HPY100124	50%	97.5%	99.1%
ECO101684	KPN301692	99%	100%	100%
ECO101684	LPN101410	79%	100%	99.2%
ECO101684	LMO100743	60%	100%	99.2%
ECO101684	MAV106548	60%	99.2%	89.3%
ECO101684	MBV101274	60%	99.2%	90.7%
ECO101684	MLP100866	58%	99.2%	90.7%
ECO101684	MTU201622	60%	99.2%	90.7%
ECO101684	MGE100200	49%	94.9%	90.3%
ECO101684	MPN100037	52%	95.8%	89.0%
ECO101684	NGO101855	79%	100%	99.2%
ECO101684	NME200857	79%	100%	99.2%
ECO101684	PMU100604	96%	99.2%	100%
ECO101684	PRT101306	92%	100%	100%
ECO101684	PAE202739	83%	100%	100%
ECO101684	PPU111376	82%	100%	100%
ECO101684	PSY109131	83%	100%	100%
ECO101684	SPA100657	100%	95.8%	94.2%
ECO101684	STY101118	100%	100%	100%
ECO101684	STM103448	100%	100%	100%
ECO101684	SAU801678	61%	99.2%	99.2%
ECO101684	SEP201662	62%	99.2%	99.2%
ECO101684	SHA100082	61%	99.2%	99.2%
ECO101684	SMU100912	60%	99.2%	98.3%
ECO101684	SPN400863	62%	99.2%	98.3%
ECO101684	SPY200598	61%	99.2%	98.3%
ECO101684	TPA100839	45%	89.0%	86.1%
ECO101684	UUR100231	49%	93.2%	96.7%
ECO101684	VCH103020	89%	99.2%	100%
ECO101684	YPS003061	97%	100%	100%
ECO101685	ABA102503	56%	98.5%	85.1%
ECO101685	BAN113355	59%	83.1%	81.8%
ECO101685	BAN109536	59%	83.1%	81.8%
ECO101685	BFR104500	61%	67.7%	69.8%
ECO101685	BPT100293	52%	100%	100%
ECO101685	BBU100188	46%	95.4%	93.9%
ECO101685	BCE106262	51%	95.4%	100%
ECO101685	BFU102444	51%	95.4%	100%
ECO101685	BMA105698	53%	100%	100%
ECO101685	CJU100216	55%	69.2%	69.8%
ECO101685	CPN200848	40%	87.7%	89.1%
ECO101685	CTR200217	38%	87.7%	89.1%
ECO101685	CAC101588	51%	98.5%	98.5%
ECO101685	CBO102406	51%	98.5%	98.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101685	CDF104095	54%	98.5%	100%
ECO101685	CDP100973	46%	80%	81.2%
ECO101685	EBC102982	92%	100%	100%
ECO101685	EFA203061	51%	83.1%	81.8%
ECO101685	EFM202134	55%	83.1%	81.8%
ECO101685	ECO101685	100%	100%	100%
ECO101685	HIN101285	78%	100%	73.0%
ECO101685	HPY100123	56%	67.7%	67.2%
ECO101685	KPN301691	100%	100%	100%
ECO101685	LPN101798	61%	72.3%	75.8%
ECO101685	LMO101064	55%	83.1%	81.8%
ECO101685	MAV106547	46%	83.1%	84.4%
ECO101685	MBV101273	41%	95.4%	96.9%
ECO101685	MLP100865	44%	83.1%	84.4%
ECO101685	MTU201621	41%	95.4%	96.9%
ECO101685	MGE100199	50%	80%	88.1%
ECO101685	MPN100038	47%	78.5%	86.4%
ECO101685	NGO101853	58%	100%	100%
ECO101685	NME200856	58%	100%	100%
ECO101685	PMU100603	78%	100%	100%
ECO101685	PRT103408	89%	100%	100%
ECO101685	PAE202740	63%	89.2%	89.1%
ECO101685	PPU103712	58%	89.2%	82.6%
ECO101685	PSY107471	56%	89.2%	89.1%
ECO101685	SPA100656	100%	100%	100%
ECO101685	STY101126	100%	100%	100%
ECO101685	STM103447	100%	100%	100%
ECO101685	SAU801679	48%	98.5%	97.0%
ECO101685	SEP201663	50%	98.5%	97.0%
ECO101685	SHA100081	50%	98.5%	97.0%
ECO101685	SMU100910	51%	83.1%	81.8%
ECO101685	SPN400862	48%	95.4%	93.9%
ECO101685	SPY200597	51%	83.1%	83.1%
ECO101685	TPA100840	57%	100%	100%
ECO101685	UUR100230	44%	89.2%	90.6%
ECO101685	VCH103019	61%	100%	100%
ECO101685	YPS003064	89%	100%	100%
ECO101686	ABA102498	61%	62.8%	100%
ECO101686	BAN104142	51%	90.6%	94.7%
ECO101686	BAN107901	53%	90.6%	83.1%
ECO101686	BFR100214	49%	92.8%	83.3%
ECO101686	BPT101959	71%	86.7%	94.5%
ECO101686	BBU100189	44%	92.8%	89.2%
ECO101686	BCE106172	69%	87.2%	100%
ECO101686	BFU107897	66%	87.2%	100%
ECO101686	BMA109299	68%	87.2%	100%
ECO101686	CJU100195	43%	91.1%	94.8%
ECO101686	CPN200849	47%	92.8%	91.9%
ECO101686	CTR200216	47%	92.8%	91.9%
ECO101686	CAC103337	47%	91.1%	93.1%
ECO101686	CBO100172	50%	91.1%	88.6%
ECO101686	CDF100791	48%	77.2%	97.9%
ECO101686	CDP100970	49%	81.1%	98.0%
ECO101686	EBC102980	95%	80%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101686	EFA200363	48%	93.3%	96.5%
ECO101686	EFM200354	44%	47.2%	94.4%
ECO101686	ECO101686	100%	100%	100%
ECO101686	HIN101284	83%	74.4%	99.3%
ECO101686	HPY100122	42%	92.2%	81.3%
ECO101686	KPN301690	97%	80%	100%
ECO101686	LMO102427	50%	90%	94.2%
ECO101686	MCA103235	56%	81.7%	100%
ECO101686	MAV106545	47%	77.8%	80.3%
ECO101686	MBV103903	45%	85%	82.6%
ECO101686	MLP100864	45%	85%	82.2%
ECO101686	MTU201620	46%	91.7%	81.6%
ECO101686	MGE100198	29%	78.3%	75.7%
ECO101686	MPN100039	30%	99.4%	89.1%
ECO101686	NGO101851	66%	86.7%	100%
ECO101686	NME200855	66%	93.9%	97.1%
ECO101686	PMU100602	81%	83.3%	97.4%
ECO101686	PRT100107	88%	62.2%	100%
ECO101686	PAE202741	64%	100%	96.7%
ECO101686	PPU111378	63%	100%	96.7%
ECO101686	PSY102598	64%	100%	100%
ECO101686	SPA100655	97%	100%	100%
ECO101686	STY101129	98%	100%	100%
ECO101686	STM103446	100%	80%	100%
ECO101686	SAU801680	53%	90.6%	94.2%
ECO101686	SEP201664	53%	90.6%	92.6%
ECO101686	SMU100907	51%	90%	80.5%
ECO101686	SPN400861	53%	90%	82.6%
ECO101686	SPY200596	51%	90%	91.5%
ECO101686	TPA100841	45%	92.8%	92.7%
ECO101686	UUR100229	31%	94.4%	96.6%
ECO101686	YPS003067	89%	100%	100%
ECO101687	ABA102500	63%	98.9%	99.1%
ECO101687	BAN104316	43%	98.4%	99.5%
ECO101687	BAN100978	46%	98.4%	98.7%
ECO101687	BFR103141	41%	79.4%	99.2%
ECO101687	BPT101956	56%	98.9%	98.5%
ECO101687	BBU100719	42%	88.2%	97.6%
ECO101687	BCE105528	58%	98.8%	99.7%
ECO101687	BFU105096	58%	98.8%	97.7%
ECO101687	BMA106934	59%	98.8%	99.7%
ECO101687	CJU100194	42%	93.8%	99.2%
ECO101687	CPN201046	40%	91.0%	91.5%
ECO101687	CTR200859	40%	95.6%	96.5%
ECO101687	CAC102528	48%	98.4%	98.9%
ECO101687	CBO100249	48%	98.6%	95.0%
ECO101687	CDF102396	48%	98.4%	93.2%
ECO101687	CDP100262	38%	93.6%	92.1%
ECO101687	EBC102990	94%	100%	100%
ECO101687	EFA200266	41%	98.6%	99.2%
ECO101687	EFM200127	41%	98.6%	99.1%
ECO101687	ECO101687	100%	100%	100%
ECO101687	HIN101333	78%	100%	99.8%
ECO101687	HPY100121	42%	88.6%	92.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101687	KPN300773	94%	96.9%	100%
ECO101687	LPN100924	57%	94.5%	99.7%
ECO101687	LMO102823	42%	98.0%	99.2%
ECO101687	MCA103158	63%	98.9%	99.2%
ECO101687	MAV102514	39%	94.7%	93.1%
ECO101687	MBV100785	40%	88.6%	85.7%
ECO101687	MLP100282	40%	88.6%	85.0%
ECO101687	MTU202577	40%	88.6%	86.3%
ECO101687	MGE100386	29%	86.3%	99.6%
ECO101687	MPN100289	28%	86.3%	98.8%
ECO101687	NGO101849	61%	98.0%	96.8%
ECO101687	NME200854	62%	98.0%	98.4%
ECO101687	PMU100593	79%	100%	99.8%
ECO101687	PRT105628	84%	100%	100%
ECO101687	PAE202742	65%	99.8%	100%
ECO101687	PPU103710	65%	99.8%	100%
ECO101687	PSY102599	65%	99.8%	100%
ECO101687	SPA100654	92%	77.3%	100%
ECO101687	STY101132	97%	100%	100%
ECO101687	STM103445	96%	100%	100%
ECO101687	SAU801683	43%	98.1%	98.4%
ECO101687	SEP201666	42%	98.1%	98.4%
ECO101687	SHA102097	45%	98.8%	97.5%
ECO101687	SMU101079	40%	98.6%	98.6%
ECO101687	SPN401471	41%	98.6%	97.0%
ECO101687	SPY200371	41%	98.6%	98.6%
ECO101687	TPA100828	48%	89.6%	97.5%
ECO101687	UUR100540	36%	87.7%	98.3%
ECO101687	VCH103018	75%	100%	100%
ECO101687	YPS003070	88%	100%	100%
ECO101688	ECO101688	100%	100%	100%
ECO101689	ECO103911	29%	97.7%	76.2%
ECO101689	ECO101689	100%	100%	100%
ECO101689	YPS000041	34%	30.8%	38.5%
ECO101689	YPS001066	29%	55.2%	54.6%
ECO101698	ECO101698	100%	100%	100%
ECO101700	ABA103947	58%	90.6%	96.9%
ECO101700	BAN112207	51%	72.9%	81.5%
ECO101700	BAN103415	54%	90.7%	99.8%
ECO101700	BFR12345	43%	65.5%	99.0%
ECO101700	BPT102828	42%	64.9%	92.3%
ECO101700	BCE114338	42%	11.6%	88.7%
ECO101700	BCE109764	43%	56.6%	82.5%
ECO101700	BFU104726	56%	96.3%	100%
ECO101700	BMA109166	47%	51.1%	74.7%
ECO101700	CJU101309	45%	57.1%	88.0%
ECO101700	EBC102119	86%	98.5%	99.1%
ECO101700	EFA201830	44%	64.4%	98.5%
ECO101700	ECO101700	100%	100%	100%
ECO101700	HIN100907	41%	64.9%	93.9%
ECO101700	HPY100862	43%	64.0%	94.1%
ECO101700	KPN302795	81%	99.1%	99.2%
ECO101700	LMO102038	44%	64.9%	97.5%
ECO101700	MCA101882	40%	64.9%	94.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101700	MAV104721	50%	92.3%	96.9%
ECO101700	NGO100702	41%	65.2%	95.0%
ECO101700	NME200047	42%	65.2%	95.0%
ECO101700	PMU100032	42%	64.1%	97.1%
ECO101700	PRT101830	40%	64.9%	96.2%
ECO101700	PAE202145	59%	91.9%	96.8%
ECO101700	PPU100583	58%	94.2%	99.9%
ECO101700	PSY101358	58%	76.4%	100%
ECO101700	SPA101365	89%	88.8%	100%
ECO101700	STY101168	88%	99.6%	99.7%
ECO101700	SAU801334	39%	65.3%	95.7%
ECO101700	SEP201991	38%	65.3%	96.2%
ECO101700	VCH101561	39%	64.7%	83.1%
ECO101700	YPS000256	42%	65.1%	99.4%
ECO101711	BCE113211	29%	48.4%	31.0%
ECO101711	BFU115576	21%	88.2%	71.8%
ECO101711	BMA101083	20%	80.1%	67.5%
ECO101711	EBC102266	81%	100%	100%
ECO101711	ECO101711	100%	100%	100%
ECO101711	KPN302804	81%	100%	100%
ECO101711	LPN101454	27%	56.5%	69.1%
ECO101711	NGO100202	28%	78.9%	84.0%
ECO101711	NME201292	27%	78.9%	84.0%
ECO101711	PAE203203	34%	90.1%	86.3%
ECO101711	PSY103109	29%	93.8%	89.0%
ECO101711	SPA103118	85%	100%	100%
ECO101711	STY101200	88%	100%	100%
ECO101711	STM103422	89%	100%	100%
ECO101712	ABA104594	44%	98.8%	98.8%
ECO101712	BPT103254	26%	19.6%	19.8%
ECO101712	BCE114029	43%	92.2%	98.1%
ECO101712	BFU112337	46%	98.8%	92.9%
ECO101712	BMA102153	47%	98.8%	92.8%
ECO101712	EBC102265	63%	100%	100%
ECO101712	ECO101712	100%	100%	100%
ECO101712	KPN302783	63%	100%	100%
ECO101712	PAE200900	38%	98.8%	97.6%
ECO101712	PPU101071	38%	98.8%	96.4%
ECO101712	PSY103122	39%	98.8%	96.4%
ECO101712	SPA103117	69%	99.7%	100%
ECO101712	STY101202	70%	99.7%	99.7%
ECO101712	STM103421	70%	99.7%	99.7%
ECO101712	VCH101223	34%	99.4%	94.4%
ECO101712	YPS002643	49%	99.7%	97.6%
ECO101714	ABA105742	68%	98.2%	98.8%
ECO101714	BCE107495	57%	98.4%	99.4%
ECO101714	BFU112434	56%	98.4%	99.0%
ECO101714	BMA105262	55%	98.4%	99.4%
ECO101714	EBC102263	79%	99.8%	52.7%
ECO101714	ECO101714	100%	100%	100%
ECO101714	KPN302790	77%	98.8%	98.8%
ECO101714	LPN101241	50%	97.8%	97.0%
ECO101714	PAE200897	62%	98.2%	99.0%
ECO101714	PPU106933	60%	98.2%	99.2%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101714	PSY103136	60%	98.8%	99.4%
ECO101714	SPA100702	82%	98.6%	100%
ECO101714	STY101206	82%	87.0%	100%
ECO101714	STM103417	83%	99.0%	99.0%
ECO101714	VCH102579	57%	98.6%	99.8%
ECO101714	YPS002625	65%	98.4%	95.8%
ECO101729	ABA105584	71%	98.7%	95.7%
ECO101729	BAN113279	29%	88.1%	89.1%
ECO101729	BAN112245	31%	84.1%	96.8%
ECO101729	BFR11684	56%	98.9%	99.8%
ECO101729	BFR102226	59%	97.8%	98.6%
ECO101729	BPT102499	72%	98.7%	95.3%
ECO101729	BCE100574	34%	79.6%	81.1%
ECO101729	BFU102258	23%	67.1%	85.4%
ECO101729	BMA107852	34%	65.1%	87.3%
ECO101729	CPN200930	20%	70.9%	82.1%
ECO101729	CAC103455	54%	98.2%	99.1%
ECO101729	CBO101019	32%	88.8%	89.7%
ECO101729	CDF101512	32%	88.8%	93.1%
ECO101729	CDP101183	59%	98.7%	98.4%
ECO101729	EBC101589	91%	98.9%	100%
ECO101729	EFA202330	55%	100%	100%
ECO101729	EFM200836	39%	13.0%	82.9%
ECO101729	ECO101729	100%	100%	100%
ECO101729	HIN100179	74%	99.8%	99.8%
ECO101729	HPY100376	57%	98.4%	99.6%
ECO101729	KPN307117	90%	100%	100%
ECO101729	LPN100778	22%	65.5%	71.7%
ECO101729	LMO102007	57%	97.1%	94.8%
ECO101729	MCA100007	54%	98.9%	99.8%
ECO101729	NGO100595	66%	98.2%	99.1%
ECO101729	NME201813	66%	98.2%	99.1%
ECO101729	PMU100043	74%	99.8%	99.8%
ECO101729	PRT101534	82%	100%	100%
ECO101729	PAE204586	65%	99.3%	99.8%
ECO101729	PPU101007	65%	98.9%	98.7%
ECO101729	SPA100748	92%	100%	100%
ECO101729	STY101224	92%	100%	100%
ECO101729	STM101795	33%	80.1%	79.1%
ECO101729	SAU800958	29%	88.6%	93.0%
ECO101729	SEP200164	29%	88.6%	93.0%
ECO101729	SHA100738	37%	18.6%	47.3%
ECO101729	SHA101571	30%	88.6%	92.5%
ECO101729	SMU100896	57%	98.2%	98.0%
ECO101729	SPN401180	55%	98.7%	98.4%
ECO101729	YPS002504	83%	100%	100%
ECO101739	BAN104442	33%	96.0%	97.7%
ECO101739	BAN102029	33%	99.7%	99.7%
ECO101739	BPT100971	32%	98.5%	88.5%
ECO101739	BBU100527	27%	92.0%	88.3%
ECO101739	CDF101932	24%	97.9%	73.7%
ECO101739	EFM202426	36%	96.0%	96.5%
ECO101739	ECO101739	100%	100%	100%
ECO101739	LMO101114	33%	100%	94.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101739	MAV104842	36%	96.0%	92.1%
ECO101739	PAE201126	35%	99.7%	94.8%
ECO101739	SAU800600	33%	97.2%	97.1%
ECO101739	SEP200145	32%	96.0%	95.8%
ECO101739	SHA100813	33%	97.2%	97.4%
ECO101752	BAN103600	24%	80.3%	75.4%
ECO101752	BAN104592	26%	95.8%	93.6%
ECO101752	BPT101378	49%	98.6%	99.5%
ECO101752	BCE113273	54%	97.7%	97.9%
ECO101752	BFU100576	54%	98.6%	98.8%
ECO101752	CJU100856	30%	18.7%	71.8%
ECO101752	CAC102209	28%	95.8%	95.7%
ECO101752	EBC102642	95%	98.8%	100%
ECO101752	ECO101752	100%	100%	100%
ECO101752	KPN300345	94%	32.3%	93.2%
ECO101752	KPN302879	91%	99.8%	99.8%
ECO101752	LPN103620	53%	98.6%	99.5%
ECO101752	PAE200586	58%	98.6%	99.3%
ECO101752	PPU100631	56%	99.3%	100%
ECO101752	PSY103401	56%	98.6%	99.3%
ECO101752	SPA100434	76%	66.3%	100%
ECO101752	STY101256	94%	99.1%	99.1%
ECO101752	VCH101843	73%	99.1%	100%
ECO101752	YPS000696	86%	98.6%	99.1%
ECO101753	ABA100639	33%	37.5%	72.5%
ECO101753	BFR106061	21%	25.1%	33.2%
ECO101753	BPT101941	29%	35.6%	49.6%
ECO101753	BCE106878	24%	87.2%	96.5%
ECO101753	CAC102460	31%	35.2%	29.4%
ECO101753	CDF100180	33%	33.0%	49.4%
ECO101753	EBC100307	33%	44.4%	97.8%
ECO101753	ECO100999	38%	89.4%	97.3%
ECO101753	ECO101753	100%	100%	100%
ECO101753	HPY200297	27%	25.1%	49.0%
ECO101753	KPN300785	27%	80.2%	87.9%
ECO101753	LPN102390	32%	43.2%	30.7%
ECO101753	LMO101448	27%	40.5%	56%
ECO101753	LMO102375	28%	36.9%	50.3%
ECO101753	NME201936	31%	22.8%	29.1%
ECO101753	SPA101696	34%	35.8%	49.2%
ECO101753	STY104535	34%	35.8%	49.2%
ECO101753	SMU101724	27%	25.1%	77.0%
ECO101753	SPY103619	30%	15.9%	63.4%
ECO101753	TPA100971	33%	32.8%	41.3%
ECO101753	UUR100526	20%	22.8%	19.0%
ECO101753	VCH101352	23%	79.4%	92.1%
ECO101763	ABA105513	40%	90.2%	86.7%
ECO101763	BAN100828	36%	92.7%	87.8%
ECO101763	BFR105380	39%	61.0%	95.1%
ECO101763	BPT100872	37%	92.7%	89.2%
ECO101763	BCE101273	47%	97.6%	67.2%
ECO101763	CDP101886	35%	97.6%	92.0%
ECO101763	EBC100161	90%	100%	100%
ECO101763	EFA200147	27%	92.7%	90%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101763	EFM200246	28%	97.6%	100%
ECO101763	ECO101763	100%	100%	100%
ECO101763	KPN302997	87%	75.6%	100%
ECO101763	MCA102133	43%	86.6%	78.4%
ECO101763	MAV103677	38%	98.8%	76.0%
ECO101763	MBV102010	35%	98.8%	79.2%
ECO101763	MLP101243	32%	98.8%	79.8%
ECO101763	MTU201828	35%	98.8%	79.2%
ECO101763	PRT106179	75%	92.7%	92.7%
ECO101763	PAE205419	41%	98.8%	97.5%
ECO101763	PPU103670	47%	98.8%	97.5%
ECO101763	PSY103272	42%	98.8%	97.5%
ECO101763	SPA103813	95%	100%	100%
ECO101763	STY101269	95%	100%	100%
ECO101763	STM103357	95%	100%	100%
ECO101763	SAU800374	38%	91.5%	85.5%
ECO101763	SEP201355	38%	91.5%	84.5%
ECO101763	SPN400255	32%	91.5%	93.4%
ECO101763	SPY200974	28%	92.7%	87.8%
ECO101763	YPS000210	82%	100%	76.6%
ECO101764	ECO101764	100%	100%	100%
ECO101764	KPN303650	49%	91.7%	66.3%
ECO101764	PRT104545	53%	90%	46.5%
ECO101764	SPA103812	96%	100%	100%
ECO101764	STY101560	95%	100%	100%
ECO101764	STM103355	96%	100%	100%
ECO101765	ECO101765	100%	100%	100%
ECO101765	KPN303648	68%	88.2%	95.5%
ECO101765	PRT105988	60%	88.2%	95.5%
ECO101765	SPA103810	84%	100%	99.2%
ECO101765	STY101562	84%	100%	99.2%
ECO101765	STM103353	83%	100%	99.2%
ECO101780	ABA104139	38%	79.0%	77.7%
ECO101780	BAN105904	31%	80.8%	83.4%
ECO101780	BAN105947	36%	93.8%	89.8%
ECO101780	CJU100801	35%	55.6%	42.1%
ECO101780	CDF101312	45%	83.4%	61.5%
ECO101780	CDP101238	40%	58.1%	31.4%
ECO101780	EBC102374	74%	98.7%	98.9%
ECO101780	ECO101780	100%	100%	100%
ECO101780	HPY100289	35%	63.4%	52.6%
ECO101780	KPN304841	76%	99.1%	99.6%
ECO101780	LPN100163	38%	99.1%	99.8%
ECO101780	PRT104174	60%	97.8%	94.3%
ECO101780	PAE201757	47%	95.1%	94.0%
ECO101780	PPU111323	45%	95.4%	95.7%
ECO101780	PSY106827	46%	92.9%	99.5%
ECO101780	SPA101635	76%	98.0%	99.8%
ECO101780	STY101751	76%	99.8%	99.6%
ECO101780	STM101879	76%	99.8%	99.6%
ECO101780	SPN201794	38%	59.2%	46.8%
ECO101780	SPY201530	35%	59.2%	46.0%
ECO101780	VCH101284	59%	99.6%	98.9%
ECO101780	YPS001281	66%	97.4%	96.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101781	ABA105027	38%	80.7%	75.1%
ECO101781	BPT100243	42%	79.7%	64.3%
ECO101781	BCE101466	42%	83.9%	73.7%
ECO101781	BFU102068	43%	79.7%	71.4%
ECO101781	BMA100553	42%	80.7%	31.0%
ECO101781	CBO100995	25%	71.4%	74.9%
ECO101781	CDF101386	25%	90.6%	95.1%
ECO101781	CDP101714	32%	90.6%	71.7%
ECO101781	EBC102375	84%	100%	100%
ECO101781	ECO101781	100%	100%	100%
ECO101781	KPN304842	84%	100%	100%
ECO101781	LPN101532	30%	69.3%	98.5%
ECO101781	LMO102769	33%	45.3%	36.8%
ECO101781	MCA102435	37%	82.3%	64.2%
ECO101781	MAV102732	34%	80.7%	61.4%
ECO101781	MBV103988	34%	80.2%	60.8%
ECO101781	MLP101366	35%	79.2%	61.7%
ECO101781	MTU203618	34%	80.2%	60.8%
ECO101781	PRT106168	52%	94.3%	97.8%
ECO101781	PAE203751	40%	92.7%	87.7%
ECO101781	PPU107780	46%	80.2%	80.6%
ECO101781	PSY103810	43%	92.2%	89.4%
ECO101781	SPA101637	70%	89.6%	100%
ECO101781	STY101753	87%	100%	100%
ECO101781	STM101882	89%	97.4%	97.4%
ECO101781	SPY201658	25%	77.6%	78.9%
ECO101781	VCH101283	34%	95.8%	95.6%
ECO101781	YPS001278	55%	95.3%	95.5%
ECO101782	ABA105163	54%	99.6%	99.6%
ECO101782	BFR11775	41%	94.5%	98.4%
ECO101782	BPT100261	53%	99.1%	98.5%
ECO101782	BCE110535	53%	99.1%	98.9%
ECO101782	BFU101746	52%	99.1%	98.9%
ECO101782	BMA107390	52%	99.1%	98.9%
ECO101782	CJU101530	45%	99.3%	99.3%
ECO101782	CBO100452	33%	60.4%	91.2%
ECO101782	CDP101615	63%	98.5%	97.2%
ECO101782	EBC102376	89%	100%	100%
ECO101782	EFA202451	34%	61.2%	92.6%
ECO101782	ECO101782	100%	100%	100%
ECO101782	HIN100274	69%	100%	100%
ECO101782	HPY100130	45%	99.3%	99.1%
ECO101782	KPN304852	89%	100%	100%
ECO101782	MCA100203	53%	98.7%	99.6%
ECO101782	MAV102729	34%	10.8%	10.3%
ECO101782	MBV106198	50%	99.1%	98.0%
ECO101782	MTU200069	50%	99.1%	98.0%
ECO101782	PMU100036	68%	99.8%	99.8%
ECO101782	PRT106079	80%	100%	100%
ECO101782	PAE202441	53%	99.1%	98.9%
ECO101782	PPU104035	53%	99.1%	98.9%
ECO101782	SPA101021	87%	100%	100%
ECO101782	STY101754	94%	100%	100%
ECO101782	STM101885	94%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101782	VCH101281	75%	99.8%	100%
ECO101782	YPS001275	84%	99.8%	99.8%
ECO101785	BPT101965	29%	31.6%	81.1%
ECO101785	BCE100539	29%	40.2%	79.5%
ECO101785	BFU102714	31%	41.8%	71.0%
ECO101785	BMA103652	30%	40.2%	79.6%
ECO101785	CAC100528	27%	43.7%	86.6%
ECO101785	CDF101085	32%	97.8%	100%
ECO101785	CDF102264	28%	99.1%	100%
ECO101785	EBC100373	97%	21.4%	98.6%
ECO101785	EFA200641	43%	98.5%	97.3%
ECO101785	EFM201694	23%	34.1%	80.1%
ECO101785	EFM202558	42%	98.5%	97.3%
ECO101785	ECO101785	100%	100%	100%
ECO101785	KPN304856	94%	100%	100%
ECO101785	LMO102369	42%	98.5%	97.2%
ECO101785	NGO101815	28%	40.6%	91.0%
ECO101785	NME200364	30%	40.6%	91.0%
ECO101785	PMU100834	64%	99.1%	98.8%
ECO101785	SPA100142	93%	97.8%	100%
ECO101785	STY101758	95%	100%	100%
ECO101785	STM101897	95%	100%	100%
ECO101785	SMU101286	39%	99.1%	98.8%
ECO101785	SPN400261	39%	99.1%	97.9%
ECO101785	SPY201337	39%	99.1%	98.8%
ECO101785	YPS000675	81%	100%	100%
ECO101796	BFR104413	55%	90.9%	95.9%
ECO101796	BPT102042	44%	89.7%	95.0%
ECO101796	BCE112542	59%	90.5%	97.8%
ECO101796	BFU104304	59%	90.9%	94.3%
ECO101796	BMA105070	57%	90.5%	97.4%
ECO101796	CAC101675	32%	82.6%	84.0%
ECO101796	CBO102946	31%	81.0%	83.9%
ECO101796	CDF100814	32%	82.8%	32.4%
ECO101796	CDP100150	29%	90.3%	96.8%
ECO101796	EBC101616	86%	35.8%	100%
ECO101796	EFA202385	32%	84.2%	87.2%
ECO101796	ECO101796	100%	100%	100%
ECO101796	KPN301541	79%	92.1%	99.8%
ECO101796	MBV105656	28%	81.6%	77.6%
ECO101796	MTU202299	28%	81.6%	75.6%
ECO101796	PAE200245	29%	83.0%	82.8%
ECO101796	SPA100492	89%	91.5%	100%
ECO101796	STM101923	90%	92.5%	100%
ECO101796	SMU103098	25%	34.0%	93.0%
ECO101796	VCH101573	28%	82.0%	84.9%
ECO101796	YPS000541	70%	90.5%	98.2%
ECO101812	ABA105060	28%	95.9%	96.9%
ECO101812	BFR12043	23%	94.1%	91.4%
ECO101812	BCE102658	29%	69.1%	79.2%
ECO101812	CPN200090	25%	97.7%	88.8%
ECO101812	CTR200812	27%	87.7%	80.8%
ECO101812	CAC103515	35%	66.4%	50.7%
ECO101812	EBC102091	88%	98.6%	98.6%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101812	ECO101812	100%	100%	100%
ECO101812	KPN301983	87%	98.6%	99.1%
ECO101812	MAV103787	32%	69.1%	75.3%
ECO101812	SPA101082	90%	99.5%	100%
ECO101812	STY102242	90%	99.5%	94.4%
ECO101812	STM101972	90%	99.5%	94.4%
ECO101822	BPT102404	59%	99.2%	97.7%
ECO101822	BCE107531	52%	98.8%	85.4%
ECO101822	BFU103511	51%	99.6%	75.9%
ECO101822	BMA100592	52%	98.8%	98.7%
ECO101822	EBC101988	96%	99.8%	100%
ECO101822	ECO101822	100%	100%	100%
ECO101822	HIN101541	77%	100%	100%
ECO101822	KPN301976	95%	100%	100%
ECO101822	LPN100837	44%	94.4%	99.8%
ECO101822	NGO101773	49%	100%	98.6%
ECO101822	NME200171	49%	100%	98.6%
ECO101822	PMU100653	78%	100%	100%
ECO101822	PRT102540	85%	100%	100%
ECO101822	PAE204327	57%	99.0%	98.6%
ECO101822	PPU103342	57%	99.0%	98.3%
ECO101822	PSY105033	55%	99.0%	98.6%
ECO101822	SPA101027	96%	38.1%	100%
ECO101822	STY102252	98%	100%	100%
ECO101822	STM101984	98%	100%	100%
ECO101822	VCH101978	68%	99.8%	99.8%
ECO101822	YPS003477	89%	100%	100%
ECO101830	BCE101208	46%	73.0%	70.2%
ECO101830	ECO101830	100%	100%	100%
ECO101830	SPA102453	80%	82.4%	96.5%
ECO101830	STY102261	80%	82.4%	96.5%
ECO101830	STM102393	80%	82.4%	96.5%
ECO101834	ABA101157	59%	98.8%	98.5%
ECO101834	BAN109213	38%	98.6%	99.5%
ECO101834	BAN103380	52%	99.5%	99.3%
ECO101834	BFR10266	48%	78.3%	99.1%
ECO101834	BPT101790	57%	98.8%	99.0%
ECO101834	BBU100445	41%	85.1%	99.0%
ECO101834	BCE104313	44%	14.9%	70.2%
ECO101834	BCE111669	56%	98.8%	98.3%
ECO101834	BFU111015	58%	98.8%	98.5%
ECO101834	BMA100432	58%	98.8%	98.3%
ECO101834	CJU100601	51%	98.8%	99.1%
ECO101834	CPN200083	44%	98.6%	99.1%
ECO101834	CTR200818	45%	98.6%	99.5%
ECO101834	CAC102618	48%	99.5%	98.3%
ECO101834	CBO100008	47%	99.5%	98.5%
ECO101834	CDF100502	52%	98.6%	97.6%
ECO101834	CDP100396	47%	96.4%	95.7%
ECO101834	EBC102309	92%	100%	100%
ECO101834	EFA202213	53%	98.6%	98.6%
ECO101834	EFM202626	53%	99.5%	99.5%
ECO101834	ECO101834	100%	100%	100%
ECO101834	HIN100302	76%	99.2%	99.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101834	HPY100610	49%	99.2%	100%
ECO101834	KPN301306	93%	51.5%	96.8%
ECO101834	LPN101576	55%	98.8%	98.8%
ECO101834	LMO101015	52%	99.7%	99.5%
ECO101834	MCA100604	56%	99.3%	99.3%
ECO101834	MAV103031	47%	87.3%	99.8%
ECO101834	MBV101554	46%	96.4%	93.5%
ECO101834	MLP100306	45%	96.4%	96.4%
ECO101834	MTU202535	46%	96.4%	95.8%
ECO101834	MGE100036	33%	95.3%	95.3%
ECO101834	MPN100108	35%	95.6%	94.4%
ECO101834	NGO101633	55%	98.8%	99.5%
ECO101834	NME201865	56%	99.5%	99.0%
ECO101834	PMU100983	77%	99.2%	99.5%
ECO101834	PRT100115	78%	98.6%	100%
ECO101834	PAE200962	64%	98.8%	98.6%
ECO101834	PPU112195	62%	98.8%	98.6%
ECO101834	PSY106866	63%	90.7%	98.5%
ECO101834	SPA102449	91%	66.6%	99.7%
ECO101834	STY102265	94%	100%	100%
ECO101834	SAU801630	54%	98.6%	99.1%
ECO101834	SEP201575	53%	98.6%	99.1%
ECO101834	SHA100663	53%	98.6%	99.1%
ECO101834	SMU101272	50%	99.8%	99.0%
ECO101834	SPN401921	50%	98.6%	98.1%
ECO101834	SPY201648	49%	98.6%	99.0%
ECO101834	TPA100975	42%	98.6%	96.7%
ECO101834	UUR100288	39%	98.1%	99.0%
ECO101834	VCH101147	75%	98.8%	98.6%
ECO101834	YPS003419	82%	99.3%	98.0%
ECO101844	ABA102360	23%	99.7%	99.3%
ECO101844	BAN106237	31%	74.2%	92.4%
ECO101844	BAN106908	33%	93.2%	93.7%
ECO101844	BFR10875	26%	95.0%	94.7%
ECO101844	BPT101508	24%	99.1%	99.8%
ECO101844	BBU100593	22%	95.3%	93.2%
ECO101844	BCE100461	27%	99.7%	98.7%
ECO101844	BFU103077	25%	99.7%	98.7%
ECO101844	BMA100457	26%	99.7%	98.7%
ECO101844	CJU101100	22%	92.2%	92.8%
ECO101844	CPN200176	39%	96.2%	95.7%
ECO101844	CTR200729	39%	99.7%	98.8%
ECO101844	CAC101790	33%	94.5%	94.7%
ECO101844	CBO100741	32%	94.5%	94.7%
ECO101844	CDF104545	33%	93.8%	93.6%
ECO101844	CDP100057	25%	95.3%	94%
ECO101844	EBC100321	88%	52.9%	100%
ECO101844	EFA200290	31%	100%	100%
ECO101844	EFM201011	30%	100%	100%
ECO101844	ECO101844	100%	100%	100%
ECO101844	HIN101550	71%	100%	100%
ECO101844	HPY100315	22%	93.2%	93.7%
ECO101844	KPN301304	92%	100%	100%
ECO101844	LPN101161	23%	99.7%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101844	LMO101656	27%	99.5%	98.7%
ECO101844	MCA100331	67%	100%	100%
ECO101844	MAV106525	26%	99.3%	97.3%
ECO101844	MBV105559	25%	99.8%	99.3%
ECO101844	MLP100693	24%	99.8%	99.3%
ECO101844	MTU201275	25%	99.8%	99.3%
ECO101844	MGE100389	27%	27.9%	30.2%
ECO101844	MPN100286	22%	90.5%	89.9%
ECO101844	NGO100228	56%	100%	100%
ECO101844	NME201566	57%	100%	100%
ECO101844	PMU100551	71%	97.6%	100%
ECO101844	PRT100545	77%	100%	100%
ECO101844	PAE205046	53%	99.7%	98.6%
ECO101844	PPU109126	55%	99.7%	99.3%
ECO101844	PSY103569	56%	99.7%	98.6%
ECO101844	SPA103053	90%	100%	100%
ECO101844	STY102666	95%	100%	100%
ECO101844	STM102429	95%	100%	100%
ECO101844	SAU800607	25%	99.7%	98.9%
ECO101844	SEP200171	25%	99.5%	98.6%
ECO101844	SHA101545	26%	99.7%	98.9%
ECO101844	SMU101264	33%	100%	100%
ECO101844	SPN401887	33%	92.2%	92.4%
ECO101844	SPY201643	34%	92.2%	92.4%
ECO101844	TPA100822	26%	91.9%	91.2%
ECO101844	UUR100280	21%	99.0%	98.9%
ECO101844	VCH102042	71%	100%	96.3%
ECO101844	YPS003380	83%	100%	100%
ECO101848	BAN109475	29%	89.3%	99.1%
ECO101848	BAN107115	30%	89.8%	56.3%
ECO101848	BPT101039	54%	97.6%	97.4%
ECO101848	BBU100271	26%	91.6%	94.4%
ECO101848	BCE101394	43%	83.8%	99.4%
ECO101848	BFU107593	49%	97.6%	92.1%
ECO101848	BMA106909	47%	97.6%	79.6%
ECO101848	CJU100304	37%	93.2%	98.3%
ECO101848	CPN200429	28%	94.2%	99.4%
ECO101848	CTR200360	27%	89.8%	95%
ECO101848	CAC101540	34%	90.3%	56.6%
ECO101848	CBO103112	37%	90.8%	56.8%
ECO101848	CDF101537	35%	90.6%	57.3%
ECO101848	CDP100831	24%	50%	24.0%
ECO101848	EBC101868	82%	75.4%	99.7%
ECO101848	ECO101848	100%	100%	100%
ECO101848	HPY100757	34%	91.1%	96.6%
ECO101848	LPN102387	37%	96.9%	96.6%
ECO101848	LMO101348	32%	88.5%	96.0%
ECO101848	PRT101697	56%	99.7%	99.7%
ECO101848	PAE201448	41%	97.1%	98.1%
ECO101848	PPU100957	42%	97.1%	98.2%
ECO101848	PSY104645	39%	97.1%	98.1%
ECO101848	SPA103608	30%	89.8%	96.9%
ECO101848	STY102681	90%	99.5%	99.5%
ECO101848	STM104011	30%	89.8%	96.9%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101848	TPA100707	31%	88.0%	89.4%
ECO101848	VCH102087	42%	95.8%	97.6%
ECO101848	YPS001340	65%	99.5%	98.7%
ECO101849	BPT100969	66%	93.0%	93.8%
ECO101849	BCE102972	54%	95.3%	90.5%
ECO101849	BFU101753	52%	94.9%	94.5%
ECO101849	BMA100242	54%	92.5%	88.4%
ECO101849	EBC102526	86%	100%	100%
ECO101849	ECO101849	100%	100%	100%
ECO101849	PRT101698	68%	97.7%	97.7%
ECO101849	PAE201456	36%	90.7%	79.8%
ECO101849	PPU107239	34%	90.7%	80.2%
ECO101849	PSY104628	36%	90.7%	80.5%
ECO101849	STY102684	92%	100%	100%
ECO101849	VCH102032	34%	95.3%	87.4%
ECO101849	YPS000444	79%	95.8%	95.8%
ECO101850	BPT100968	78%	98.4%	98.4%
ECO101850	BBU100569	37%	91.5%	97.6%
ECO101850	BCE114763	76%	96.9%	95.4%
ECO101850	BFU101848	77%	94.6%	96.1%
ECO101850	BMA102452	77%	96.9%	95.4%
ECO101850	CJU101044	48%	91.5%	91.5%
ECO101850	EBC102527	92%	100%	100%
ECO101850	ECO101850	100%	100%	100%
ECO101850	HPY101050	49%	91.5%	96.0%
ECO101850	PRT101699	83%	100%	100%
ECO101850	PAE201455	60%	94.6%	98.4%
ECO101850	PPU107240	58%	86.0%	98.2%
ECO101850	PSY108633	62%	96.9%	97.7%
ECO101850	STY102690	97%	100%	100%
ECO101850	VCH102033	66%	96.9%	96.2%
ECO101850	YPS000441	90%	100%	100%
ECO101855	ABA100537	23%	61.7%	57.9%
ECO101855	BAN103169	26%	85.0%	47%
ECO101855	BAN111824	26%	85.0%	47.6%
ECO101855	BPT100964	74%	91.6%	85.6%
ECO101855	BBU100564	33%	86.8%	87.8%
ECO101855	BCE102043	71%	89.2%	87.1%
ECO101855	BFU104019	70%	89.8%	84.3%
ECO101855	BMA106471	71%	89.2%	85.1%
ECO101855	CJU100254	32%	79.6%	79.8%
ECO101855	CAC101201	34%	83.2%	82.1%
ECO101855	CBO101893	31%	86.8%	98.0%
ECO101855	CDF100179	31%	86.8%	84.3%
ECO101855	EBC101567	93%	100%	100%
ECO101855	ECO101855	100%	100%	100%
ECO101855	HPY100387	30%	82.0%	82.4%
ECO101855	LMO100168	28%	85.0%	46.4%
ECO101855	PRT101704	82%	92.2%	92.8%
ECO101855	PAE200177	65%	92.2%	96.9%
ECO101855	PPU100206	31%	89.8%	94.3%
ECO101855	PSY104621	31%	94.6%	99.4%
ECO101855	SPA102291	92%	100%	100%
ECO101855	STY102699	91%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101855	STM100698	23%	80.2%	42.3%
ECO101855	TPA100435	31%	85.0%	85.9%
ECO101855	VCH103807	38%	88.6%	97.4%
ECO101855	YPS000402	84%	97.6%	98.8%
ECO101862	EBC104539	95%	100%	100%
ECO101862	EBC103941	96%	100%	100%
ECO101862	EBC100826	96%	100%	100%
ECO101862	EBC103716	96%	100%	100%
ECO101862	EBC103336	100%	100%	100%
ECO101862	EFM200791	25%	84.6%	24.9%
ECO101862	EFM200545	27%	63.7%	21.3%
ECO101862	EFM201822	26%	86.8%	24.6%
ECO101862	EFM202619	26%	86.8%	24.6%
ECO101862	EFM200291	26%	86.8%	24.6%
ECO101862	EFM201961	26%	86.8%	24.6%
ECO101862	EFM200014	26%	86.8%	24.6%
ECO101862	EFM202174	28%	86.8%	27.1%
ECO101862	ECO101862	100%	100%	100%
ECO101862	ECO103367	100%	100%	100%
ECO101862	ECO100022	100%	100%	100%
ECO101868	BCE102392	53%	98.8%	96.7%
ECO101868	BCE113790	55%	98.6%	99.0%
ECO101868	BFU102747	53%	42.3%	81.2%
ECO101868	BMA100031	54%	98.6%	97.6%
ECO101868	EBC102563	88%	100%	100%
ECO101868	ECO101868	100%	100%	100%
ECO101868	KPN301529	87%	100%	98.6%
ECO101868	PPU103879	39%	46.6%	95.0%
ECO101868	PSY105277	60%	97.4%	96.8%
ECO101868	YPS001717	79%	47.0%	96.3%
ECO101870	EBC102565	63%	100%	100%
ECO101870	ECO101870	100%	100%	100%
ECO101870	KPN301537	50%	97.0%	95.9%
ECO101870	SPA102034	76%	100%	100%
ECO101870	STY102732	76%	100%	100%
ECO101870	STM102496	76%	100%	100%
ECO101871	ECO101871	100%	100%	100%
ECO101871	KPN308700	50%	75%	76.4%
ECO101872	EBC102561	48%	78.5%	100%
ECO101872	ECO101872	100%	100%	100%
ECO101872	KPN207037	25%	51.4%	93.2%
ECO101872	SPA102033	57%	91.6%	100%
ECO101872	STY102735	60%	97.2%	93.7%
ECO101872	STM102500	61%	97.2%	93.7%
ECO101882	BCE114633	55%	98%	95.2%
ECO101882	BFU102808	59%	96.4%	94.8%
ECO101882	CAC100722	52%	99.2%	100%
ECO101882	CAC102757	56%	99.2%	100%
ECO101882	CBO102646	54%	97.2%	98.0%
ECO101882	EBC100445	92%	100%	100%
ECO101882	EFA200396	58%	98%	99.6%
ECO101882	ECO101882	100%	100%	100%
ECO101882	HIN101054	57%	97.6%	94.9%
ECO101882	KPN300045	89%	40.8%	85%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101882	KPN300885	89%	66%	87.8%
ECO101882	LMO100107	58%	98%	99.2%
ECO101882	PPU109960	77%	99.2%	97.6%
ECO101882	PSY103670	74%	97.2%	98.4%
ECO101882	SPA102746	90%	100%	100%
ECO101882	STY102765	92%	100%	100%
ECO101882	SAU801857	53%	99.2%	100%
ECO101882	SEP200471	53%	99.2%	100%
ECO101882	YPS001591	77%	99.2%	98.0%
ECO101897	BAN101612	26%	73.6%	91.9%
ECO101897	BFU101528	26%	88.7%	78.0%
ECO101897	BMA102559	29%	54.7%	39.2%
ECO101897	CAC103410	23%	63.5%	70.5%
ECO101897	ECO101897	100%	100%	100%
ECO101897	KPN302916	29%	95.6%	94.4%
ECO101916	EBC104124	22%	85.5%	89.4%
ECO101916	ECO101916	100%	100%	100%
ECO101916	KPN300872	61%	60.9%	96.9%
ECO101916	LMO101661	31%	23.2%	20.3%
ECO101916	PRT103362	21%	93.7%	96.5%
ECO101916	SPA102250	88%	100%	100%
ECO101916	STY102835	87%	100%	100%
ECO101916	STM102569	87%	100%	100%
ECO101916	YPS003114	23%	89.4%	93.1%
ECO101932	ECO101932	100%	100%	100%
ECO101932	HPY101345	27%	43.4%	45.8%
ECO101932	PAE204881	32%	95.4%	95.0%
ECO101932	PSY102848	34%	94.5%	94.4%
ECO101932	SPA103998	54%	99.3%	98.9%
ECO101932	STY103627	54%	99.3%	98.9%
ECO101939	BPT100783	32%	86.3%	94.2%
ECO101939	BCE106818	33%	82.0%	87.0%
ECO101939	BFU100112	34%	82.0%	86.6%
ECO101939	BMA106390	33%	82.0%	85.8%
ECO101939	EBC101415	81%	95.3%	100%
ECO101939	ECO101939	100%	100%	100%
ECO101939	KPN301295	78%	74.8%	99.5%
ECO101939	PAE204027	39%	83.5%	84.8%
ECO101939	PPU108189	39%	84.9%	87.8%
ECO101939	PSY102145	38%	86.0%	89.6%
ECO101939	SPA100917	80%	99.3%	100%
ECO101939	STY102854	84%	89.9%	94.3%
ECO101939	STM103015	85%	89.9%	94.3%
ECO101939	YPS000612	66%	89.9%	92.6%
ECO101940	ABA106057	24%	15.3%	83.5%
ECO101940	ABA101677	23%	20.1%	85.4%
ECO101940	ABA105636	22%	28.0%	95.0%
ECO101940	ABA102772	23%	22.0%	89.0%
ECO101940	ABA100270	24%	47.8%	51.6%
ECO101940	ABA105476	21%	23.2%	80.5%
ECO101940	ABA100269	23%	58.7%	46.7%
ECO101940	ABA103692	22%	45.7%	93.5%
ECO101940	BAN103564	18%	40.9%	91.9%
ECO101940	BAN110387	20%	49.7%	98.9%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101940	BAN100594	22%	45.3%	74.1%
ECO101940	BAN103966	20%	29.1%	86.4%
ECO101940	BAN106993	21%	29.7%	86.0%
ECO101940	BAN112238	21%	70.8%	35.0%
ECO101940	BPT101815	27%	79.9%	71.4%
ECO101940	BCE112364	20%	29.0%	39.2%
ECO101940	BCE102526	22%	75.8%	5.6%
ECO101940	CAC100010	21%	30.3%	72.2%
ECO101940	CBO100633	24%	7.4%	32.6%
ECO101940	CDF100798	20%	7.3%	35.6%
ECO101940	CDF104552	19%	72.1%	39.7%
ECO101940	EFA203172	20%	7.8%	64.8%
ECO101940	EFA200715	22%	63.6%	81.9%
ECO101940	EFM201066	22%	44.1%	27.4%
ECO101940	ECO101940	100%	100%	100%
ECO101940	LPN100835	22%	12.5%	89.5%
ECO101940	LPN102554	21%	28.5%	89.5%
ECO101940	LPN101177	20%	74.3%	71.6%
ECO101940	LMO102668	20%	61.8%	43.8%
ECO101940	LMO101179	20%	7.8%	15.1%
ECO101940	LMO101791	20%	4.4%	41.4%
ECO101940	PRT101411	26%	81.2%	83.6%
ECO101940	PAE201873	21%	28.9%	78.2%
ECO101940	PPU104136	20%	69.1%	30.2%
ECO101940	SPA102738	40%	13.9%	93.9%
ECO101940	STM102843	19%	8.2%	54.6%
ECO101940	SPN401402	22%	56.7%	15.3%
ECO101940	YPS002407	28%	90.0%	76.3%
ECO101943	ABA102320	38%	94.7%	83.6%
ECO101943	BPT100469	37%	93.8%	88.7%
ECO101943	BCE104326	72%	96.8%	88.7%
ECO101943	BFU103848	74%	98.9%	98.6%
ECO101943	BMA105236	40%	95.2%	94.3%
ECO101943	EBC102095	90%	99.3%	99.3%
ECO101943	ECO101943	100%	100%	100%
ECO101943	KPN308062	85%	98.9%	100%
ECO101943	MAV105065	39%	95.0%	87.8%
ECO101943	SPA102653	39%	93.4%	94.5%
ECO101943	STM103556	41%	94.7%	96.5%
ECO101944	BFR10768	28%	57.4%	90.3%
ECO101944	BPT102655	48%	97.5%	94.8%
ECO101944	BCE111329	47%	98.1%	67.2%
ECO101944	BFU111886	47%	97.7%	94.9%
ECO101944	BMA107275	48%	98.1%	95.3%
ECO101944	CPN200955	27%	60.1%	86.7%
ECO101944	CTR200127	26%	57.6%	81.7%
ECO101944	EBC102094	90%	97.3%	100%
ECO101944	ECO101944	100%	100%	100%
ECO101944	KPN301247	88%	100%	100%
ECO101944	PRT103047	86%	42.8%	100%
ECO101944	PAE203967	54%	98.3%	95.8%
ECO101944	PPU107622	56%	98.3%	98.2%
ECO101944	PSY105099	53%	98.3%	98.2%
ECO101944	SPA100713	90%	93.6%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101944	STY102855	90%	100%	100%
ECO101944	YPS001830	72%	96.9%	87.7%
ECO101945	BAN112031	60%	68.9%	100%
ECO101945	BAN104148	56%	98.7%	98.3%
ECO101945	BAN104405	58%	98.7%	98.3%
ECO101945	EFA200256	62%	98.7%	98.3%
ECO101945	EFM201788	64%	99.2%	98.7%
ECO101945	ECO101945	100%	100%	100%
ECO101945	LMO101499	62%	98.7%	98.3%
ECO101945	SPA102952	96%	100%	100%
ECO101945	STY104391	95%	100%	98.8%
ECO101945	SAU800669	48%	60.1%	97.9%
ECO101945	SEP200711	56%	98.7%	98.7%
ECO101945	SHA102248	56%	98.7%	98.7%
ECO101945	SMU101096	77%	100%	100%
ECO101945	SPN401736	74%	98.7%	98.7%
ECO101945	SPY200231	78%	99.6%	99.6%
ECO101945	VCH102742	42%	98.3%	98.3%
ECO101953	ABA105612	27%	29.0%	31.2%
ECO101953	BFU100696	50%	91.4%	95.6%
ECO101953	EBC104763	92%	18.6%	100%
ECO101953	EBC107253	93%	18.6%	100%
ECO101953	EBC101291	100%	16.9%	100%
ECO101953	EBC102182	96%	29.6%	99.0%
ECO101953	EBC101203	93%	32.2%	100%
ECO101953	EBC104566	98%	39.3%	100%
ECO101953	EBC100510	87%	46.7%	100%
ECO101953	EBC103428	98%	41.7%	100%
ECO101953	EBC104220	96%	45.0%	100%
ECO101953	EBC101223	99%	55.6%	96.4%
ECO101953	EBC104973	92%	100%	100%
ECO101953	ECO102150	99%	100%	100%
ECO101953	ECO100251	99%	100%	100%
ECO101953	ECO100542	99%	100%	100%
ECO101953	ECO102916	99%	100%	100%
ECO101953	ECO101302	99%	100%	100%
ECO101953	ECO101989	99%	100%	100%
ECO101953	ECO103428	99%	100%	100%
ECO101953	ECO100646	99%	100%	100%
ECO101953	ECO103148	99%	100%	100%
ECO101953	ECO101953	100%	100%	100%
ECO101953	KPN206674	93%	26.9%	98.9%
ECO101953	KPN201650	96%	96.2%	99.7%
ECO101953	LPN101936	20%	68.3%	89.6%
ECO101953	MBV101126	23%	36.7%	47.1%
ECO101953	MTU203341	23%	36.7%	52.1%
ECO101953	NGO101896	26%	25.1%	58.4%
ECO101953	NGO100681	26%	25.1%	58.4%
ECO101953	NGO100569	26%	25.1%	58.4%
ECO101953	NGO100201	26%	25.1%	58.4%
ECO101953	NGO101807	26%	25.1%	58.4%
ECO101953	NGO100715	26%	25.1%	58.4%
ECO101953	NME200429	23%	24.0%	79.0%
ECO101953	NME201600	26%	24.0%	79.0%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101953	NME201634	26%	25.4%	78.6%
ECO101953	NME201479	26%	25.4%	72.1%
ECO101953	NME201478	27%	59.8%	93.8%
ECO101953	NME201635	28%	59.8%	95.1%
ECO101953	NME201501	27%	62.7%	94.5%
ECO101953	NME201597	28%	60.7%	79.2%
ECO101953	NME200676	27%	68.9%	79.7%
ECO101953	NME201125	30%	60.7%	76.2%
ECO101953	NME200427	26%	86.1%	91.6%
ECO101953	NME201028	27%	86.1%	90.7%
ECO101953	NME201153	27%	86.1%	90.7%
ECO101953	NME201109	27%	86.1%	90.7%
ECO101953	NME200210	28%	86.1%	90.7%
ECO101953	PPU111071	58%	92.3%	95.7%
ECO101953	PSY108820	28%	32.5%	87.5%
ECO101953	PSY100971	37%	28.1%	79.8%
ECO101953	PSY107786	56%	17.2%	84.1%
ECO101953	PSY108012	58%	14.8%	52.1%
ECO101953	PSY100713	50%	15.4%	69.3%
ECO101953	PSY105545	51%	29.3%	0.9%
ECO101953	PSY102628	55%	46.2%	95.1%
ECO101953	PSY105342	66%	42.3%	98.6%
ECO101953	PSY102624	54%	47.0%	98.8%
ECO101953	PSY108079	54%	56.8%	93.6%
ECO101953	PSY100132	58%	61.8%	93.7%
ECO101953	PSY105328	57%	65.7%	94.5%
ECO101953	PSY108150	53%	77.5%	96.3%
ECO101953	PSY108972	53%	77.5%	98.9%
ECO101953	PSY101764	57%	79.9%	92.8%
ECO101953	PSY100142	58%	77.5%	92.9%
ECO101953	PSY100923	55%	88.8%	97.1%
ECO101953	PSY100425	56%	89.1%	94.9%
ECO101953	PSY100530	56%	91.7%	95.1%
ECO101953	PSY106503	57%	91.7%	95.1%
ECO101953	PSY106678	57%	91.4%	95.7%
ECO101953	PSY107045	57%	91.7%	95.1%
ECO101953	PSY103445	57%	91.7%	95.1%
ECO101953	PSY100366	57%	91.7%	95.1%
ECO101953	PSY106085	57%	91.7%	95.1%
ECO101953	PSY105970	57%	91.7%	95.1%
ECO101953	PSY103492	57%	91.7%	95.1%
ECO101953	PSY106670	57%	91.7%	95.1%
ECO101953	PSY108825	57%	91.7%	95.1%
ECO101953	PSY106530	57%	91.7%	95.1%
ECO101953	PSY106607	57%	91.7%	95.1%
ECO101953	PSY100555	57%	91.7%	95.1%
ECO101953	PSY100919	57%	91.7%	95.1%
ECO101953	PSY108757	57%	91.7%	95.1%
ECO101953	PSY101541	57%	91.7%	91.4%
ECO101953	PSY107011	57%	91.7%	95.1%
ECO101953	PSY108510	57%	91.7%	95.1%
ECO101953	PSY108390	57%	91.7%	95.1%
ECO101953	PSY106920	57%	91.7%	95.1%
ECO101953	PSY100368	57%	91.7%	95.1%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101953	PSY100686	57%	91.7%	95.1%
ECO101953	PSY100026	57%	91.7%	95.1%
ECO101953	PSY107134	57%	91.7%	95.1%
ECO101953	PSY107080	57%	91.7%	95.1%
ECO101953	PSY100200	57%	91.7%	95.1%
ECO101953	PSY101963	57%	91.7%	95.1%
ECO101953	PSY108098	57%	91.7%	95.1%
ECO101953	PSY106521	57%	91.7%	95.1%
ECO101953	PSY107158	57%	91.7%	95.1%
ECO101953	PSY108313	57%	91.7%	95.1%
ECO101953	PSY106814	57%	91.7%	95.1%
ECO101953	PSY107065	57%	91.7%	95.1%
ECO101953	PSY102698	57%	91.7%	95.1%
ECO101953	PSY108019	57%	91.7%	95.1%
ECO101953	PSY107438	57%	91.7%	95.1%
ECO101953	PSY106301	57%	91.7%	95.1%
ECO101953	PSY108294	57%	91.7%	95.1%
ECO101953	SAU302002	99%	100%	100%
ECO101953	VCH103198	82%	96.2%	99.7%
ECO101953	VCH103013	82%	96.2%	99.7%
ECO101961	BFU102395	46%	95.3%	65.3%
ECO101961	EBC103227	81%	61.5%	90.1%
ECO101961	ECO102590	77%	94.6%	87.5%
ECO101961	ECO100239	81%	100%	93.7%
ECO101961	ECO101961	100%	100%	100%
ECO101961	LPN103162	46%	70.9%	95.5%
ECO101961	SEP200678	43%	40.5%	57.1%
ECO101962	EBC107300	65%	75.3%	98.2%
ECO101962	ECO101962	100%	100%	100%
ECO101977	ECO101977	100%	100%	100%
ECO101977	STY104903	100%	68.8%	84.6%
ECO101978	ABA100967	32%	72.9%	99.0%
ECO101978	BAN110750	27%	67.9%	96.1%
ECO101978	BAN104616	29%	72.9%	98.6%
ECO101978	BFR10274	46%	97.7%	99.3%
ECO101978	BPT102118	35%	63.5%	84.3%
ECO101978	BCE111202	31%	67.9%	91.2%
ECO101978	BFU102918	31%	67.9%	85.3%
ECO101978	BMA100478	31%	67.9%	90.8%
ECO101978	CJU101503	66%	100%	100%
ECO101978	CAC100618	30%	75.6%	100%
ECO101978	CBO103224	31%	72.2%	96.7%
ECO101978	CDF101429	32%	67.9%	92.8%
ECO101978	CDP101163	31%	96.3%	97.9%
ECO101978	EBC101407	95%	100%	100%
ECO101978	ECO101978	100%	100%	100%
ECO101978	HIN100448	71%	100%	100%
ECO101978	KPN307753	93%	100%	100%
ECO101978	LPN101189	53%	98.3%	99.0%
ECO101978	LMO102293	35%	69.2%	93.9%
ECO101978	MCA100763	34%	65.6%	85.3%
ECO101978	MAV101032	32%	96.3%	97.9%
ECO101978	MBV101983	31%	96.3%	97.9%
ECO101978	MLP100814	29%	96.3%	97.2%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101978	MTU202088	31%	96.3%	97.9%
ECO101978	NGO101357	32%	74.9%	98.2%
ECO101978	NME201627	32%	74.9%	100%
ECO101978	PMU101195	74%	99.7%	99.7%
ECO101978	PRT102221	87%	100%	100%
ECO101978	PAE204447	33%	72.9%	98.1%
ECO101978	PPU111032	34%	70.9%	97.2%
ECO101978	PSY104792	34%	70.9%	97.2%
ECO101978	SPA101158	88%	100%	100%
ECO101978	STY103477	95%	100%	100%
ECO101978	STM103244	95%	100%	100%
ECO101978	SAU802679	32%	70.9%	96.6%
ECO101978	SEP202153	31%	70.6%	96.1%
ECO101978	SMU100230	33%	73.6%	96.7%
ECO101978	VCH101113	68%	98.3%	96.7%
ECO101978	YPS002977	87%	100%	100%
ECO101987	ABA103119	23%	64.2%	68.1%
ECO101987	BAN110772	28%	64.7%	58.3%
ECO101987	BAN111921	29%	86.9%	75.5%
ECO101987	BFR101373	56%	100%	98.6%
ECO101987	BPT102039	29%	87.1%	81.4%
ECO101987	BCE109316	29%	97.2%	83.9%
ECO101987	BFU100399	29%	67.5%	97.2%
ECO101987	BFU112557	27%	94.3%	86.4%
ECO101987	BFU102079	29%	87.1%	78.4%
ECO101987	BMA106683	28%	88.4%	79.6%
ECO101987	CJU101360	51%	100%	99.7%
ECO101987	CDF103450	30%	87.1%	77.4%
ECO101987	CDP101551	30%	76.3%	81.8%
ECO101987	EBC102062	88%	46.6%	100%
ECO101987	EFM202675	43%	23.5%	84.2%
ECO101987	EFM201814	59%	100%	98.6%
ECO101987	ECO101987	100%	100%	100%
ECO101987	KPN300804	81%	100%	100%
ECO101987	MCA101063	21%	46.4%	43.1%
ECO101987	MAV101246	29%	86.9%	81.4%
ECO101987	MBV102120	27%	81.2%	79.1%
ECO101987	MTU200321	28%	86.9%	81.0%
ECO101987	PMU100776	59%	99.7%	99.2%
ECO101987	PRT105811	75%	99.7%	99.5%
ECO101987	PAE203557	28%	88.4%	78.2%
ECO101987	PPU110693	28%	92.8%	85.7%
ECO101987	PSY108023	28%	86.9%	76.8%
ECO101987	SPA109961	87%	100%	100%
ECO101987	STY103507	88%	100%	100%
ECO101987	SPN400318	59%	100%	100%
ECO101987	SPY201684	54%	100%	100%
ECO101987	VCH103500	69%	100%	100%
ECO101987	YPS000760	29%	88.4%	81.5%
ECO101989	ABA105612	27%	29.0%	31.2%
ECO101989	BFU100696	49%	91.4%	95.6%
ECO101989	EBC104763	92%	18.6%	100%
ECO101989	EBC107253	93%	18.6%	100%
ECO101989	EBC101291	100%	16.9%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101989	EBC102182	96%	29.6%	99.0%
ECO101989	EBC101203	93%	32.2%	100%
ECO101989	EBC104566	98%	39.3%	100%
ECO101989	EBC100510	87%	46.7%	100%
ECO101989	EBC103428	98%	41.7%	100%
ECO101989	EBC104220	96%	45.0%	100%
ECO101989	EBC101223	99%	55.6%	96.4%
ECO101989	EBC104973	92%	100%	100%
ECO101989	ECO103148	100%	100%	100%
ECO101989	ECO100251	100%	100%	100%
ECO101989	ECO100542	100%	100%	100%
ECO101989	ECO100646	100%	100%	100%
ECO101989	ECO101302	100%	100%	100%
ECO101989	ECO103428	100%	100%	100%
ECO101989	ECO102150	100%	100%	100%
ECO101989	ECO102916	100%	100%	100%
ECO101989	ECO101989	100%	100%	100%
ECO101989	KPN206674	94%	26.9%	98.9%
ECO101989	KPN201650	96%	96.2%	99.7%
ECO101989	LPN101936	20%	68.3%	89.6%
ECO101989	MBV101126	23%	36.7%	47.1%
ECO101989	MTU203341	23%	36.7%	52.1%
ECO101989	NGO101896	26%	25.1%	58.4%
ECO101989	NGO100681	26%	25.1%	58.4%
ECO101989	NGO100569	26%	25.1%	58.4%
ECO101989	NGO100201	26%	25.1%	58.4%
ECO101989	NGO101807	26%	25.1%	58.4%
ECO101989	NGO100715	26%	25.1%	58.4%
ECO101989	NME200429	23%	24.0%	79.0%
ECO101989	NME201600	26%	24.0%	79.0%
ECO101989	NME201634	26%	25.4%	78.6%
ECO101989	NME201479	26%	25.4%	72.1%
ECO101989	NME201478	27%	59.8%	93.8%
ECO101989	NME201635	28%	59.8%	95.1%
ECO101989	NME201501	27%	62.7%	94.5%
ECO101989	NME201597	28%	60.7%	79.2%
ECO101989	NME200676	27%	68.9%	79.7%
ECO101989	NME201125	30%	60.7%	76.2%
ECO101989	NME200427	26%	86.1%	91.6%
ECO101989	NME201028	27%	86.1%	90.7%
ECO101989	NME201153	27%	86.1%	90.7%
ECO101989	NME201109	27%	86.1%	90.7%
ECO101989	NME200210	28%	86.1%	90.7%
ECO101989	PPU111071	58%	92.3%	95.7%
ECO101989	PSY108820	27%	32.5%	87.5%
ECO101989	PSY100971	36%	28.1%	79.8%
ECO101989	PSY107786	55%	17.2%	84.1%
ECO101989	PSY108012	56%	14.8%	52.1%
ECO101989	PSY100713	50%	15.4%	69.3%
ECO101989	PSY105545	50%	29.3%	0.9%
ECO101989	PSY102628	55%	46.2%	95.1%
ECO101989	PSY105342	66%	42.3%	98.6%
ECO101989	PSY102624	54%	47.0%	98.8%
ECO101989	PSY108079	54%	56.8%	93.6%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101989	PSY100132	58%	61.8%	93.7%
ECO101989	PSY105328	57%	65.7%	94.5%
ECO101989	PSY108150	53%	77.5%	96.3%
ECO101989	PSY108972	53%	77.5%	98.9%
ECO101989	PSY101764	56%	79.9%	92.8%
ECO101989	PSY100142	58%	77.5%	92.9%
ECO101989	PSY100923	55%	88.8%	97.1%
ECO101989	PSY100425	56%	89.1%	94.9%
ECO101989	PSY100530	56%	91.7%	95.1%
ECO101989	PSY106503	56%	91.7%	95.1%
ECO101989	PSY106678	57%	91.4%	95.7%
ECO101989	PSY107045	57%	91.7%	95.1%
ECO101989	PSY103445	57%	91.7%	95.1%
ECO101989	PSY100366	57%	91.7%	95.1%
ECO101989	PSY106085	57%	91.7%	95.1%
ECO101989	PSY105970	57%	91.7%	95.1%
ECO101989	PSY103492	57%	91.7%	95.1%
ECO101989	PSY106670	57%	91.7%	95.1%
ECO101989	PSY108825	57%	91.7%	95.1%
ECO101989	PSY106530	57%	91.7%	95.1%
ECO101989	PSY106607	57%	91.7%	95.1%
ECO101989	PSY101541	57%	91.7%	91.4%
ECO101989	PSY100919	57%	91.7%	95.1%
ECO101989	PSY108757	57%	91.7%	95.1%
ECO101989	PSY100555	57%	91.7%	95.1%
ECO101989	PSY107011	57%	91.7%	95.1%
ECO101989	PSY108510	57%	91.7%	95.1%
ECO101989	PSY108390	57%	91.7%	95.1%
ECO101989	PSY106920	57%	91.7%	95.1%
ECO101989	PSY100368	57%	91.7%	95.1%
ECO101989	PSY100686	57%	91.7%	95.1%
ECO101989	PSY100026	57%	91.7%	95.1%
ECO101989	PSY107134	57%	91.7%	95.1%
ECO101989	PSY107080	57%	91.7%	95.1%
ECO101989	PSY100200	57%	91.7%	95.1%
ECO101989	PSY101963	57%	91.7%	95.1%
ECO101989	PSY108098	57%	91.7%	95.1%
ECO101989	PSY106521	57%	91.7%	95.1%
ECO101989	PSY107158	57%	91.7%	95.1%
ECO101989	PSY108313	57%	91.7%	95.1%
ECO101989	PSY106814	57%	91.7%	95.1%
ECO101989	PSY107065	57%	91.7%	95.1%
ECO101989	PSY102698	57%	91.7%	95.1%
ECO101989	PSY108019	57%	91.7%	95.1%
ECO101989	PSY107438	57%	91.7%	95.1%
ECO101989	PSY106301	57%	91.7%	95.1%
ECO101989	PSY108294	57%	91.7%	95.1%
ECO101989	SAU302002	100%	100%	100%
ECO101989	VCH103198	82%	96.2%	99.7%
ECO101989	VCH103013	82%	96.2%	99.7%
ECO101994	BAN104507	24%	45.9%	30.4%
ECO101994	BFU115854	23%	59.5%	53.9%
ECO101994	CJU100398	25%	27.1%	28.2%
ECO101994	CDF101229	25%	33.2%	66.2%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO101994	EFA202758	25%	22.4%	45.2%
ECO101994	ECO101994	100%	100%	100%
ECO101994	SAU800598	22%	29.1%	53.4%
ECO101995	ABA100286	32%	24.5%	19.8%
ECO101995	BAN112682	39%	10.4%	7.8%
ECO101995	BAN101794	39%	10.4%	7.8%
ECO101995	BAN107558	50%	10.4%	7.9%
ECO101995	BCE113421	41%	75.2%	94.2%
ECO101995	CJU101358	60%	98.6%	98.1%
ECO101995	CAC100692	37%	98.9%	99.7%
ECO101995	CBO103801	63%	98.4%	98.6%
ECO101995	CDP100618	45%	98.4%	97.4%
ECO101995	EFA200263	60%	97.8%	95.8%
ECO101995	ECO101995	100%	100%	100%
ECO101995	KPN300283	40%	55.3%	89.4%
ECO101995	LPN100642	48%	11.2%	8.3%
ECO101995	MAV105101	44%	99.2%	91.1%
ECO101995	MBV105249	43%	99.2%	94.7%
ECO101995	MLP100062	43%	99.2%	91.5%
ECO101995	MTU203754	43%	99.2%	94.7%
ECO101995	MGE100139	31%	99.2%	95.0%
ECO101995	MPN100557	31%	98.9%	96.2%
ECO101995	PSY100373	39%	97.0%	90.1%
ECO101995	SPA103753	39%	96.2%	92.4%
ECO101995	STY101896	38%	89.4%	90.4%
ECO101995	STM101645	39%	96.2%	92.4%
ECO101995	SHA101771	26%	45.5%	37.6%
ECO101995	SPN400319	61%	53.4%	97.5%
ECO101995	YPS001684	20%	64.0%	58.3%
ECO101996	BAN112783	18%	96.4%	81.8%
ECO101996	BAN105601	19%	96.4%	82.0%
ECO101996	BFR10318	21%	89.2%	94.4%
ECO101996	BCE102578	30%	96.6%	92.6%
ECO101996	BFU109796	25%	96.4%	90.1%
ECO101996	BMA102055	28%	60.2%	96.2%
ECO101996	CAC103498	28%	96.1%	92.6%
ECO101996	CBO102105	18%	88.4%	76.8%
ECO101996	EFA103494	20%	96.1%	84.3%
ECO101996	EFM202571	22%	65.5%	90.8%
ECO101996	ECO101996	100%	100%	100%
ECO101996	MCA103135	26%	49.4%	46.7%
ECO101996	SAU800132	22%	98.3%	84.5%
ECO101996	SHA100902	27%	37.3%	54.4%
ECO101996	SPN401149	20%	96.4%	80.4%
ECO102017	EBC102686	90%	99.4%	98.8%
ECO102017	ECO102017	100%	100%	100%
ECO102017	PPU110717	36%	96.3%	89.7%
ECO102017	SPA101233	88%	98.8%	98.8%
ECO102017	STY103559	90%	98.8%	98.8%
ECO102018	BAN106184	50%	13.6%	16.4%
ECO102018	BAN101034	43%	33.0%	40.6%
ECO102018	BAN113598	32%	56.3%	54.7%
ECO102018	BCE115140	40%	38.0%	24.7%
ECO102018	BFU111005	35%	33.0%	25.6%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102018	BFU102835	34%	35.5%	30.3%
ECO102018	BMA100943	24%	76.7%	39.6%
ECO102018	CJU101054	33%	40.9%	37.2%
ECO102018	CBO100253	34%	35.8%	11.2%
ECO102018	CDF102522	39%	44.8%	46.2%
ECO102018	CDF100756	39%	36.9%	39.9%
ECO102018	EBC102685	91%	98.6%	100%
ECO102018	EFA101670	35%	43.4%	54.3%
ECO102018	EFA101668	26%	73.1%	18.5%
ECO102018	ECO102018	100%	100%	100%
ECO102018	HIN101661	23%	87.1%	82.3%
ECO102018	KPN206346	32%	93.9%	89.3%
ECO102018	PSY104048	28%	45.2%	25.0%
ECO102018	SPA101232	90%	99.3%	98.9%
ECO102018	STM104358	27%	33.3%	31.8%
ECO102018	SMU100170	29%	36.6%	33.4%
ECO102018	SPN400136	35%	41.6%	37.9%
ECO102018	SPY200581	26%	41.6%	38.7%
ECO102023	BFR103686	22%	54.0%	38.5%
ECO102023	BPT103136	24%	27.1%	44.5%
ECO102023	EBC102773	70%	100%	100%
ECO102023	ECO102023	100%	100%	100%
ECO102023	HIN100127	19%	31.6%	45.3%
ECO102023	KPN305530	62%	100%	100%
ECO102023	LPN102648	16%	28.5%	33.5%
ECO102023	MAV101053	25%	19.3%	38.7%
ECO102023	NGO102494	18%	36.1%	29%
ECO102023	NME201800	21%	36.1%	28.0%
ECO102023	PMU100950	19%	30.5%	42.6%
ECO102023	PRT101807	35%	100%	100%
ECO102023	PAE205141	18%	17.7%	27.6%
ECO102023	PPU100174	21%	16.7%	24.5%
ECO102023	PSY107421	29%	84.1%	84.6%
ECO102023	SPA100423	63%	75.0%	100%
ECO102023	STY103566	75%	100%	100%
ECO102023	VCH101020	22%	99.7%	99.4%
ECO102023	YPS002349	46%	100%	100%
ECO102033	BAN106562	18%	82.8%	96.7%
ECO102033	BPT102716	50%	85.8%	94.0%
ECO102033	BCE108874	44%	82.5%	84.9%
ECO102033	BFU100768	44%	81.5%	82.9%
ECO102033	CDF100611	23%	67.9%	85.8%
ECO102033	EBC100477	78%	76.9%	100%
ECO102033	EFA202080	21%	59.1%	68.8%
ECO102033	ECO102033	100%	100%	100%
ECO102033	HIN100874	26%	62.3%	74.9%
ECO102033	HPY100954	21%	58.2%	71.0%
ECO102033	KPN307304	79%	86.9%	100%
ECO102033	LPN100326	30%	69.8%	86.1%
ECO102033	PMU101134	26%	72.8%	87.9%
ECO102033	PRT103182	57%	87.5%	98.1%
ECO102033	PAE202526	43%	86.6%	94.1%
ECO102033	PPU101036	50%	78.7%	93.1%
ECO102033	PSY102464	54%	65.1%	89.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102033	SPA100386	78%	98.5%	100%
ECO102033	STY104172	83%	89.4%	100%
ECO102033	STM103909	82%	89.4%	100%
ECO102033	SAU800197	20%	38.4%	43.8%
ECO102033	SEP201308	21%	69.6%	87.9%
ECO102033	SMU100791	25%	44.0%	49.2%
ECO102033	SPN400693	21%	71.8%	88.5%
ECO102033	VCH100897	27%	72.6%	89.2%
ECO102033	YPS003133	64%	87.3%	91.2%
ECO102035	ABA100532	30%	98.7%	98.8%
ECO102035	BAN104054	21%	39.2%	92.3%
ECO102035	BAN113400	23%	92.4%	93.5%
ECO102035	BAN111342	24%	98.8%	98.3%
ECO102035	BAN109301	26%	47.2%	98.6%
ECO102035	BPT102713	60%	98.9%	98.5%
ECO102035	BFU114052	49%	31.6%	84.8%
ECO102035	BFU103150	41%	62.5%	97.5%
ECO102035	BFU100826	52%	99.1%	99.0%
ECO102035	BMA107834	48%	99.1%	34.6%
ECO102035	CDF100351	26%	20.6%	99.5%
ECO102035	CDF103505	27%	98.6%	96.6%
ECO102035	CDP100571	24%	25.2%	29.9%
ECO102035	EBC101451	90%	97.5%	49.3%
ECO102035	ECO102035	100%	100%	100%
ECO102035	HPY100600	29%	97.4%	97.5%
ECO102035	KPN300214	93%	9.4%	95.0%
ECO102035	KPN304474	91%	100%	100%
ECO102035	LMO101639	21%	22.5%	23.7%
ECO102035	MAV103710	25%	18.8%	19.9%
ECO102035	PRT102326	72%	99.3%	99.1%
ECO102035	PAE202524	63%	48.2%	98.3%
ECO102035	PPU101032	55%	98.6%	98.1%
ECO102035	PSY101154	55%	99.2%	98.6%
ECO102035	SPA104062	86%	98.3%	100%
ECO102035	STY104175	91%	100%	99.9%
ECO102035	STM103911	91%	100%	99.9%
ECO102035	SHA100824	25%	98.0%	93.8%
ECO102035	SPY201593	25%	16.2%	30.0%
ECO102035	YPS003145	80%	99.4%	99.5%
ECO102040	ABA105133	66%	96.7%	97.1%
ECO102040	BAN113695	28%	85.7%	86.7%
ECO102040	BAN110083	31%	95.4%	93.7%
ECO102040	CJU100651	33%	89.2%	87.1%
ECO102040	CAC103116	36%	92.1%	93.6%
ECO102040	CAC103516	38%	92.1%	93.8%
ECO102040	CBO101395	37%	92.1%	92.9%
ECO102040	CDF101858	38%	96.0%	96.6%
ECO102040	EBC101308	88%	52.8%	100%
ECO102040	EFA200766	34%	94.3%	94.7%
ECO102040	EFM201535	34%	94.9%	95.9%
ECO102040	ECO102040	100%	100%	100%
ECO102040	HIN100399	79%	99.3%	98.7%
ECO102040	HPY100166	36%	87.2%	84.6%
ECO102040	KPN300020	88%	22.1%	99.0%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102040	KPN300423	98%	20.8%	89.5%
ECO102040	KPN304482	95%	99.8%	99.8%
ECO102040	LMO102686	33%	95.6%	97.1%
ECO102040	MCA100567	64%	94.5%	98.9%
ECO102040	NGO100452	58%	95.4%	97.8%
ECO102040	NME201774	60%	95.4%	97.8%
ECO102040	PMU100233	78%	99.8%	99.3%
ECO102040	PRT102329	83%	99.6%	98.3%
ECO102040	PAE205435	74%	99.6%	95.5%
ECO102040	PPU111450	72%	96.9%	97.1%
ECO102040	SPA104056	94%	94.0%	100%
ECO102040	STY104182	96%	100%	100%
ECO102040	STM103916	96%	100%	100%
ECO102040	SAU801612	33%	87.2%	85.3%
ECO102040	SEP201130	33%	87.2%	85.3%
ECO102040	SHA101196	31%	86.8%	84.8%
ECO102040	SMU100046	32%	94.9%	92.3%
ECO102040	SPN401281	22%	54.5%	88.4%
ECO102040	SPN401283	32%	94.9%	91.0%
ECO102040	SPY200427	33%	94.9%	92.3%
ECO102040	VCH100704	78%	99.8%	98.7%
ECO102040	YPS003165	83%	99.8%	97.4%
ECO102041	BCE114538	40%	51.4%	45.1%
ECO102041	EBC100818	72%	100%	100%
ECO102041	ECO102041	100%	100%	100%
ECO102041	KPN300790	58%	93.1%	100%
ECO102041	SPA102924	56%	93.1%	100%
ECO102041	STY102620	54%	86.1%	86.1%
ECO102041	STY102604	55%	93.1%	93.1%
ECO102041	STY103062	56%	93.1%	93.1%
ECO102041	YPS002733	53%	72.2%	64.2%
ECO102051	CAC101149	25%	85.8%	82.8%
ECO102051	CDF103902	45%	90.2%	96.2%
ECO102051	EFA200471	27%	85.8%	83.3%
ECO102051	EFM202569	31%	96.0%	94.9%
ECO102051	ECO102051	100%	100%	100%
ECO102051	KPN302059	87%	88.7%	97.8%
ECO102051	LMO102456	41%	91.4%	48.0%
ECO102051	SPA103907	87%	74.5%	94.4%
ECO102051	STY100949	85%	98.9%	97.6%
ECO102051	STM101688	85%	98.9%	97.6%
ECO102051	SAU800247	44%	91.4%	98.6%
ECO102056	BFR10950	64%	95.5%	97.8%
ECO102056	CPN200470	62%	93.6%	100%
ECO102056	CTR200480	62%	93.6%	100%
ECO102056	EBC101305	96%	51.3%	100%
ECO102056	ECO102056	100%	100%	100%
ECO102056	KPN300375	94%	29.7%	100%
ECO102056	KPN300279	80%	54.0%	100%
ECO102056	KPN305930	95%	93.6%	100%
ECO102056	PRT102331	88%	93.6%	100%
ECO102056	SPA100768	93%	99.2%	99.2%
ECO102056	STY104185	96%	93.6%	100%
ECO102057	EBC100332	90%	65.2%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102057	EFM103335	21%	66.8%	84.8%
ECO102057	ECO102057	100%	100%	100%
ECO102057	KPN300480	37%	24.7%	77.1%
ECO102057	KPN304405	37%	94.4%	100%
ECO102057	PRT104586	34%	94.6%	94.7%
ECO102057	SPA101211	89%	43.5%	100%
ECO102057	STY104186	94%	100%	100%
ECO102057	STM103926	94%	100%	100%
ECO102060	BPT100571	27%	89.9%	75.3%
ECO102060	BCE114915	32%	91.9%	93.4%
ECO102060	BFU102711	33%	92.7%	94.3%
ECO102060	BMA106091	31%	91.9%	91.9%
ECO102060	EBC100259	85%	79.4%	100%
ECO102060	ECO102060	100%	100%	100%
ECO102060	LMO102040	29%	87.9%	90.6%
ECO102060	PAE203754	30%	99.6%	98.8%
ECO102060	SPA101208	92%	100%	100%
ECO102060	STY104189	92%	100%	100%
ECO102060	YPS002288	28%	90.7%	84.9%
ECO102061	ABA105449	35%	74.5%	81.0%
ECO102061	BAN100724	32%	64.4%	100%
ECO102061	BFR103764	40%	85.5%	85.3%
ECO102061	CAC101945	25%	70.9%	52.4%
ECO102061	CAC102333	27%	68%	55.1%
ECO102061	CAC103064	27%	68%	55.2%
ECO102061	CAC100916	27%	75.6%	57.3%
ECO102061	CDP101400	36%	78.2%	58.1%
ECO102061	BFA201783	27%	69.5%	59.4%
ECO102061	ECO102061	100%	100%	100%
ECO102061	MAV105422	23%	62.9%	39.5%
ECO102061	PSY107807	29%	66.9%	95.2%
ECO102061	SEP201350	21%	68.7%	68.0%
ECO102061	SHA102214	21%	68.7%	72.0%
ECO102061	SMU101599	24%	58.9%	77.5%
ECO102065	BAN105349	45%	11.3%	39.1%
ECO102065	BPT100515	25%	92.0%	72.4%
ECO102065	BBU100615	33%	22.6%	16.2%
ECO102065	BFU110329	38%	17.9%	15.1%
ECO102065	CAC103749	38%	12.4%	22.9%
ECO102065	CBO102313	46%	16.4%	11.0%
ECO102065	CDP101428	29%	42.0%	32.3%
ECO102065	EBC101349	63%	99.6%	99.6%
ECO102065	ECO102065	100%	100%	100%
ECO102065	HPY101411	41%	11.7%	41.7%
ECO102065	HPY101406	47%	14.6%	53.3%
ECO102065	KPN302399	60%	99.3%	100%
ECO102065	LPN100694	26%	37.6%	40.4%
ECO102065	MAV106643	38%	21.2%	44.1%
ECO102065	MTU411238	33%	14.2%	10.3%
ECO102065	MGE100151	48%	9.9%	10.3%
ECO102065	PPU110820	60%	7.3%	20.7%
ECO102065	PSY108075	60%	99.3%	99.3%
ECO102065	SPA103445	75%	55.5%	90.5%
ECO102065	STM100110	77%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102065	TPA100552	25%	77.4%	59.9%
ECO102065	YPS003304	22%	75.9%	58.8%
ECO102066	ABA104340	37%	26.2%	35.4%
ECO102066	BCE100985	27%	34.3%	47.2%
ECO102066	BFU111670	34%	28.5%	37.4%
ECO102066	BMA108444	33%	31.4%	42.9%
ECO102066	EBC101816	63%	65.1%	100%
ECO102066	ECO102066	100%	100%	100%
ECO102066	KPN304485	66%	61.6%	94.3%
ECO102066	PPU110423	30%	55.2%	88.5%
ECO102066	PSY105412	28%	54.7%	86.6%
ECO102066	SPA103081	78%	66.3%	99.1%
ECO102066	STY104192	80%	64.0%	100%
ECO102066	STM103938	80%	64.0%	100%
ECO102075	ECO102077	35%	98.9%	58.8%
ECO102075	ECO102075	100%	100%	100%
ECO102087	BAN109609	38%	68.3%	32.8%
ECO102087	BAN103939	42%	72.4%	34.6%
ECO102087	BCE113462	50%	88.5%	84.3%
ECO102087	BFU103320	40%	78.6%	89.4%
ECO102087	BMA101918	48%	88.5%	77.9%
ECO102087	CDP101960	25%	82.3%	88.4%
ECO102087	EBC101969	79%	100%	99.2%
ECO102087	EFA201197	37%	76.1%	36.2%
ECO102087	EFM100592	41%	79.8%	77.6%
ECO102087	ECO102087	100%	100%	100%
ECO102087	KPN300432	73%	54.7%	89.3%
ECO102087	KPN308952	75%	99.2%	98.4%
ECO102087	MAV103177	31%	78.6%	72.7%
ECO102087	PAE203887	41%	78.6%	88.2%
ECO102087	PPU103928	43%	78.6%	89.4%
ECO102087	PSY104886	42%	78.6%	89.4%
ECO102087	SPA101283	85%	100%	100%
ECO102087	STY104213	85%	100%	100%
ECO102087	SAU800723	42%	77.8%	36.9%
ECO102087	SEP200779	42%	75.7%	35.7%
ECO102087	SHA101684	42%	77.8%	52.2%
ECO102087	SMU100859	36%	77.0%	36.6%
ECO102087	SPN401675	36%	76.1%	36.2%
ECO102087	SPY200861	37%	79.8%	37.5%
ECO102087	YPS000242	62%	97.5%	85.3%
ECO102091	BFR12227	47%	95.4%	99.5%
ECO102091	BFR100173	47%	95.9%	96.7%
ECO102091	BCE106341	29%	92.2%	96.0%
ECO102091	BCE114157	28%	94.8%	93.2%
ECO102091	BMA104139	32%	35.6%	71.2%
ECO102091	CAC101425	27%	74.2%	87.2%
ECO102091	EBC100545	93%	75.0%	100%
ECO102091	EFA200665	38%	94.0%	97.9%
ECO102091	ECO102091	100%	100%	100%
ECO102091	KPN308152	91%	100%	100%
ECO102091	LMO100590	40%	95.0%	98.8%
ECO102091	MAV102142	27%	83.8%	86.2%
ECO102091	MBV102634	28%	83.8%	88.0%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102091	MTU200185	28%	83.8%	88.0%
ECO102091	PAE201725	62%	100%	100%
ECO102091	PPU103399	60%	99.2%	99.9%
ECO102091	PSY103958	60%	100%	100%
ECO102091	SPA101478	92%	53.6%	99.8%
ECO102091	STY104221	92%	100%	100%
ECO102091	YPS001925	37%	95.4%	97.4%
ECO102096	CAC100302	38%	96.4%	98.0%
ECO102096	EBC102712	82%	67.6%	99.4%
ECO102096	EFA200448	32%	96.0%	93.8%
ECO102096	EFM201601	32%	96.0%	93.9%
ECO102096	ECO102096	100%	100%	100%
ECO102096	LPN101451	31%	96.0%	97.7%
ECO102096	PRT104799	35%	96.0%	92.5%
ECO102096	PSY105439	34%	98.0%	95.9%
ECO102096	SPA101528	78%	99.2%	100%
ECO102096	STY104231	80%	99.2%	99.2%
ECO102104	ECO102104	100%	100%	100%
ECO102104	SPA103486	56%	100%	100%
ECO102104	STY104257	59%	100%	97.5%
ECO102104	STM104010	59%	100%	97.5%
ECO102113	BPT102072	52%	99.3%	98.6%
ECO102113	BCE108135	37%	15.5%	19.4%
ECO102113	BCE103599	51%	99.3%	99.3%
ECO102113	BFU100632	53%	99.6%	98.6%
ECO102113	EBC101993	82%	99.3%	99.3%
ECO102113	ECO102113	100%	100%	100%
ECO102113	KPN302658	82%	99.3%	99.3%
ECO102113	MCA100219	55%	99.3%	99.3%
ECO102113	MAV104224	25%	69.1%	66.3%
ECO102113	MBV105322	30%	37.8%	32.0%
ECO102113	MLP101567	29%	30.2%	26.7%
ECO102113	MTU200768	30%	37.8%	31.1%
ECO102113	PAE203626	63%	99.3%	97.9%
ECO102113	PPU112106	62%	95.7%	94.7%
ECO102113	PSY100252	60%	91.0%	98.8%
ECO102113	SPA102638	85%	99.3%	100%
ECO102113	STY104279	87%	99.3%	96.8%
ECO102113	STM104028	86%	86.7%	98.4%
ECO102113	SMU101450	57%	99.3%	97.9%
ECO102113	YPS002263	73%	99.3%	97.9%
ECO102129	BFU103431	27%	96.7%	89.5%
ECO102129	EBC101476	87%	45.0%	100%
ECO102129	ECO102129	100%	100%	100%
ECO102129	KPN300529	77%	41.5%	100%
ECO102129	KPN301280	81%	100%	100%
ECO102129	MCA100396	21%	37.2%	38.2%
ECO102129	PSY105004	22%	90.3%	93.6%
ECO102129	SPA101502	89%	97.5%	97.9%
ECO102129	STY104305	90%	100%	100%
ECO102129	STM104054	90%	100%	100%
ECO102129	SAU800673	26%	94.9%	94.1%
ECO102129	SEP200718	25%	94.9%	94.5%
ECO102129	SPN401865	29%	31.8%	20%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102129	SPY102942	31%	19.3%	12.8%
ECO102136	ABA100843	34%	91.1%	98.4%
ECO102136	BCE108968	37%	93.6%	93.3%
ECO102136	BFU100533	36%	96.0%	91.1%
ECO102136	BMA105246	36%	45.4%	89.2%
ECO102136	EBC102152	77%	98.7%	99.5%
ECO102136	ECO102136	100%	100%	100%
ECO102136	HPY101235	38%	96.9%	98.8%
ECO102136	KPN305265	76%	98.7%	99.5%
ECO102136	PAE202056	40%	95.2%	96.3%
ECO102136	PAE201809	42%	93.7%	92.4%
ECO102136	PPU101200	43%	91.4%	89.7%
ECO102136	PSY103874	40%	94.4%	93.2%
ECO102136	SPA102470	87%	95.7%	100%
ECO102136	STY104319	86%	99.2%	100%
ECO102136	STM100148	86%	99.2%	100%
ECO102136	VCH103315	53%	95.2%	94.8%
ECO102136	YPS000357	68%	97.4%	98.0%
ECO102141	ABA104746	48%	11.9%	92.2%
ECO102141	ABA101188	29%	99.5%	97.8%
ECO102141	BAN112388	27%	97.5%	97.0%
ECO102141	BAN108740	30%	97.5%	92.8%
ECO102141	BFR101333	28%	90.4%	90.8%
ECO102141	BFR106060	28%	98.5%	95.5%
ECO102141	BPT102363	33%	96.5%	96.5%
ECO102141	BCE105915	41%	39.1%	62%
ECO102141	BFU106774	36%	91.2%	87.0%
ECO102141	BMA106590	33%	99.0%	96.5%
ECO102141	CJU100035	28%	98.2%	97.5%
ECO102141	CDP101654	29%	82.1%	89.8%
ECO102141	EBC102913	87%	99.7%	100%
ECO102141	EFM201550	22%	90.4%	93.8%
ECO102141	ECO102141	100%	100%	100%
ECO102141	HIN101214	42%	96.5%	96.0%
ECO102141	KPN301781	84%	99.7%	100%
ECO102141	MCA101373	30%	91.7%	90.4%
ECO102141	NME201886	30%	90.7%	88.3%
ECO102141	PMU100004	42%	97.0%	97.0%
ECO102141	PRT101139	61%	94.7%	100%
ECO102141	PAE204133	36%	94.7%	93.3%
ECO102141	PPU108255	30%	96.5%	97.2%
ECO102141	PSY102166	31%	97.2%	96.7%
ECO102141	SPA100234	91%	53.8%	100%
ECO102141	STY104329	93%	100%	100%
ECO102141	SAU802355	29%	95.2%	93.5%
ECO102141	SEP200901	32%	97.0%	94.8%
ECO102141	SHA101965	29%	97.2%	95.8%
ECO102141	VCH101607	48%	95.7%	94.5%
ECO102141	YPS000345	68%	100%	99.2%
ECO102144	ABA100156	46%	98.9%	96.9%
ECO102144	BFR10466	30%	91.5%	41.8%
ECO102144	BPT100615	48%	94.7%	44.1%
ECO102144	BBU100785	27%	93.6%	40.7%
ECO102144	BCE100941	47%	90.4%	42.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102144	BFU104372	34%	53.2%	30.7%
ECO102144	BMA104337	47%	90.4%	40.9%
ECO102144	CTR200177	25%	88.3%	46.5%
ECO102144	CBO100877	32%	78.7%	40.6%
ECO102144	CDP100213	27%	95.7%	43.9%
ECO102144	EBC102919	79%	100%	100%
ECO102144	EFA200510	25%	95.7%	45.0%
ECO102144	EFM200879	23%	95.7%	45.3%
ECO102144	ECO102144	100%	100%	100%
ECO102144	HIN101596	63%	98.9%	97.9%
ECO102144	KPN301785	87%	100%	100%
ECO102144	LPN100134	45%	63.8%	92.4%
ECO102144	LMO100830	27%	95.7%	43.0%
ECO102144	MCA100395	46%	97.9%	42.2%
ECO102144	MAV105518	38%	94.7%	40.2%
ECO102144	MBV105580	36%	94.7%	40.9%
ECO102144	MLP100176	33%	94.7%	40.9%
ECO102144	MTU201004	36%	94.7%	40.9%
ECO102144	NGO101086	40%	95.7%	47.4%
ECO102144	NME201008	40%	95.7%	47.4%
ECO102144	PMU100639	61%	98.9%	98.9%
ECO102144	PRT101142	65%	100%	100%
ECO102144	PAE204668	38%	97.9%	45.6%
ECO102144	PPU104091	39%	97.9%	46.7%
ECO102144	PSY102433	43%	97.9%	45.8%
ECO102144	STY104335	91%	100%	100%
ECO102144	STM100156	91%	100%	100%
ECO102144	SAU800501	26%	97.9%	42.4%
ECO102144	SEP201834	26%	97.9%	42.0%
ECO102144	SHA100294	26%	97.9%	41.6%
ECO102144	TPA100368	29%	88.3%	42.3%
ECO102144	VCH101613	60%	93.6%	94.6%
ECO102144	YPS000333	69%	98.9%	98.9%
ECO102158	BAN113007	25%	37.3%	54.4%
ECO102158	BAN100196	25%	56.4%	51.9%
ECO102158	BFU101537	38%	58.2%	100%
ECO102158	CBO100009	24%	45.5%	43.4%
ECO102158	CDP100250	29%	73.2%	58.1%
ECO102158	ECO102158	100%	100%	100%
ECO102158	HIN101066	65%	99.5%	99.1%
ECO102158	KPN303268	72%	95.9%	96.3%
ECO102158	LPN103411	42%	98.6%	96.0%
ECO102158	MCA100276	38%	88.6%	87.1%
ECO102158	MAV103621	25%	95.5%	76.8%
ECO102158	MBV100934	26%	81.4%	65.9%
ECO102158	MLP100370	26%	96.8%	77.4%
ECO102158	MTU201436	26%	81.4%	65.9%
ECO102158	PMU100006	66%	99.5%	99.1%
ECO102158	PAE201475	55%	99.1%	97.8%
ECO102158	PPU100226	54%	99.1%	98.2%
ECO102158	PSY101789	54%	99.1%	97.8%
ECO102158	SPA105501	67%	65.5%	86.4%
ECO102158	STY105178	86%	98.6%	99.5%
ECO102158	STY104020	85%	99.5%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102158	VCH102024	67%	98.6%	97.7%
ECO102158	YPS002274	77%	99.5%	100%
ECO102174	EBC104807	80%	39.9%	97.0%
ECO102174	ECO102174	100%	100%	100%
ECO102174	KPN305315	72%	39.4%	96.7%
ECO102174	PRT100254	30%	99.0%	99.8%
ECO102174	SPA102837	83%	100%	100%
ECO102174	STY100497	84%	100%	100%
ECO102174	STM100221	84%	100%	100%
ECO102175	BPT101953	31%	94.0%	77.9%
ECO102175	BCE104891	29%	98.1%	94.2%
ECO102175	BCE110834	42%	93.1%	86.2%
ECO102175	BCE110631	42%	93.1%	84.1%
ECO102175	BFU103402	30%	98.1%	93.9%
ECO102175	BFU101073	42%	94.4%	84.8%
ECO102175	BMA107754	37%	93.5%	96.2%
ECO102175	EBC101339	97%	100%	100%
ECO102175	ECO102175	100%	100%	100%
ECO102175	KPN302345	96%	100%	100%
ECO102175	PRT100255	90%	97.2%	96.3%
ECO102175	PAE204077	38%	94.4%	94.9%
ECO102175	PSY104929	41%	96.3%	100%
ECO102175	SPA102836	99%	100%	100%
ECO102175	STY100502	98%	100%	100%
ECO102175	STM100225	99%	100%	100%
ECO102175	YPS000270	91%	100%	99.5%
ECO102177	BAN100878	33%	35.7%	100%
ECO102177	BAN110444	33%	54.1%	97.6%
ECO102177	BFR10050	26%	37.8%	65.1%
ECO102177	BFR10471	23%	65.8%	90.1%
ECO102177	BFR103847	23%	66.4%	91.5%
ECO102177	BFR104769	31%	34.4%	91.3%
ECO102177	BFR102132	23%	64.0%	92.0%
ECO102177	BPT100807	27%	66.6%	60.9%
ECO102177	BBU100763	26%	55.1%	88.0%
ECO102177	BCE110046	33%	39.0%	67.8%
ECO102177	BFU102307	27%	45.6%	95.3%
ECO102177	BFU104735	25%	57.1%	23.6%
ECO102177	BFU115698	25%	26.8%	5.9%
ECO102177	BFU102033	27%	26.8%	5.8%
ECO102177	BFU108758	27%	26.8%	5.8%
ECO102177	CJU100732	32%	35.7%	62.5%
ECO102177	CPN200162	25%	54.8%	85.3%
ECO102177	CTR200741	25%	56.7%	92.6%
ECO102177	ECO102177	100%	100%	100%
ECO102177	HPY100240	28%	36.0%	55.4%
ECO102177	LPN100223	28%	54.8%	91.0%
ECO102177	NGO101717	23%	67.4%	60.3%
ECO102177	NME200153	23%	67.1%	60.1%
ECO102177	PMU101380	24%	70.1%	51.9%
ECO102177	PRT101476	23%	91.4%	74.8%
ECO102177	PAE201097	29%	66.6%	92.5%
ECO102177	PPU101155	31%	54.9%	55.0%
ECO102177	PSY103867	31%	54.9%	54.9%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102177	SAU800019	22%	98.0%	98.2%
ECO102177	SHA101256	25%	72.4%	73.4%
ECO102177	VCH101497	32%	49.5%	42.8%
ECO102186	BFR105684	34%	28.3%	24.6%
ECO102186	BCE102555	24%	22.8%	61.0%
ECO102186	BFU113675	44%	99.0%	82.5%
ECO102186	ECO102186	100%	100%	100%
ECO102186	PAE204487	54%	98.2%	86.4%
ECO102192	ABA101391	28%	96.3%	94.3%
ECO102192	ABA103347	28%	97.8%	95.5%
ECO102192	BFR100918	27%	91.6%	82.2%
ECO102192	BPT102917	28%	85.3%	67.3%
ECO102192	BCE106131	30%	84.1%	64.7%
ECO102192	BFU106485	29%	85.3%	65.5%
ECO102192	BMA101166	30%	84.1%	62.2%
ECO102192	CJU100024	28%	98.4%	99.7%
ECO102192	CPN200856	29%	95.8%	72.5%
ECO102192	CTR200209	31%	89.8%	67.8%
ECO102192	CAC101459	26%	90.0%	93.5%
ECO102192	CBO100410	27%	95.7%	97.8%
ECO102192	EBC104912	92%	43.2%	100%
ECO102192	ECO102192	100%	100%	100%
ECO102192	HIN101624	83%	100%	96.8%
ECO102192	HPY100672	26%	98.7%	99.9%
ECO102192	KPN309027	93%	100%	100%
ECO102192	LPN101523	28%	97.9%	82.3%
ECO102192	MCA102664	76%	40.1%	100%
ECO102192	NGO100273	77%	98.2%	99.9%
ECO102192	NME201367	77%	99.6%	99.3%
ECO102192	PMU100717	80%	100%	100%
ECO102192	PRT101668	85%	100%	100%
ECO102192	PAE201155	29%	85.9%	68.6%
ECO102192	PPU108076	28%	85.9%	68.9%
ECO102192	PSY104529	27%	85.9%	68.0%
ECO102192	SPA100868	94%	41.4%	100%
ECO102192	STY100522	96%	100%	100%
ECO102192	STM100241	96%	100%	100%
ECO102192	VCH101237	80%	100%	100%
ECO102192	YPS000266	90%	100%	100%
ECO102193	ABA103998	24%	83.0%	85.8%
ECO102193	ABA101388	23%	85.4%	94.2%
ECO102193	BFR10832	23%	90.4%	90.3%
ECO102193	BPT102919	25%	76.6%	67.8%
ECO102193	BCE105994	26%	76.9%	67.2%
ECO102193	BFU106488	27%	76.9%	65.9%
ECO102193	BMA101937	26%	76.9%	67.2%
ECO102193	CJU100204	25%	94.9%	96.8%
ECO102193	CPN200855	24%	76.9%	77.7%
ECO102193	CTR200210	25%	76.9%	77.7%
ECO102193	CAC103499	23%	91.2%	91.9%
ECO102193	CBO100701	22%	96.3%	97.1%
ECO102193	EBC102449	95%	100%	100%
ECO102193	ECO102193	100%	100%	100%
ECO102193	HIN101625	85%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102193	HPY100360	24%	91.8%	92.4%
ECO102193	KPN302355	97%	100%	100%
ECO102193	LPN102663	24%	77.7%	74.7%
ECO102193	LMO101175	25%	92.3%	91.7%
ECO102193	MCA101601	70%	100%	100%
ECO102193	NGO100274	82%	100%	98.2%
ECO102193	NME201364	81%	100%	100%
ECO102193	PMU100719	84%	100%	100%
ECO102193	PRT105222	88%	100%	100%
ECO102193	PAE201154	25%	76.9%	65.3%
ECO102193	PPU108078	25%	76.9%	65.1%
ECO102193	PSY104507	24%	76.9%	65.3%
ECO102193	SPA102116	93%	57.7%	100%
ECO102193	STY100524	98%	100%	100%
ECO102193	STM100243	98%	100%	100%
ECO102193	VCH101236	81%	100%	96.9%
ECO102193	YPS000265	88%	100%	100%
ECO102201	BCE103326	26%	98.2%	89.6%
ECO102201	BMA108589	26%	98.2%	91.2%
ECO102201	EBC100985	84%	99.2%	100%
ECO102201	ECO102201	100%	100%	100%
ECO102201	HIN100664	58%	99.2%	93.7%
ECO102201	HPY100658	23%	99.7%	98.2%
ECO102201	KPN302356	81%	99.7%	99.7%
ECO102201	MBV102204	20%	87.9%	41.3%
ECO102201	MLP101488	20%	87.9%	37.3%
ECO102201	PMU101440	59%	99.2%	93.7%
ECO102201	PRT102600	71%	99.7%	99.5%
ECO102201	SPA103570	87%	99.0%	100%
ECO102201	STY100540	94%	99.7%	99.7%
ECO102201	STM100259	94%	99.7%	99.7%
ECO102201	VCH103469	59%	99.2%	95.9%
ECO102201	YPS001321	72%	99.5%	97.8%
ECO102210	ECO102210	100%	100%	100%
ECO102210	PPU107669	36%	59%	50.9%
ECO102210	PSY104950	33%	54%	60.2%
ECO102210	PSY106018	34%	56.5%	48.7%
ECO102210	SPA103571	67%	99%	99.0%
ECO102210	STY100562	67%	99%	99.0%
ECO102210	SMU101847	28%	36.5%	40.3%
ECO102213	BCE112594	47%	97.7%	98.9%
ECO102213	BFU101145	58%	42.7%	76.8%
ECO102213	BMA102261	45%	98.2%	100%
ECO102213	EBC107404	77%	100%	100%
ECO102213	ECO102213	100%	100%	100%
ECO102213	KPN300107	55%	13.9%	86.0%
ECO102213	KPN304792	77%	99.5%	99.4%
ECO102213	PRT100983	68%	98.6%	98.6%
ECO102213	PAE203552	69%	98.3%	97.9%
ECO102213	SPA103579	86%	50.9%	98.8%
ECO102213	STY100570	79%	100%	100%
ECO102213	STM100287	79%	100%	100%
ECO102213	YPS003031	71%	98.6%	97.6%
ECO102216	BMA101178	31%	35.6%	63.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102216	CBO102059	30%	50.9%	93.2%
ECO102216	EBC104300	50%	56.8%	97.7%
ECO102216	ECO102216	100%	100%	100%
ECO102216	KPN304764	51%	56.8%	100%
ECO102216	PRT101259	38%	53.2%	90.2%
ECO102216	PAE203556	36%	53.2%	83.2%
ECO102216	SPA100716	56%	97.3%	100%
ECO102216	STY100576	68%	55.0%	97.6%
ECO102216	STM100295	68%	55.0%	97.6%
ECO102216	SMU100452	30%	41.4%	44.9%
ECO102216	YPS003015	33%	55.9%	96.9%
ECO102227	ECO102227	100%	100%	100%
ECO102227	SPA103572	28%	88.8%	96.2%
ECO102227	STY100542	28%	83.6%	97.2%
ECO102227	STM100261	29%	83.6%	97.2%
ECO102229	BFR104644	31%	32.6%	34.1%
ECO102229	BCE105027	36%	27.7%	29.8%
ECO102229	BMA104789	29%	43.4%	32.8%
ECO102229	ECO102229	100%	100%	100%
ECO102229	LPN102350	25%	83.4%	62.5%
ECO102229	LPN102353	26%	62.5%	68.9%
ECO102229	VCH103533	31%	38.8%	25.1%
ECO102233	BPT103695	32%	20.5%	26.9%
ECO102233	ECO102233	100%	100%	100%
ECO102233	STY103757	27%	43.8%	18.7%
ECO102253	EBC103027	89%	100%	100%
ECO102253	ECO102253	100%	100%	100%
ECO102253	HIN101178	44%	93.4%	98.6%
ECO102253	KPN300467	95%	45.0%	100%
ECO102253	KPN301394	89%	100%	100%
ECO102253	PMU100703	47%	93.4%	98.6%
ECO102253	PRT104902	65%	100%	100%
ECO102253	SPA102050	95%	82.8%	100%
ECO102253	STY100981	94%	100%	100%
ECO102253	VCH101080	44%	95.4%	96.1%
ECO102253	YPS000483	70%	100%	100%
ECO102255	ABA104878	49%	99.3%	99.0%
ECO102255	BAN106141	33%	43.8%	99.7%
ECO102255	BAN102570	46%	43.8%	96.9%
ECO102255	BFR101415	47%	42.9%	93.2%
ECO102255	CJU100638	48%	45.4%	64.9%
ECO102255	CAC102832	45%	43.8%	96.4%
ECO102255	CDF100616	23%	44.1%	97.3%
ECO102255	CDF100432	25%	43.0%	94.1%
ECO102255	CDP101294	42%	59.5%	91.4%
ECO102255	EBC104962	90%	100%	100%
ECO102255	EFA202248	44%	42.7%	93.9%
ECO102255	EFM200028	39%	26.9%	93.7%
ECO102255	ECO102255	100%	100%	100%
ECO102255	HIN101176	69%	99.7%	100%
ECO102255	HPY200837	49%	31.8%	8.5%
ECO102255	KPN305976	96%	99.3%	99.9%
ECO102255	LMO100950	47%	43.1%	94.8%
ECO102255	MCA101508	63%	23.8%	1.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102255	MAV101929	37%	97.5%	96.7%
ECO102255	MBV102834	37%	99.3%	98.8%
ECO102255	MTU200407	37%	99.3%	98.8%
ECO102255	MPN100413	36%	44.1%	97.5%
ECO102255	NGO100804	67%	15.5%	11.2%
ECO102255	NMB200777	67%	15.5%	11.2%
ECO102255	PMU100705	69%	99.7%	100%
ECO102255	PRT100628	82%	99.4%	100%
ECO102255	PAE200834	55%	99.0%	98.9%
ECO102255	PPU103956	49%	98.7%	100%
ECO102255	PSY102379	51%	97.6%	99.4%
ECO102255	SPA102048	88%	70.4%	93.3%
ECO102255	STY100983	96%	100%	99.9%
ECO102255	STM100723	96%	100%	99.9%
ECO102255	SAU800588	42%	43.0%	94.8%
ECO102255	SEP200137	44%	43.0%	94.8%
ECO102255	SHA101700	45%	43.0%	94.8%
ECO102255	SMU100210	45%	42.7%	92.7%
ECO102255	SPN401007	48%	43.1%	95.1%
ECO102255	SPY200858	44%	43.3%	94.0%
ECO102255	UUR100064	24%	35.4%	82.9%
ECO102255	VCH101078	74%	100%	99.9%
ECO102255	YPS000496	87%	99.7%	99.2%
ECO102259	ABA103937	50%	98.6%	100%
ECO102259	BPT100934	51%	93.9%	85.5%
ECO102259	BCE105657	29%	67.8%	71.4%
ECO102259	BFU101725	25%	86.9%	83.9%
ECO102259	EBC103024	70%	76.6%	100%
ECO102259	ECO102259	100%	100%	100%
ECO102259	KPN302840	71%	79.4%	100%
ECO102259	PAE204399	30%	85.0%	86.3%
ECO102259	PPU107709	26%	88.3%	92.9%
ECO102259	PSY103869	27%	85.5%	91.5%
ECO102259	SPA103767	80%	100%	100%
ECO102259	STY100992	81%	100%	100%
ECO102266	ABA105182	60%	98.7%	98.3%
ECO102266	BCE111438	62%	99.6%	99.1%
ECO102266	BFU115309	62%	99.6%	97.4%
ECO102266	BMA105998	61%	99.6%	99.1%
ECO102266	EBC103021	91%	100%	100%
ECO102266	ECO102266	100%	100%	100%
ECO102266	KPN302806	86%	100%	100%
ECO102266	MCA102171	40%	99.6%	95%
ECO102266	PAE202922	63%	98.2%	97.8%
ECO102266	PPU106919	51%	100%	100%
ECO102266	PSY100833	57%	98.7%	88.6%
ECO102266	SPA103776	91%	99.6%	100%
ECO102266	STY100997	91%	100%	100%
ECO102266	VCH101832	47%	96.5%	92.3%
ECO102266	YPS002431	77%	100%	100%
ECO102267	BCE106677	54%	99.6%	92.8%
ECO102267	BMA104068	55%	99.2%	78.7%
ECO102267	EBC103019	93%	100%	100%
ECO102267	ECO102267	100%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102267	KPN302841	90%	99.6%	99.6%
ECO102267	PAE202921	50%	97.7%	96.6%
ECO102267	SPA103777	98%	100%	100%
ECO102267	STY100998	97%	100%	100%
ECO102267	YPS002427	76%	99.6%	98.9%
ECO102274	ABA101266	56%	88.2%	89.3%
ECO102274	BAN103283	52%	85.2%	88.6%
ECO102274	BFR11899	25%	61.8%	34.0%
ECO102274	BFR11219	26%	61.2%	33.5%
ECO102274	BFR11611	29%	61.8%	34.2%
ECO102274	BPT100791	62%	91.8%	96.9%
ECO102274	BCE105100	71%	43.4%	97.1%
ECO102274	BFU114977	63%	92.8%	98.6%
ECO102274	BMA103750	63%	92.8%	98.6%
ECO102274	CJU100116	53%	82.6%	89.6%
ECO102274	CPN200705	52%	82.6%	81.5%
ECO102274	CTR200558	52%	82.6%	88.7%
ECO102274	CAC103552	51%	88.8%	93.7%
ECO102274	CDF101011	52%	85.9%	90.8%
ECO102274	CDP100046	34%	74.3%	44.1%
ECO102274	EBC101249	98%	82.9%	100%
ECO102274	EFA200246	45%	85.9%	89.2%
ECO102274	EFM200144	43%	86.2%	89.3%
ECO102274	ECO102274	100%	100%	100%
ECO102274	HIN101232	75%	93.1%	96.3%
ECO102274	HPY100934	49%	83.6%	87.9%
ECO102274	KPN302817	97%	100%	100%
ECO102274	LPN101645	69%	67.4%	93.6%
ECO102274	LMO101514	47%	90.5%	92.5%
ECO102274	MCA101005	62%	60.2%	97.3%
ECO102274	MAV105603	36%	82.2%	48.4%
ECO102274	MBV105423	39%	80.6%	48.3%
ECO102274	MLP100443	27%	61.2%	31.5%
ECO102274	MTU200895	39%	80.6%	48.3%
ECO102274	NGO100954	60%	91.1%	96.9%
ECO102274	NME200815	60%	91.1%	96.9%
ECO102274	PMU100636	75%	93.1%	94.1%
ECO102274	PRT103138	75%	29.6%	72.6%
ECO102274	PRT100424	81%	99.7%	96.6%
ECO102274	PAE203110	71%	88.8%	93.1%
ECO102274	PPU105860	67%	92.1%	93.6%
ECO102274	PSY101722	69%	93.4%	93.1%
ECO102274	SPA100127	63%	70.7%	100%
ECO102274	STY101011	98%	100%	100%
ECO102274	SAU801701	47%	86.8%	91.6%
ECO102274	SEP201705	46%	86.8%	91.6%
ECO102274	SHA100922	46%	86.8%	90.6%
ECO102274	SMU100531	44%	89.5%	91.7%
ECO102274	SPN400386	43%	86.2%	89.6%
ECO102274	SPY201343	45%	84.5%	87.8%
ECO102274	VCH100983	73%	100%	98.7%
ECO102274	YPS002401	86%	97.4%	98.0%
ECO102277	BAN105110	35%	68.2%	95.2%
ECO102277	BAN110285	34%	97.6%	97.1%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102277	BFR101725	35%	97.3%	98.2%
ECO102277	BPT104802	28%	33.8%	22.8%
ECO102277	CJU100951	33%	98.8%	98.8%
ECO102277	CPN200789	26%	70.6%	68.2%
ECO102277	CTR200632	23%	82.2%	79.6%
ECO102277	CAC102778	25%	32.0%	34.7%
ECO102277	CAC100810	20%	100%	100%
ECO102277	CBO102584	33%	97.6%	87.9%
ECO102277	CDF102483	33%	96.1%	96.4%
ECO102277	CDP101635	31%	96.7%	99.1%
ECO102277	EBC101246	88%	100%	100%
ECO102277	EFA200749	32%	98.2%	96.6%
ECO102277	BFM202572	32%	96.7%	96.1%
ECO102277	ECO102277	100%	100%	100%
ECO102277	HIN101399	31%	97.6%	97.8%
ECO102277	HPY101172	27%	96.1%	97.1%
ECO102277	KPN302836	88%	100%	100%
ECO102277	LPN102579	40%	99.7%	100%
ECO102277	LMO102054	32%	98.8%	98.8%
ECO102277	MAV103165	34%	97.3%	98.8%
ECO102277	MBV102870	32%	94.1%	99.7%
ECO102277	MLP101382	31%	98.8%	99.1%
ECO102277	MTU203654	32%	98.2%	99.4%
ECO102277	PMU100486	32%	99.1%	99.4%
ECO102277	PRT101099	59%	100%	100%
ECO102277	PAE203114	38%	99.7%	100%
ECO102277	PPU105849	39%	98.8%	99.1%
ECO102277	PSY101677	37%	90.8%	100%
ECO102277	SPA102819	88%	100%	100%
ECO102277	STY101017	89%	100%	100%
ECO102277	SAU801394	29%	97.0%	97.6%
ECO102277	SEP202102	29%	96.7%	97.3%
ECO102277	SHA100967	30%	96.7%	97.3%
ECO102277	SMU100090	28%	97.3%	95.0%
ECO102277	SPN400918	32%	97.3%	95.0%
ECO102277	VCH102075	47%	99.4%	99.4%
ECO102277	YPS002391	71%	100%	100%
ECO102278	ABA100261	41%	92.9%	97.5%
ECO102278	BFR105970	40%	93.9%	99.1%
ECO102278	EBC101245	88%	99.7%	99.7%
ECO102278	ECO102278	100%	100%	100%
ECO102278	KPN300235	87%	37.3%	96.6%
ECO102278	KPN302833	85%	100%	100%
ECO102278	LPN100171	32%	83.3%	100%
ECO102278	MCA101758	36%	92.3%	98.9%
ECO102278	PRT101100	69%	98.9%	99.7%
ECO102278	PAE201374	47%	93.7%	94.7%
ECO102278	PPU100882	45%	93.7%	94.5%
ECO102278	PSY104726	50%	93.7%	94.5%
ECO102278	SPA102820	85%	99.7%	100%
ECO102278	STY101019	89%	99.7%	99.7%
ECO102278	VCH102076	49%	97.9%	95.9%
ECO102278	YPS002383	72%	97.9%	98.7%
ECO102294	BCE109553	50%	55.2%	80.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102294	EBC101870	53%	93.2%	100%
ECO102294	ECO102294	100%	100%	100%
ECO102294	KPN300579	41%	88.4%	98.7%
ECO102294	PRT103789	43%	86%	86.6%
ECO102294	PRT105512	48%	96.4%	98.0%
ECO102294	PRT100542	51%	92.4%	93.7%
ECO102294	SPA103175	62%	95.2%	96%
ECO102294	STY103518	51%	93.6%	92.2%
ECO102294	STM103181	62%	95.2%	96%
ECO102294	YPS002774	43%	93.2%	97.1%
ECO102295	ECO102295	100%	100%	100%
ECO102299	BPT101732	31%	96.8%	96.0%
ECO102299	BCE107836	35%	84.3%	95.4%
ECO102299	BFU100376	38%	18.6%	73.4%
ECO102299	BFU101790	36%	97.3%	95.1%
ECO102299	BMA108007	33%	96.9%	98.6%
ECO102299	EBC103285	81%	96.9%	100%
ECO102299	ECO102299	100%	100%	100%
ECO102299	KPN302810	77%	98.9%	99.0%
ECO102299	LPN101186	32%	92.7%	95.1%
ECO102299	MAV106193	34%	94.7%	97.9%
ECO102299	MAV102403	34%	95.0%	97.5%
ECO102299	MBV101858	34%	94.4%	97.9%
ECO102299	MLP101294	33%	95.7%	98.3%
ECO102299	MTU200851	34%	95.7%	98.2%
ECO102299	PRT104299	59%	98.7%	100%
ECO102299	SPA101277	84%	96.1%	99.7%
ECO102299	STY101059	85%	99.7%	99.6%
ECO102299	VCH101028	56%	98.9%	97.7%
ECO102299	YPS002312	64%	98.7%	93.7%
ECO102300	ABA105679	38%	96.6%	80.7%
ECO102300	BFU113756	39%	96.6%	97.7%
ECO102300	EBC103287	93%	100%	98.6%
ECO102300	ECO102300	100%	100%	100%
ECO102300	KPN302809	88%	100%	99.1%
ECO102300	LPN103520	34%	97.0%	96.1%
ECO102300	MCA101138	38%	96.8%	99.1%
ECO102300	MAV102113	37%	98.6%	88.7%
ECO102300	MBV104788	38%	96.8%	97.0%
ECO102300	MLP101512	36%	96.8%	93.4%
ECO102300	MTU200242	38%	96.8%	97.0%
ECO102300	PRT104089	76%	97.2%	97.7%
ECO102300	PAE204781	37%	96.6%	98.6%
ECO102300	PPU105718	39%	97.5%	99.5%
ECO102300	PSY102192	39%	88.8%	97.7%
ECO102300	SPA101278	81%	100%	100%
ECO102300	STY101068	93%	100%	100%
ECO102300	SMU101700	25%	15.6%	28.8%
ECO102300	VCH101027	73%	98.2%	88.4%
ECO102300	YPS002308	80%	100%	100%
ECO102301	EBC103289	80%	98.0%	100%
ECO102301	ECO102301	100%	100%	100%
ECO102301	HIN100380	44%	90.2%	96.8%
ECO102301	KPN302808	85%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102301	PMU101070	50%	90.2%	85.2%
ECO102301	PRT106011	58%	92.2%	95.9%
ECO102301	SPA101279	90%	100%	100%
ECO102301	STY101071	93%	92.2%	100%
ECO102301	YPS002304	63%	92.2%	95.9%
ECO102302	ABA100283	20%	55.1%	57.5%
ECO102302	BFU113190	21%	85.3%	89.4%
ECO102302	EBC103291	75%	100%	100%
ECO102302	ECO102302	100%	100%	100%
ECO102302	HIN100381	39%	98.2%	99.3%
ECO102302	HPY100826	19%	78.3%	71.7%
ECO102302	KPN300868	76%	84.4%	100%
ECO102302	LPN103173	25%	94.0%	90.4%
ECO102302	MCA101962	22%	60.3%	49.4%
ECO102302	NGO101776	25%	46.0%	79.5%
ECO102302	NME200172	23%	93.8%	90.9%
ECO102302	PMU101069	45%	100%	97.1%
ECO102302	PRT101022	59%	99.6%	100%
ECO102302	PAE201287	25%	94.0%	93.2%
ECO102302	PPU104562	26%	98.9%	99.8%
ECO102302	PSY104544	27%	97.8%	97.9%
ECO102302	SPA103147	94%	44.4%	99.5%
ECO102302	STY101074	91%	100%	100%
ECO102302	STM100858	91%	100%	100%
ECO102302	SAU301338	26%	19.0%	47.1%
ECO102302	VCH103582	38%	97.8%	99.0%
ECO102302	YPS002300	63%	100%	100%
ECO102303	CAC101472	28%	40.3%	25.6%
ECO102303	CBO100325	26%	40.3%	82.5%
ECO102303	ECO102303	100%	100%	100%
ECO102303	SMU100480	27%	21.9%	54.9%
ECO102304	ABA100317	37%	77.3%	63.5%
ECO102304	BPT102103	35%	96.0%	91.3%
ECO102304	BCE101609	36%	94.8%	77.2%
ECO102304	BFU102908	37%	92.8%	65.7%
ECO102304	BMA105727	38%	89.6%	70.2%
ECO102304	CJU101295	32%	77.3%	82.8%
ECO102304	EBC103292	88%	100%	100%
ECO102304	ECO102304	100%	100%	100%
ECO102304	HIN100697	41%	98.8%	98.8%
ECO102304	KPN300867	88%	100%	100%
ECO102304	NGO101284	32%	84.1%	76.2%
ECO102304	NME200455	32%	82.1%	73.8%
ECO102304	PMU101501	48%	98.0%	98.0%
ECO102304	PRT104688	67%	99.2%	94.3%
ECO102304	PAE202798	33%	91.2%	92.3%
ECO102304	PPU109914	33%	90.8%	94.5%
ECO102304	PSY102933	33%	82.5%	86.7%
ECO102304	SPA103149	93%	84.9%	100%
ECO102304	STY101077	94%	100%	100%
ECO102304	VCH102018	46%	88.4%	87.4%
ECO102304	YPS002296	75%	99.6%	99.2%
ECO102306	EBC101290	42%	69.1%	96.0%
ECO102306	EBC103212	47%	98.7%	95.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102306	ECO102306	100%	100%	100%
ECO102306	PRT104903	47%	98.7%	95.5%
ECO102306	PSY100759	35%	97.4%	94.5%
ECO102306	PSY104073	36%	97.9%	98.0%
ECO102306	SPN202986	22%	86.0%	93.9%
ECO102306	SPN201140	23%	86.0%	93.6%
ECO102306	YPS002735	47%	97.9%	96.2%
ECO102309	BAN101643	28%	27.5%	13.0%
ECO102309	BAN102231	28%	27.5%	35.8%
ECO102309	BFR101716	23%	17.4%	20.3%
ECO102309	BBU100071	22%	71.6%	71.0%
ECO102309	CAC100251	24%	95.9%	93.6%
ECO102309	CBO100594	28%	19.6%	44.6%
ECO102309	ECO102309	100%	100%	100%
ECO102309	SPA107090	21%	32.3%	35.9%
ECO102309	STY105066	21%	32.3%	35.9%
ECO102309	SAU802647	29%	12.4%	12.2%
ECO102309	SPN202910	24%	33.4%	40.1%
ECO102310	ECO101129	93%	83.3%	47.5%
ECO102310	ECO102310	100%	100%	100%
ECO102310	STY100513	59%	79.8%	44.4%
ECO102310	STY102589	85%	90.4%	49.7%
ECO102324	CDF100186	28%	77.5%	84.5%
ECO102324	EFM101276	25%	78.5%	99.5%
ECO102324	ECO102324	100%	100%	100%
ECO102324	MLP100958	25%	80.7%	78.5%
ECO102324	MTU203196	26%	80.3%	39.4%
ECO102324	MTU203674	27%	82.4%	40.3%
ECO102324	SAU802352	27%	95.9%	75.9%
ECO102324	SEP200058	26%	94.3%	72.9%
ECO102324	SMU101282	28%	79.3%	86.9%
ECO102324	SMU101105	26%	78.7%	71.1%
ECO102325	BAN112247	28%	28.4%	49.1%
ECO102325	BAN106780	34%	28.4%	50.2%
ECO102325	BBU100140	23%	24.8%	29.6%
ECO102325	ECO102325	100%	100%	100%
ECO102325	KPN105518	45%	33.9%	97.0%
ECO102325	SAU802353	31%	9.0%	35.3%
ECO102325	SEP200059	30%	29.2%	51.6%
ECO102325	SHA101967	32%	28.4%	50.2%
ECO102325	VCH101389	39%	87.9%	92.9%
ECO102327	BAN105225	32%	31.9%	98.1%
ECO102327	BFR103042	23%	10.5%	45.1%
ECO102327	BFR101189	21%	12.6%	23.2%
ECO102327	BFR105724	27%	9.4%	22.0%
ECO102327	BFR100047	23%	16.2%	95.5%
ECO102327	BFR104792	38%	8.3%	27.0%
ECO102327	BFR106019	34%	9.3%	84.8%
ECO102327	BFR104322	32%	9.4%	87.5%
ECO102327	BFR10160	24%	22.6%	88.4%
ECO102327	BFR11362	30%	14.6%	56.4%
ECO102327	BFR101143	34%	12.3%	61.1%
ECO102327	BFR100846	26%	21.6%	37.9%
ECO102327	BFR101230	28%	20.8%	36.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102327	BFR101426	28%	20.8%	47.7%
ECO102327	BFR100955	30%	19.5%	99.1%
ECO102327	BFR104184	26%	29.7%	27.9%
ECO102327	BFR102180	24%	26.3%	90.7%
ECO102327	BFR101650	31%	20.8%	29.7%
ECO102327	BFR105953	32%	19.5%	30.9%
ECO102327	BFR101152	25%	33.1%	31.4%
ECO102327	BFR10010	30%	20.0%	95.1%
ECO102327	BFR100177	28%	20.4%	38.3%
ECO102327	BFR10421	30%	21.0%	63.9%
ECO102327	BFR105397	27%	33.9%	50.4%
ECO102327	BFR100838	25%	30.8%	29.0%
ECO102327	BFR100736	32%	20.7%	61.7%
ECO102327	BFR101753	33%	21.3%	26.4%
ECO102327	BFR11164	36%	19.7%	42.2%
ECO102327	BFR11210	25%	39.3%	90.7%
ECO102327	BFR12194	26%	31.2%	61.9%
ECO102327	BFR100523	33%	20.9%	28.0%
ECO102327	BFR100487	27%	35.1%	32.1%
ECO102327	BFR102042	29%	32.4%	46.3%
ECO102327	BFR100456	32%	30.6%	56.0%
ECO102327	BFR104593	28%	39.4%	60.0%
ECO102327	BFR11399	32%	32.2%	45.8%
ECO102327	BFR101340	30%	32.6%	37.6%
ECO102327	BFR102465	33%	30.9%	97.9%
ECO102327	BPT101258	28%	98.7%	97.7%
ECO102327	BCE113373	26%	21.2%	85.6%
ECO102327	BCE110418	33%	33.3%	89.7%
ECO102327	BFU107834	32%	32.7%	36.0%
ECO102327	BMA108695	31%	29.7%	48.3%
ECO102327	CDF101251	22%	57.6%	98.8%
ECO102327	ECO102327	100%	100%	100%
ECO102327	KPN301629	48%	8.5%	1.2%
ECO102327	PAE203042	33%	51.6%	84.3%
ECO102327	PAE203943	28%	97.0%	97.3%
ECO102327	PPU101764	28%	95.8%	95.2%
ECO102327	PSY105580	34%	38.9%	99.4%
ECO102327	VCH101626	23%	92.5%	98.3%
ECO102335	ABA103657	35%	83.5%	98.2%
ECO102335	ABA100510	33%	91.5%	96.5%
ECO102335	EBC101559	83%	93.6%	86.0%
ECO102335	ECO102335	100%	100%	100%
ECO102335	HPY100276	23%	76.2%	79.3%
ECO102335	KPN300200	71%	46.0%	100%
ECO102335	KPN308311	70%	91.8%	99.3%
ECO102335	MCA102793	31%	88.7%	86.7%
ECO102335	NME103365	28%	79.3%	88.8%
ECO102335	SPA103016	87%	99.7%	100%
ECO102335	STY101117	91%	93.3%	100%
ECO102335	STM100888	90%	93.3%	100%
ECO102335	YPS003046	67%	91.5%	98.4%
ECO102336	ABA101400	26%	91.7%	93.4%
ECO102336	BAN111058	36%	81.3%	89.0%
ECO102336	BAN110656	38%	86.4%	90.1%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102336	BFR105861	34%	87.6%	98.9%
ECO102336	BPT101343	79%	95.4%	99.5%
ECO102336	BCE112311	29%	93.0%	96.0%
ECO102336	BMA108485	28%	93.9%	92.8%
ECO102336	CJU100139	53%	93.4%	98%
ECO102336	CPN200256	24%	89.8%	93.2%
ECO102336	CTR200659	26%	84.0%	87.8%
ECO102336	CAC101393	31%	91.3%	96.6%
ECO102336	CBO103831	28%	86.7%	90.0%
ECO102336	CDP100538	27%	86.4%	92.6%
ECO102336	EBC101560	94%	71.4%	98.7%
ECO102336	EFA100818	30%	86.2%	89.8%
ECO102336	EFM201340	30%	86.2%	90.5%
ECO102336	ECO102336	100%	100%	100%
ECO102336	KPN301772	96%	98.1%	100%
ECO102336	LPN101493	64%	95.6%	99.2%
ECO102336	LMO101321	37%	93.7%	97.5%
ECO102336	MBV101440	30%	90.3%	97.5%
ECO102336	MLP100918	31%	90.3%	96.2%
ECO102336	MTU201162	30%	90.3%	97.5%
ECO102336	NGO101128	26%	93.4%	99.5%
ECO102336	NME201026	26%	93.4%	99.5%
ECO102336	PAE204711	90%	98.3%	98.5%
ECO102336	PPU109673	89%	96.8%	99.3%
ECO102336	PSY103563	88%	97.1%	99.5%
ECO102336	SPA103017	94%	100%	100%
ECO102336	STY101128	95%	100%	100%
ECO102336	SAU802560	32%	84.7%	89.6%
ECO102336	SEP201196	32%	84.7%	89.1%
ECO102336	SHA101775	31%	86.4%	90.9%
ECO102336	SMU101230	29%	86.2%	90.3%
ECO102336	SPN400035	30%	86.9%	91.5%
ECO102336	SPY200468	26%	89.3%	93.2%
ECO102336	YPS000566	87%	99.8%	100%
ECO102340	ECO102340	100%	100%	100%
ECO102340	PAE203757	32%	79.2%	76.8%
ECO102346	BAN100855	23%	90.2%	92.9%
ECO102346	CDP100903	24%	38.5%	56.9%
ECO102346	EBC100292	78%	57.2%	100%
ECO102346	ECO102346	100%	100%	100%
ECO102346	KPN301764	77%	97.6%	99.3%
ECO102346	LMO102180	20%	78.9%	82.4%
ECO102346	MLP101425	23%	36.6%	50.5%
ECO102346	PPU103355	25%	30.9%	28.2%
ECO102346	SPA100138	79%	56.7%	96.7%
ECO102346	STY101134	80%	97.6%	99.3%
ECO102346	STM100894	80%	97.6%	99.3%
ECO102351	ECO100572	100%	99.5%	100%
ECO102351	ECO100016	100%	99.5%	100%
ECO102351	ECO102351	100%	100%	100%
ECO102351	KPN301837	28%	24.5%	33.5%
ECO102351	KPN301756	28%	24.5%	25.9%
ECO102351	PPU112458	31%	21.5%	17.3%
ECO102351	PPU110183	31%	21.5%	18.0%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102351	PPU100534	31%	21.5%	17.3%
ECO102351	PPU111918	31%	21.5%	17.3%
ECO102351	PPU111424	31%	21.5%	17.3%
ECO102351	PPU109580	31%	21.5%	17.3%
ECO102351	STY100108	28%	24.5%	25.9%
ECO102355	ABA100922	34%	98.5%	97.5%
ECO102355	BAN110804	31%	97.7%	98.6%
ECO102355	BAN108869	35%	97.7%	99.2%
ECO102355	BFR102616	29%	94.3%	99.6%
ECO102355	BPT102905	52%	96.6%	92.7%
ECO102355	BBU100371	34%	99.4%	100%
ECO102355	BCE100150	61%	57.3%	98.6%
ECO102355	BFU100071	49%	95.1%	98.5%
ECO102355	BMA103736	49%	97.5%	98.9%
ECO102355	CJU101212	43%	97.7%	98.3%
ECO102355	CPN200187	32%	96.6%	92.3%
ECO102355	CTR200720	30%	98.1%	93.5%
ECO102355	CAC101596	36%	97.9%	98.4%
ECO102355	CBO103047	38%	97.9%	97.1%
ECO102355	CDF100252	36%	97.0%	98.4%
ECO102355	CDP100231	32%	96.6%	96.0%
ECO102355	EBC100212	90%	98.5%	100%
ECO102355	EFA200192	38%	97.7%	98.4%
ECO102355	EFM202131	38%	97.9%	99.6%
ECO102355	ECO102355	100%	100%	100%
ECO102355	HIN100261	72%	98.5%	96.5%
ECO102355	HPY100472	42%	97.5%	98.9%
ECO102355	KPN300278	93%	47.8%	100%
ECO102355	LPN103492	59%	99.2%	99.1%
ECO102355	LMO101411	37%	97.0%	97.8%
ECO102355	MCA102322	33%	98.1%	96.1%
ECO102355	MAV101415	33%	93.4%	97.7%
ECO102355	MBV101327	34%	97.2%	100%
ECO102355	MLP101032	34%	97.5%	96.0%
ECO102355	MTU202954	34%	98.1%	98.2%
ECO102355	MGE100471	32%	97.9%	98.6%
ECO102355	MPN100164	34%	95.8%	96.5%
ECO102355	NGO100018	46%	97.0%	99.6%
ECO102355	NME200234	48%	97.0%	99.6%
ECO102355	PMU101115	73%	98.5%	96.5%
ECO102355	PRT100735	85%	99.6%	99.4%
ECO102355	PAE203132	37%	98.1%	95.3%
ECO102355	PPU101878	35%	99.6%	97.6%
ECO102355	PSY105734	36%	99.6%	97.6%
ECO102355	SPA103535	84%	100%	100%
ECO102355	STY101161	95%	92.6%	92.0%
ECO102355	SAU800528	37%	97.2%	99.0%
ECO102355	SEP201872	38%	96.8%	98.6%
ECO102355	SHA101478	36%	93.8%	99.6%
ECO102355	SMU100660	37%	97.9%	98.8%
ECO102355	SPN401878	38%	98.5%	99.2%
ECO102355	SPY200174	37%	97.5%	99.2%
ECO102355	TPA100665	34%	97.9%	97.4%
ECO102355	UUR100606	32%	98.5%	99.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102355	VCH102180	69%	99.4%	92.5%
ECO102355	YPS000590	84%	100%	100%
ECO102363	ABA103642	25%	41.8%	40.3%
ECO102363	BAN108766	23%	45.4%	55.4%
ECO102363	BCE101681	29%	35.7%	76.4%
ECO102363	BCE111898	32%	30.2%	68.3%
ECO102363	EBC101051	87%	47.6%	100%
ECO102363	ECO102363	100%	100%	100%
ECO102363	HIN101075	28%	95.4%	98.5%
ECO102363	KPN301039	65%	81.1%	100%
ECO102363	MBV104175	29%	31.4%	5.3%
ECO102363	MBV100194	34%	23.2%	27.8%
ECO102363	MTU300292	33%	34.8%	23.7%
ECO102363	MPN100388	27%	49.4%	66.8%
ECO102363	PMU101695	30%	97.0%	99.7%
ECO102363	PRT102268	41%	99.1%	99.1%
ECO102363	PAE201527	37%	50%	57.4%
ECO102363	PPU105011	27%	97.0%	95.3%
ECO102363	PSY103901	36%	45.7%	52.1%
ECO102363	SPA103530	80%	100%	100%
ECO102363	STY101188	80%	100%	100%
ECO102363	TPA100365	33%	36.0%	20.7%
ECO102363	VCH100954	39%	98.5%	97.9%
ECO102363	YPS000610	53%	99.7%	99.1%
ECO102403	CJU100562	20%	70.3%	61.7%
ECO102403	CDF102160	47%	95.8%	94.9%
ECO102403	CDF104311	53%	96.6%	97.0%
ECO102403	EFA201797	54%	95.8%	96.4%
ECO102403	ECO102403	100%	100%	100%
ECO102403	KPN306809	88%	52.0%	100%
ECO102403	LMO101643	55%	95.8%	94.6%
ECO102403	NME201309	27%	30.6%	27.8%
ECO102403	PAE201490	30%	97.3%	95.1%
ECO102403	SPA100275	83%	100%	100%
ECO102403	STY101540	96%	100%	100%
ECO102403	SMU102926	24%	21.3%	27.3%
ECO102415	ABA100008	42%	55.1%	100%
ECO102415	ABA100811	51%	97.8%	94.8%
ECO102415	CPN200680	48%	97.5%	94.2%
ECO102415	CTR200579	50%	97.5%	94.8%
ECO102415	CDP100260	36%	30.4%	24.7%
ECO102415	EBC103692	84%	100%	100%
ECO102415	ECO102415	100%	100%	100%
ECO102415	HPY201384	24%	88.0%	88.9%
ECO102415	KPN304355	85%	100%	99.4%
ECO102415	MAV101559	35%	43.7%	63.8%
ECO102415	MBV100249	34%	43.7%	36.5%
ECO102415	MLP100365	35%	43.7%	36.3%
ECO102415	MTU201429	34%	43.7%	36.5%
ECO102415	NGO100798	31%	47.2%	41.9%
ECO102415	NME300318	34%	47.2%	41.9%
ECO102415	SPA100353	82%	49.4%	92.3%
ECO102415	STY101570	89%	100%	100%
ECO102415	STM101333	89%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102420	BAN105583	28%	36.6%	52.9%
ECO102420	BAN102074	28%	36.6%	52.7%
ECO102420	CDF103262	24%	34.8%	47.0%
ECO102420	EBC100809	63%	51.8%	88.8%
ECO102420	ECO102420	100%	100%	100%
ECO102420	HIN100254	38%	97.9%	98.9%
ECO102420	MAV102966	31%	35.9%	23.8%
ECO102420	NGO100196	27%	94.5%	95.6%
ECO102420	NME201296	28%	95.4%	96.4%
ECO102420	PMU101591	41%	97.9%	98.6%
ECO102420	PPU111874	33%	33.7%	81.1%
ECO102420	SPA100988	86%	82.7%	100%
ECO102420	STY101591	87%	99.8%	99.8%
ECO102420	STM101354	88%	99.5%	99.5%
ECO102420	VCH103397	42%	98.4%	96.6%
ECO102425	EBC102366	59%	98.5%	98.9%
ECO102425	ECO102425	100%	100%	100%
ECO102425	HIN101226	37%	43.7%	84.1%
ECO102425	KPN306928	63%	99.4%	99.9%
ECO102425	PMU101043	39%	87.0%	90.5%
ECO102425	PRT102552	44%	97.2%	100%
ECO102425	SPA100012	67%	8.6%	100%
ECO102425	SPA102785	67%	94.3%	100%
ECO102425	STY101609	71%	98.7%	98.5%
ECO102425	VCH103825	31%	69.0%	66.2%
ECO102425	YPS000834	51%	95.8%	94.4%
ECO102432	ABA100511	31%	32.1%	65.4%
ECO102432	CAC100970	32%	32.6%	11.1%
ECO102432	ECO102432	100%	100%	100%
ECO102432	MCA100789	33%	24.8%	50.5%
ECO102432	PRT105668	54%	94.0%	100%
ECO102432	PSY106056	28%	34.9%	78.5%
ECO102454	BFR101754	22%	27.2%	58.1%
ECO102454	BBU100362	26%	48.2%	53.1%
ECO102454	EBC102725	68%	68.0%	98.8%
ECO102454	EFM201772	25%	18.1%	20.3%
ECO102454	ECO102454	100%	100%	100%
ECO102454	KPN305737	63%	47.9%	99.2%
ECO102454	SPA103104	72%	98.1%	100%
ECO102454	STY101669	72%	98.1%	99.5%
ECO102454	SMU100183	23%	34.9%	32.4%
ECO102462	ABA100688	52%	97.0%	98.5%
ECO102462	BAN111369	34%	90.1%	98.2%
ECO102462	BAN112079	40%	90.1%	97.9%
ECO102462	BFR10077	37%	23.5%	71.0%
ECO102462	BPT100007	51%	93.2%	99.8%
ECO102462	BBU100507	31%	71.6%	34.4%
ECO102462	BCE100856	49%	92.8%	98.4%
ECO102462	BFU105505	51%	92.8%	99.8%
ECO102462	BMA102074	51%	92.8%	99.8%
ECO102462	CJU100354	32%	89.7%	96.5%
ECO102462	CPN201006	32%	72.6%	32.0%
ECO102462	CTR200076	33%	72.8%	32.0%
ECO102462	CAC100098	40%	91.5%	99.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102462	CBO101866	39%	90.9%	98.4%
ECO102462	CDF102465	36%	90.9%	98.0%
ECO102462	CDP101065	34%	90.9%	78.2%
ECO102462	EBC102035	92%	97.4%	100%
ECO102462	EFA201884	38%	90.1%	97.9%
ECO102462	ECO102462	100%	100%	100%
ECO102462	HIN100129	70%	97.0%	99.2%
ECO102462	HPY100821	31%	93.6%	99.8%
ECO102462	KPN305977	91%	97.4%	100%
ECO102462	LPN101429	55%	97.4%	100%
ECO102462	LMO102523	41%	90.1%	97.9%
ECO102462	MCA101523	54%	30.4%	71.6%
ECO102462	MAV102019	35%	92.6%	93.8%
ECO102462	MBV105348	35%	92.6%	94.4%
ECO102462	MLP100852	34%	73.4%	34.4%
ECO102462	MTU201691	35%	92.6%	94.4%
ECO102462	MGE100337	34%	90.3%	96.7%
ECO102462	MPN100366	34%	15.5%	43.5%
ECO102462	NGO101003	48%	97.4%	95.3%
ECO102462	NME200978	48%	97.4%	95.3%
ECO102462	PMU100105	69%	97.0%	99.2%
ECO102462	PRT102921	79%	97.4%	100%
ECO102462	PAE203796	59%	97.0%	98.0%
ECO102462	PPU112339	60%	97.0%	98.2%
ECO102462	PSY106808	64%	65.6%	85.2%
ECO102462	PSY103809	59%	97.0%	97.4%
ECO102462	SPA102739	95%	99.8%	100%
ECO102462	STY101715	97%	97.4%	100%
ECO102462	SAU801475	42%	90.1%	97.9%
ECO102462	SEP200461	42%	90.1%	97.9%
ECO102462	SHA101409	42%	90.1%	97.9%
ECO102462	SMU101355	36%	90.3%	98.2%
ECO102462	SPN401552	37%	90.3%	98.2%
ECO102462	SPY200248	37%	90.5%	98.4%
ECO102462	TPA100681	28%	91.3%	95%
ECO102462	UUR100386	34%	90.5%	97.5%
ECO102462	VCH100750	72%	97.4%	99.8%
ECO102462	YPS003216	81%	97.4%	100%
ECO102463	ABA100690	26%	97.2%	96.6%
ECO102463	BAN100167	18%	43.9%	32.2%
ECO102463	BFR105944	23%	87.8%	41.9%
ECO102463	BFR11585	21%	90.1%	26.6%
ECO102463	BPT100009	28%	98.2%	95.8%
ECO102463	BCE109201	32%	95.9%	94.8%
ECO102463	BFU112086	31%	96.2%	95.0%
ECO102463	BMA102173	30%	90.3%	90.6%
ECO102463	CBO103865	22%	51.8%	33.7%
ECO102463	EBC102802	87%	99.5%	76.5%
ECO102463	ECO102463	100%	100%	100%
ECO102463	KPN305713	89%	100%	100%
ECO102463	LPN101809	30%	91.1%	95.1%
ECO102463	MCA101522	28%	64.0%	79.3%
ECO102463	MLP101057	28%	43.6%	45.6%
ECO102463	MTU409282	42%	13.0%	29.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102463	PRT102922	63%	100%	100%
ECO102463	PAE203797	31%	97.2%	97.4%
ECO102463	PPU103985	30%	97.2%	97.1%
ECO102463	PSY107526	28%	39.3%	98.6%
ECO102463	PSY103806	29%	87.8%	94.1%
ECO102463	SPA102740	91%	100%	100%
ECO102463	STY101717	91%	100%	100%
ECO102463	SMU100069	23%	33.7%	20.8%
ECO102463	VCH100749	45%	98.5%	97.2%
ECO102463	YPS003220	76%	100%	100%
ECO102466	ABA100666	44%	23.7%	94.6%
ECO102466	ABA101467	63%	97.3%	97.6%
ECO102466	BAN111145	46%	84.9%	86.1%
ECO102466	BAN100549	47%	97.8%	98.4%
ECO102466	BFR11690	37%	89.8%	90.2%
ECO102466	BPT100015	31%	93.0%	93.1%
ECO102466	BCE101925	31%	82.0%	75.5%
ECO102466	BFU107038	34%	88.7%	85.8%
ECO102466	BMA104846	35%	88.7%	90.4%
ECO102466	CJU100636	41%	92.7%	96.1%
ECO102466	CPN200377	38%	86.8%	91.5%
ECO102466	CTR200322	40%	84.4%	91.3%
ECO102466	CAC102226	48%	93.0%	99.1%
ECO102466	CBO102775	47%	91.9%	98.0%
ECO102466	CDF100537	49%	91.7%	97.2%
ECO102466	CDP101104	44%	97.0%	91.6%
ECO102466	EBC102799	96%	100%	100%
ECO102466	ECO102466	100%	100%	100%
ECO102466	HIN100347	88%	97.3%	98.6%
ECO102466	HPY100617	45%	95.2%	98.1%
ECO102466	KPN305822	99%	99.7%	99.5%
ECO102466	LMO102690	49%	97.0%	98.1%
ECO102466	MCA101518	59%	99.5%	99.2%
ECO102466	MAV106393	42%	94.6%	92.4%
ECO102466	MBV102284	43%	94.9%	92.9%
ECO102466	MLP100964	45%	87.4%	83.2%
ECO102466	MTU202830	43%	94.9%	91.5%
ECO102466	NGO100207	33%	92.5%	92.6%
ECO102466	NME201384	33%	92.5%	92.6%
ECO102466	PMU102010	88%	96.5%	98.1%
ECO102466	PRT106101	87%	100%	100%
ECO102466	PAE203800	73%	97.3%	97.3%
ECO102466	PPU101373	71%	97.3%	97.8%
ECO102466	PSY103798	71%	96.2%	96.7%
ECO102466	SPA101922	97%	100%	100%
ECO102466	STY101723	98%	100%	100%
ECO102466	TPA100442	38%	90.6%	86.4%
ECO102466	VCH100746	85%	100%	99.2%
ECO102466	YPS003233	86%	99.7%	99.2%
ECO102467	ABA105298	28%	10.1%	24.3%
ECO102467	BAN102965	21%	47.2%	61.1%
ECO102467	BAN100109	21%	47.2%	56.4%
ECO102467	BPT104503	23%	35.9%	77.4%
ECO102467	BCE107711	25%	93.2%	91.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102467	BFU107885	26%	93.2%	88.6%
ECO102467	BMA105226	25%	93.2%	91.1%
ECO102467	CDP101012	31%	28.5%	24.0%
ECO102467	EBC102798	79%	100%	100%
ECO102467	EFA201529	22%	82.5%	98.6%
ECO102467	ECO102467	100%	100%	100%
ECO102467	HIN100346	24%	89.3%	92.1%
ECO102467	KPN304056	77%	100%	100%
ECO102467	LPN100742	28%	53.4%	96.8%
ECO102467	LMO100900	20%	94.7%	97.1%
ECO102467	MBV100599	34%	29.1%	33.1%
ECO102467	MTU202164	34%	29.1%	33.1%
ECO102467	PMU102009	26%	93.5%	95.9%
ECO102467	PRT105472	43%	97.6%	99.1%
ECO102467	PAE203801	29%	92.6%	93.7%
ECO102467	PPU101372	30%	93.2%	94.6%
ECO102467	PSY103796	36%	16.3%	94.7%
ECO102467	SPA101923	82%	100%	100%
ECO102467	STY101725	81%	100%	100%
ECO102467	SAU501460	26%	23.7%	61.5%
ECO102467	SEP201584	26%	33.8%	90.8%
ECO102467	SMU100616	26%	43.0%	17.2%
ECO102467	SPN402025	21%	47.2%	58.3%
ECO102467	VCH100745	35%	97.0%	88.8%
ECO102467	YPS003236	57%	98.5%	100%
ECO102470	BFR106150	31%	84.4%	100%
ECO102470	BPT101227	45%	96.8%	95.7%
ECO102470	BCE114473	36%	54.0%	97.5%
ECO102470	BMA100851	31%	67.4%	76.4%
ECO102470	EBC102795	83%	58.6%	100%
ECO102470	ECO102470	100%	100%	100%
ECO102470	KPN300051	52%	7.4%	100%
ECO102470	KPN308496	76%	98.7%	98.7%
ECO102470	LPN103343	29%	94.5%	94.7%
ECO102470	PMU100644	28%	98.1%	97.8%
ECO102470	PRT102900	60%	98.2%	97.9%
ECO102470	PPU105748	59%	96.4%	97.4%
ECO102470	PSY100879	58%	97.1%	99.3%
ECO102470	SPA100488	80%	43.5%	100%
ECO102470	STY102000	82%	98.8%	98.7%
ECO102473	BAN110554	27%	34.1%	76.7%
ECO102473	BAN101059	26%	43.3%	84.8%
ECO102473	EBC103107	88%	98.9%	100%
ECO102473	ECO102473	100%	100%	100%
ECO102473	KPN308674	81%	98.9%	100%
ECO102473	PRT102904	38%	42.9%	81.6%
ECO102473	SPA102272	89%	100%	100%
ECO102473	STY102006	89%	100%	100%
ECO102473	YPS003275	43%	95.4%	84.5%
ECO102501	ECO102501	100%	100%	100%
ECO102501	KPN304071	65%	99.2%	99.2%
ECO102507	EBC101718	84%	92.7%	100%
ECO102507	ECO102507	100%	100%	100%
ECO102507	KPN300399	73%	27.0%	91.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102507	KPN303134	78%	95.0%	99.6%
ECO102507	PRT104136	60%	91.7%	100%
ECO102507	SPA101717	68%	99.6%	100%
ECO102507	STY102061	86%	92.7%	99.8%
ECO102507	YPS003367	71%	95.6%	98.1%
ECO102508	ABA104968	57%	99.9%	100%
ECO102508	BAN111337	22%	57.7%	90.6%
ECO102508	BAN102784	24%	57.7%	89.3%
ECO102508	BFR10864	33%	80.2%	98.0%
ECO102508	BPT100477	53%	99.7%	99.6%
ECO102508	BCE106362	55%	93.7%	99.9%
ECO102508	BFU101352	54%	55.6%	100%
ECO102508	BMA106567	54%	97.3%	99.8%
ECO102508	CJU100885	22%	58.1%	91.6%
ECO102508	CAC101045	22%	84.6%	83.5%
ECO102508	CBO100623	23%	85.7%	84.8%
ECO102508	CDF101443	22%	88.9%	98.3%
ECO102508	CDP101519	24%	83.8%	82.7%
ECO102508	EBC100610	92%	40.5%	100%
ECO102508	EFA200566	24%	58.1%	90.4%
ECO102508	EFM202343	26%	28.6%	89.1%
ECO102508	ECO102508	100%	100%	100%
ECO102508	HIN100732	69%	99.6%	97.9%
ECO102508	KPN300196	91%	12.1%	90.8%
ECO102508	KPN303137	91%	100%	100%
ECO102508	LPN102188	24%	33.9%	96.2%
ECO102508	LMO100467	23%	60.8%	94.3%
ECO102508	MCA101372	53%	99.7%	99.7%
ECO102508	MAV103029	26%	40.2%	93.9%
ECO102508	MBV101894	26%	57.9%	87.9%
ECO102508	MLP101323	26%	57.9%	89.3%
ECO102508	MTU200797	26%	57.9%	89.3%
ECO102508	NGO100513	55%	99.7%	99.5%
ECO102508	NME200415	55%	99.7%	99.5%
ECO102508	PMU101085	73%	99.7%	99.7%
ECO102508	PRT101464	75%	99.8%	99.8%
ECO102508	PAE203760	65%	99.6%	99.7%
ECO102508	PPU103524	65%	99.6%	99.7%
ECO102508	PSY103799	65%	99.6%	99.7%
ECO102508	SPA101716	86%	42.7%	100%
ECO102508	STY102064	93%	100%	100%
ECO102508	SAU801069	23%	62.2%	95.6%
ECO102508	SEP200756	24%	58.1%	89.6%
ECO102508	SHA101252	23%	56.6%	97.8%
ECO102508	SMU101241	25%	83.8%	82.7%
ECO102508	SPN400046	23%	83.8%	82.6%
ECO102508	SPY200019	24%	83.8%	81.6%
ECO102508	VCH100853	74%	99.9%	100%
ECO102508	YPS003373	82%	99.9%	100%
ECO102512	EBC102616	76%	100%	100%
ECO102512	ECO102512	100%	100%	100%
ECO102512	KPN303133	78%	92.2%	100%
ECO102512	SPA103316	75%	99.0%	100%
ECO102512	STY102085	82%	92.2%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102512	STM101842	83%	92.2%	100%
ECO102512	YPS003387	60%	92.2%	100%
ECO102513	ABA100098	65%	87.2%	93.7%
ECO102513	BPT103139	57%	89.5%	91.6%
ECO102513	BCE114785	61%	89.5%	86.4%
ECO102513	BFU111724	50%	72.1%	98.4%
ECO102513	BFU100595	59%	89.5%	89.4%
ECO102513	BMA105131	61%	89.5%	60.8%
ECO102513	CJU100323	49%	84.9%	88.9%
ECO102513	CAC103521	42%	65.1%	89.3%
ECO102513	CBO100419	42%	65.1%	84.7%
ECO102513	CDF103036	41%	65.1%	63.3%
ECO102513	EBC102617	91%	100%	100%
ECO102513	ECO102513	100%	100%	100%
ECO102513	HIN100506	73%	100%	100%
ECO102513	HPY100273	44%	97.7%	100%
ECO102513	KPN303135	94%	100%	100%
ECO102513	MCA100048	62%	89.5%	91.6%
ECO102513	MAV105676	27%	30.2%	50.4%
ECO102513	MAV101610	28%	46.5%	72.2%
ECO102513	NGO102756	58%	89.5%	91.6%
ECO102513	NME200144	57%	89.5%	91.6%
ECO102513	PMU101858	72%	100%	100%
ECO102513	PRT105191	75%	84.9%	100%
ECO102513	PAE200361	58%	89.5%	91.6%
ECO102513	PPU102180	62%	89.5%	91.6%
ECO102513	PSY102752	57%	52.3%	84.6%
ECO102513	SPA103322	95%	100%	100%
ECO102513	STY102097	95%	100%	100%
ECO102513	STM101854	94%	100%	100%
ECO102513	VCH100703	76%	93.0%	95.2%
ECO102513	YPS003406	79%	100%	100%
ECO102553	ABA100455	69%	96.5%	91.0%
ECO102553	BFR102397	56%	83.5%	82.1%
ECO102553	BPT100242	64%	97.4%	92.9%
ECO102553	BBU100698	49%	97.4%	93.4%
ECO102553	BCE107881	67%	97.4%	90%
ECO102553	BFU102066	65%	99.1%	92.2%
ECO102553	BMA100174	66%	97.4%	90.7%
ECO102553	CJU100664	51%	93.9%	93.2%
ECO102553	CPN200643	44%	97.4%	92.6%
ECO102553	CTR200292	43%	97.4%	92.6%
ECO102553	CAC102258	55%	97.4%	98.2%
ECO102553	CBO102492	47%	99.1%	100%
ECO102553	CDF103914	53%	100%	99.1%
ECO102553	CDP101148	52%	96.5%	98.2%
ECO102553	EBC100906	98%	100%	100%
ECO102553	EFA202298	58%	97.4%	97.4%
ECO102553	EFM202223	58%	97.4%	97.4%
ECO102553	ECO102553	100%	100%	100%
ECO102553	HIN100191	89%	99.1%	98.3%
ECO102553	HPY101130	51%	93.9%	93.2%
ECO102553	KPN301017	98%	100%	100%
ECO102553	LPN101449	69%	100%	95.9%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102553	LMO102632	57%	97.4%	98.2%
ECO102553	MCA100220	68%	99.1%	94.3%
ECO102553	MAV102886	54%	96.5%	98.2%
ECO102553	MBV102292	53%	96.5%	98.2%
ECO102553	MLP100984	52%	96.5%	98.2%
ECO102553	MTU202866	53%	96.5%	98.2%
ECO102553	MGE100453	47%	95.7%	91.6%
ECO102553	MPN100184	47%	95.7%	91.6%
ECO102553	NGO102004	67%	97.4%	95.0%
ECO102553	NME200732	68%	97.4%	95.0%
ECO102553	PMU101298	87%	99.1%	98.3%
ECO102553	PRT100819	96%	100%	98.3%
ECO102553	PAE203739	73%	98.3%	97.4%
ECO102553	PPU107802	71%	99.1%	98.3%
ECO102553	PSY103791	69%	99.1%	98.3%
ECO102553	SPA101891	97%	100%	100%
ECO102553	STY102215	97%	100%	100%
ECO102553	SAU801241	55%	94.8%	94.0%
ECO102553	SEP201534	57%	97.4%	98.3%
ECO102553	SMU100257	57%	97.4%	97.4%
ECO102553	SPN401170	58%	97.4%	97.4%
ECO102553	SPY200530	57%	97.4%	97.4%
ECO102553	TPA100899	51%	97.4%	91.1%
ECO102553	UUR100573	47%	94.8%	88.6%
ECO102553	VCH100554	83%	99.1%	97.4%
ECO102553	YPS003417	93%	99.1%	99.1%
ECO102554	ABA100452	51%	93.7%	99.2%
ECO102554	BFR103869	44%	88.6%	100%
ECO102554	BPT101155	52%	95.3%	98.8%
ECO102554	BBU100697	42%	85.9%	90.8%
ECO102554	BCE110744	55%	86.3%	84.8%
ECO102554	BFU102064	51%	96.5%	98.1%
ECO102554	BMA102082	58%	86.3%	84.8%
ECO102554	CJU100663	34%	87.5%	96.6%
ECO102554	CPN200644	52%	88.6%	61.5%
ECO102554	CTR200291	50%	87.5%	62.2%
ECO102554	CAC101341	49%	92.2%	95.5%
ECO102554	CBO102927	46%	94.1%	97.5%
ECO102554	CDF104123	47%	85.9%	95.2%
ECO102554	CDP101153	37%	89.8%	92.8%
ECO102554	EBC100905	96%	100%	100%
ECO102554	EFA202296	46%	95.3%	98.8%
ECO102554	ECO102554	100%	100%	100%
ECO102554	HIN100192	83%	95.7%	99.2%
ECO102554	HPY101131	32%	88.2%	98.3%
ECO102554	KPN300514	99%	44.3%	100%
ECO102554	LPN101866	57%	94.9%	96.8%
ECO102554	LMO102506	46%	94.1%	98.4%
ECO102554	MCA100037	51%	94.5%	99.6%
ECO102554	MAV103396	42%	87.8%	95.0%
ECO102554	MBV102286	42%	87.5%	98.3%
ECO102554	MLP100985	42%	87.5%	95.0%
ECO102554	MTU202868	42%	87.5%	98.3%
ECO102554	MGE100454	39%	87.5%	94.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102554	MPN100183	40%	82.4%	97.6%
ECO102554	NGO102006	55%	97.3%	99.6%
ECO102554	NME200733	56%	97.3%	99.6%
ECO102554	PMU101297	80%	96.1%	100%
ECO102554	PRT100820	84%	96.9%	98.8%
ECO102554	PAE203740	66%	94.1%	95.6%
ECO102554	PPU107801	65%	94.5%	96.4%
ECO102554	PSY102681	67%	94.5%	93.4%
ECO102554	SPA101890	94%	100%	100%
ECO102554	STY102217	96%	100%	100%
ECO102554	SAU801240	44%	94.5%	97.6%
ECO102554	SEP201533	44%	94.5%	97.6%
ECO102554	SMU100806	48%	95.3%	98.8%
ECO102554	SPN400687	49%	94.5%	98.3%
ECO102554	SPY200632	48%	94.5%	96.7%
ECO102554	TPA100898	43%	95.3%	97.2%
ECO102554	UUR100574	41%	88.2%	96.9%
ECO102554	VCH100553	78%	96.9%	100%
ECO102554	YPS003421	91%	95.7%	99.2%
ECO102555	ABA100450	38%	93.5%	96.2%
ECO102555	BFR104790	24%	91.9%	90.6%
ECO102555	BPT101152	29%	91.9%	93.7%
ECO102555	BBU100696	26%	78.4%	84.9%
ECO102555	BCE100840	29%	93.5%	79.1%
ECO102555	BFU106135	31%	93.5%	73.0%
ECO102555	BMA100086	27%	93.5%	77.7%
ECO102555	CJU100662	24%	88.1%	90.5%
ECO102555	CAC100852	28%	87.0%	91.0%
ECO102555	CBO102176	23%	88.1%	92.1%
ECO102555	CDF102281	25%	87.6%	90.6%
ECO102555	CDP101154	23%	84.3%	89.2%
ECO102555	EBC100904	95%	24.3%	100%
ECO102555	EFA202294	28%	91.9%	95.4%
ECO102555	ECO102555	100%	100%	100%
ECO102555	HIN100193	68%	90.8%	94.4%
ECO102555	HPY101132	24%	81.1%	85.9%
ECO102555	KPN300513	92%	74.1%	100%
ECO102555	LPN101155	37%	91.4%	95.9%
ECO102555	LMO101858	25%	87.6%	92.4%
ECO102555	MCA100472	30%	91.4%	99.4%
ECO102555	MAV103398	33%	88.6%	94.3%
ECO102555	MBV102283	29%	88.6%	93.8%
ECO102555	MLP100986	31%	88.6%	90.5%
ECO102555	MTU202869	29%	88.6%	93.8%
ECO102555	NGO102007	36%	89.2%	93.5%
ECO102555	NME200734	36%	89.2%	93.5%
ECO102555	PMU101296	65%	90.8%	94.4%
ECO102555	PRT104604	75%	100%	100%
ECO102555	PAE203741	39%	92.4%	96.6%
ECO102555	PPU103409	37%	95.7%	98.3%
ECO102555	PSY103789	37%	67.6%	100%
ECO102555	SPA101889	93%	98.4%	100%
ECO102555	STY102219	93%	98.4%	100%
ECO102555	SAU801239	25%	87.0%	92.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102555	SEP201532	25%	88.1%	94.0%
ECO102555	SMU100803	28%	87.0%	91.3%
ECO102555	SPN400686	23%	87.6%	91.9%
ECO102555	SPY200631	24%	87.6%	91.9%
ECO102555	TPA100897	30%	40.5%	42.5%
ECO102555	VCH100552	60%	100%	100%
ECO102555	YPS003425	81%	98.4%	100%
ECO102556	ABA100463	69%	98.8%	97.6%
ECO102556	BFR103669	43%	87.8%	33.0%
ECO102556	BPT101149	58%	93.9%	89.5%
ECO102556	BBU100694	44%	95.1%	88.4%
ECO102556	BCE101287	59%	98.8%	95.2%
ECO102556	BFU106133	59%	98.8%	72.7%
ECO102556	BMA105933	58%	98.8%	95.2%
ECO102556	CJU100660	45%	90.2%	96%
ECO102556	CPN200645	33%	90.2%	59.7%
ECO102556	CTR200290	35%	90.2%	61.2%
ECO102556	CAC102507	46%	91.5%	90.1%
ECO102556	CBO102241	48%	92.7%	87.1%
ECO102556	CDF104187	44%	90.2%	77.4%
ECO102556	CDP101155	38%	91.5%	46.5%
ECO102556	EFA201163	47%	92.7%	81.3%
ECO102556	ECO102556	100%	100%	100%
ECO102556	HIN100194	70%	100%	100%
ECO102556	HPY101134	47%	90.2%	94.7%
ECO102556	KPN203248	91%	84.1%	94.5%
ECO102556	LPN102433	56%	97.6%	93.0%
ECO102556	LMO101675	45%	90.2%	80%
ECO102556	MCA100471	60%	100%	100%
ECO102556	MAV103402	35%	91.5%	42.9%
ECO102556	MBV102277	37%	91.5%	45.1%
ECO102556	MLP100988	38%	91.5%	45.6%
ECO102556	MTU202871	37%	91.5%	45.1%
ECO102556	MGE100455	37%	85.4%	76.4%
ECO102556	MPN100182	32%	85.4%	77.3%
ECO102556	NGO102008	66%	93.9%	95.1%
ECO102556	NME200735	64%	98.8%	100%
ECO102556	PRT100822	76%	86.6%	74.0%
ECO102556	PAE203742	59%	98.8%	97.6%
ECO102556	PPU107799	60%	100%	75.2%
ECO102556	PSY103786	52%	97.6%	94.1%
ECO102556	SPA101888	97%	100%	80.4%
ECO102556	STY102221	97%	100%	100%
ECO102556	SAU801238	39%	92.7%	82.4%
ECO102556	SEP201531	42%	85.4%	75.8%
ECO102556	SHA102521	51%	57.3%	92.2%
ECO102556	SMU100800	50%	92.7%	81.3%
ECO102556	SPN400682	47%	92.7%	82.2%
ECO102556	SPY200625	44%	98.8%	87.8%
ECO102556	TPA100895	45%	89.0%	58.5%
ECO102556	UUR100575	40%	54.9%	44.6%
ECO102556	VCH100551	75%	100%	100%
ECO102556	YPS003446	79%	100%	100%
ECO102557	ABA100567	65%	98.2%	95.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102557	BAN113732	49%	72.0%	96.8%
ECO102557	BAN108180	54%	75.9%	99.4%
ECO102557	BFR10168	51%	84.8%	99.0%
ECO102557	BPT101335	63%	98.2%	97.9%
ECO102557	BBU100693	41%	98.0%	99.1%
ECO102557	BCE112884	65%	70.0%	99.1%
ECO102557	BFU115323	64%	98.7%	99.3%
ECO102557	BMA100755	65%	98.7%	99.3%
ECO102557	CJU100659	41%	95.8%	97.5%
ECO102557	CPN200646	38%	98.0%	98.9%
ECO102557	CTR200289	44%	98.0%	98.9%
ECO102557	CAC101092	48%	96.2%	97.3%
ECO102557	CBO101744	49%	98.5%	99.3%
ECO102557	CDF103672	50%	83.9%	97.9%
ECO102557	CDP101160	46%	100%	87.6%
ECO102557	EBC100407	96%	77.9%	94.9%
ECO102557	BFA201155	50%	99.8%	95.1%
ECO102557	BFM202293	51%	85.7%	99.5%
ECO102557	ECO102557	100%	100%	100%
ECO102557	HIN100105	79%	99.8%	97.8%
ECO102557	HPY101135	40%	98.9%	99.3%
ECO102557	KPN301264	97%	77.9%	94.7%
ECO102557	LPN101209	64%	98.2%	97.4%
ECO102557	LMO100196	53%	98.9%	98.2%
ECO102557	MCA100840	63%	98.2%	98.0%
ECO102557	MAV103395	49%	96.0%	84.7%
ECO102557	MBV102321	50%	96.0%	83.4%
ECO102557	MLP100989	49%	96.0%	84.1%
ECO102557	MTU202878	50%	96.0%	83.4%
ECO102557	MGE100048	39%	94.5%	95.3%
ECO102557	MPN100093	40%	91.2%	91.8%
ECO102557	NGO101772	65%	99.8%	99.8%
ECO102557	NME202026	67%	99.8%	99.8%
ECO102557	PMU101183	80%	98.5%	97.4%
ECO102557	PRT100858	87%	100%	100%
ECO102557	PAE203743	71%	99.6%	99.6%
ECO102557	PPU107798	70%	99.1%	98.9%
ECO102557	PSY103783	69%	99.1%	98.9%
ECO102557	SPA101887	92%	78.1%	100%
ECO102557	STY102223	98%	100%	100%
ECO102557	SAU801237	50%	98.7%	99.3%
ECO102557	SEP201530	50%	98.7%	99.3%
ECO102557	SMU100253	47%	99.3%	86.8%
ECO102557	SPN401165	47%	99.3%	85.7%
ECO102557	SPY200915	47%	99.3%	86.1%
ECO102557	TPA100412	39%	100%	100%
ECO102557	UUR100090	40%	94.7%	95.3%
ECO102557	VCH100550	76%	99.8%	98.0%
ECO102557	YPS003448	88%	100%	100%
ECO102562	ABA101740	44%	97.6%	94.4%
ECO102562	BAN112667	32%	51.4%	57.0%
ECO102562	BFR100600	34%	89.7%	91.0%
ECO102562	BPT103790	39%	97.6%	96.3%
ECO102562	BBU100310	34%	57.2%	58.0%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102562	BCE114005	38%	98.3%	87.7%
ECO102562	BFU102654	38%	99.0%	96%
ECO102562	BMA109400	38%	99.0%	83.5%
ECO102562	CJU100602	33%	79.1%	79.4%
ECO102562	CAC101559	33%	75.7%	77.5%
ECO102562	CBO102717	34%	92.8%	95.7%
ECO102562	CDF103162	26%	91.1%	94.0%
ECO102562	CDP101033	32%	77.4%	73.2%
ECO102562	EBC102479	97%	91.8%	100%
ECO102562	EFA200895	35%	49.3%	54.7%
ECO102562	EFM200968	25%	52.4%	60%
ECO102562	ECO102562	100%	100%	100%
ECO102562	HIN100070	58%	86.0%	96.9%
ECO102562	HPY101374	26%	99.0%	97.9%
ECO102562	KPN301269	94%	100%	100%
ECO102562	LPN101990	43%	94.5%	94.6%
ECO102562	LMO100773	32%	50.3%	56.1%
ECO102562	MCA101910	38%	98.3%	95.7%
ECO102562	MAV102046	34%	74.7%	67.3%
ECO102562	MBV105349	35%	68.2%	64.8%
ECO102562	MLP100841	34%	69.9%	65.6%
ECO102562	MTU201674	35%	68.2%	64.8%
ECO102562	MGE100130	29%	55.5%	58.3%
ECO102562	MPN100566	31%	56.8%	60.2%
ECO102562	NGO100871	39%	99.7%	99.7%
ECO102562	NME200939	39%	99.7%	99.7%
ECO102562	PMU100333	56%	98.3%	94.8%
ECO102562	PRT101147	77%	75.7%	100%
ECO102562	PAE203086	47%	98.3%	97.6%
ECO102562	PPU105852	48%	98.3%	97.3%
ECO102562	PSY100717	46%	98.3%	97.3%
ECO102562	SPA101531	95%	99.0%	100%
ECO102562	STY102233	96%	100%	100%
ECO102562	STM102487	96%	100%	100%
ECO102562	SAU801007	27%	53.8%	59.1%
ECO102562	SEP200233	29%	54.8%	60.2%
ECO102562	SHA100764	27%	54.8%	60.2%
ECO102562	SMU100219	29%	49.3%	52.0%
ECO102562	SPN401005	24%	73.6%	69.9%
ECO102562	SPY200856	32%	49.3%	51.8%
ECO102562	TPA100437	34%	84.9%	81.0%
ECO102562	UUR100177	22%	69.5%	73.7%
ECO102562	VCH100837	58%	100%	100%
ECO102562	YPS002057	82%	99.7%	99.3%
ECO102578	ECO102578	100%	100%	100%
ECO102578	VCH101777	23%	61.9%	61.6%
ECO102588	BFR100937	19%	35.1%	18.2%
ECO102588	CJU101174	30%	13.1%	16.7%
ECO102588	ECO102588	100%	100%	100%
ECO102588	HPY100493	18%	35.3%	47.1%
ECO102588	LPN101370	24%	37.6%	50.1%
ECO102588	MGE100322	23%	25.0%	40.9%
ECO102588	STY103166	28%	22.4%	49.6%
ECO102588	SAU800159	34%	15.7%	24.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102588	UUR100022	23%	22.0%	25.1%
ECO102593	ABA105043	21%	26.4%	58.5%
ECO102593	BPT105268	20%	32.6%	64.5%
ECO102593	BPT100671	22%	91.7%	82.0%
ECO102593	BPT100041	25%	45.4%	71.5%
ECO102593	BPT100991	31%	31.2%	61.6%
ECO102593	BCE104738	26%	25.6%	54.2%
ECO102593	BCE102211	22%	14.1%	40.1%
ECO102593	BCE110445	24%	8.2%	97.9%
ECO102593	BCE103017	24%	21.6%	83.6%
ECO102593	BCE103623	27%	30.4%	66.2%
ECO102593	BCE100403	22%	69.4%	24.8%
ECO102593	BCE110366	23%	85.7%	22.0%
ECO102593	BCE101250	23%	22.4%	95.0%
ECO102593	BCE106666	24%	30.7%	71.7%
ECO102593	BFU112047	19%	33.2%	75.6%
ECO102593	BFU113446	19%	27.2%	83.8%
ECO102593	BFU104375	21%	37.0%	89.3%
ECO102593	BFU112017	21%	6.1%	49.7%
ECO102593	BFU106700	22%	56.1%	75.9%
ECO102593	BFU113994	21%	8.8%	43.4%
ECO102593	BFU112565	20%	72.6%	31.1%
ECO102593	BFU108657	22%	25.8%	97.0%
ECO102593	BFU109807	23%	72.0%	24.6%
ECO102593	BMA109486	23%	36.3%	73.0%
ECO102593	CDF103395	22%	17.6%	37.5%
ECO102593	CDP101864	43%	1.3%	33.1%
ECO102593	EFA201471	22%	67.7%	52.6%
ECO102593	EFM101518	20%	38.2%	25.2%
ECO102593	ECO102148	41%	0.4%	70.9%
ECO102593	ECO102593	100%	100%	100%
ECO102593	HIN100971	22%	46.4%	45.3%
ECO102593	KPN203199	22%	10.8%	51.7%
ECO102593	LMO101479	20%	28.6%	59.4%
ECO102593	LMO101190	44%	4.9%	9.2%
ECO102593	LMO101803	28%	11.4%	32.4%
ECO102593	MCA102916	21%	56.7%	48.7%
ECO102593	MTU203460	27%	8.8%	9.0%
ECO102593	MTU200863	24%	23.0%	54.1%
ECO102593	MTU201807	23%	12.2%	35.9%
ECO102593	MTU200278	30%	6.1%	12.3%
ECO102593	MTU201226	26%	12.4%	31.0%
ECO102593	MTU200277	29%	6.9%	12.4%
ECO102593	MTU200575	23%	22.2%	24.4%
ECO102593	MTU201737	23%	23.2%	40.0%
ECO102593	MTU202815	23%	24.4%	53.5%
ECO102593	MTU201630	24%	7.6%	38.9%
ECO102593	NGO100136	24%	36.5%	46.6%
ECO102593	NGO101220	20%	52.5%	70.1%
ECO102593	NGO101062	25%	16.4%	15.8%
ECO102593	NME200426	22%	59.5%	67.6%
ECO102593	NME200638	23%	9.5%	17.2%
ECO102593	NME200634	21%	45.5%	52.6%
ECO102593	PRT103539	21%	57.4%	15.9%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102593	PRT105107	21%	61.6%	62.1%
ECO102593	PAE204079	21%	2.8%	88.2%
ECO102593	PAE204539	20%	70.0%	61.9%
ECO102593	PPU103891	22%	5.9%	14.1%
ECO102593	PPU101855	27%	47.2%	97.6%
ECO102593	PSY105010	26%	3.4%	93.8%
ECO102593	STM104147	20%	65.9%	2.1%
ECO102593	YPS000732	30%	14.9%	77.1%
ECO102593	YPS002481	29%	8.5%	63.3%
ECO102593	YPS003252	27%	17.7%	44.0%
ECO102599	ECO102599	100%	100%	100%
ECO102600	ECO102600	100%	100%	100%
ECO102604	BPT105939	30%	33.1%	20.5%
ECO102604	ECO102604	100%	100%	100%
ECO102604	KPN305556	85%	98.6%	100%
ECO102604	PPU108977	67%	90.3%	100%
ECO102604	SPA100787	84%	98.6%	100%
ECO102604	STY102673	86%	90.8%	99.7%
ECO102604	STM103130	86%	90.8%	99.7%
ECO102610	ABA100150	46%	99.3%	100%
ECO102610	BPT101957	49%	98.7%	97.3%
ECO102610	BBU100322	37%	35.6%	14.1%
ECO102610	BCE109062	43%	100%	99.4%
ECO102610	CBO101404	32%	55.0%	38.7%
ECO102610	CDF102194	35%	53.7%	39.3%
ECO102610	EBC102396	64%	99.3%	99.3%
ECO102610	EFA201210	47%	39.6%	28.6%
ECO102610	EFM201311	42%	38.3%	27.2%
ECO102610	EFM202034	47%	39.6%	26.9%
ECO102610	ECO102610	100%	100%	100%
ECO102610	KPN301659	64%	98.7%	98.7%
ECO102610	MCA100095	40%	99.3%	100%
ECO102610	NGO101731	46%	33.6%	11.2%
ECO102610	NME200158	40%	33.6%	12.3%
ECO102610	PMU101974	36%	99.3%	98.6%
ECO102610	PAE205173	54%	99.3%	100%
ECO102610	PPU106499	56%	99.3%	100%
ECO102610	PSY104020	52%	99.3%	100%
ECO102610	SPA103010	93%	100%	100%
ECO102610	TPA100041	42%	32.9%	15.2%
ECO102610	VCH100047	34%	47.0%	17.6%
ECO102612	ABA100902	27%	97.0%	93.1%
ECO102612	BAN102839	22%	70.7%	55.6%
ECO102612	BAN109348	23%	82.8%	90.1%
ECO102612	BAN105886	31%	83.8%	82.8%
ECO102612	BAN101705	33%	77.8%	90.6%
ECO102612	BAN106903	29%	82.8%	85.4%
ECO102612	BAN108997	32%	84.8%	77.6%
ECO102612	BAN109157	34%	82.8%	81.8%
ECO102612	BPT102914	25%	89.9%	78.4%
ECO102612	BCE100121	37%	93.9%	79.3%
ECO102612	BFU101752	38%	76.8%	32.1%
ECO102612	BMA104163	33%	97.0%	83.5%
ECO102612	CBO102999	27%	87.9%	93.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102612	EBC100370	76%	98.0%	100%
ECO102612	ECO102612	100%	100%	100%
ECO102612	KPN304418	69%	100%	100%
ECO102612	LPN102332	29%	78.8%	91.9%
ECO102612	LMO102436	26%	82.8%	82.5%
ECO102612	MAV101064	31%	90.9%	83.5%
ECO102612	MBV103014	32%	84.8%	72.3%
ECO102612	MTU201653	32%	85.9%	38.5%
ECO102612	NGO100659	36%	80.8%	84.9%
ECO102612	NME201928	37%	54.5%	79.4%
ECO102612	PMU101481	30%	93.9%	96.8%
ECO102612	PRT101996	38%	97.0%	88.8%
ECO102612	PAE204352	31%	77.8%	89%
ECO102612	PPU112349	28%	77.8%	89.1%
ECO102612	PPU101562	31%	78.8%	90%
ECO102612	PSY101769	31%	77.8%	85.6%
ECO102612	SPA103008	89%	100%	100%
ECO102612	STY106198	87%	100%	100%
ECO102612	STM103167	89%	100%	100%
ECO102612	SEP202395	30%	89.9%	75.4%
ECO102612	SMU101283	28%	89.9%	23.0%
ECO102612	VCH100665	41%	96.0%	87.0%
ECO102612	VCH103365	37%	97.0%	90.5%
ECO102619	BAN106019	41%	91.2%	95.8%
ECO102619	BAN106208	41%	91.2%	95.8%
ECO102619	CDP101420	53%	91.2%	92.2%
ECO102619	EBC101489	87%	99.3%	63.1%
ECO102619	EFA201340	40%	91.9%	60.8%
ECO102619	EFM202084	27%	90.4%	96.6%
ECO102619	ECO102619	100%	100%	100%
ECO102619	KPN304448	80%	96.3%	61.8%
ECO102619	MAV103566	61%	94.9%	88.7%
ECO102619	MBV105902	62%	94.9%	88.7%
ECO102619	MLP101068	60%	93.4%	94.9%
ECO102619	MTU203012	62%	94.9%	88.7%
ECO102619	MGE100235	55%	93.4%	84.3%
ECO102619	MPN100513	53%	92.6%	83.7%
ECO102619	PRT102698	58%	92.6%	59.3%
ECO102619	SPA100545	66%	100%	62.7%
ECO102619	STY102715	85%	100%	100%
ECO102619	STM103197	85%	100%	100%
ECO102619	SAU800730	36%	92.6%	90.2%
ECO102619	SEP201146	33%	86.8%	83.2%
ECO102619	SEP200795	37%	92.6%	85.6%
ECO102619	SHA100608	38%	66.2%	68.9%
ECO102619	SMU100587	27%	86.8%	88.9%
ECO102619	SPN400156	26%	97.1%	75.5%
ECO102619	SPY200303	52%	87.5%	74.1%
ECO102619	YPS001326	69%	97.1%	99.3%
ECO102636	ABA100197	94%	63.9%	100%
ECO102636	ABA101889	91%	91.8%	66.7%
ECO102636	BBU100183	33%	93.4%	70.4%
ECO102636	CJU101029	33%	88.5%	72%
ECO102636	CAC101250	38%	93.4%	78.1%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102636	CBO100627	34%	100%	84.7%
ECO102636	CDF101436	38%	88.5%	77.1%
ECO102636	EBC101518	100%	100%	100%
ECO102636	ECO102636	100%	100%	100%
ECO102636	HIN100793	68%	93.4%	90.5%
ECO102636	HPY101421	33%	96.7%	77.6%
ECO102636	KPN305688	100%	96.7%	100%
ECO102636	LPN100697	76%	98.4%	70.6%
ECO102636	MCA100043	86%	95.1%	69.9%
ECO102636	PMU101288	69%	85.2%	83.9%
ECO102636	PRT105141	96%	93.4%	91.9%
ECO102636	PAE200904	85%	100%	100%
ECO102636	PPU100420	75%	98.4%	98.4%
ECO102636	PSY106524	75%	100%	100%
ECO102636	STY102763	100%	100%	100%
ECO102636	TPA100649	40%	96.7%	80.8%
ECO102636	VCH100538	98%	90.2%	84.6%
ECO102636	YPS003496	95%	100%	100%
ECO102637	ABA102548	52%	8.7%	92.7%
ECO102637	ABA101894	58%	99.4%	99.3%
ECO102637	BAN112993	47%	12.1%	95.5%
ECO102637	BAN112360	40%	72.6%	99.1%
ECO102637	BAN110893	44%	99.1%	99.0%
ECO102637	BFR11415	43%	98.3%	98.7%
ECO102637	BPT101143	62%	99.4%	99.8%
ECO102637	BBU100219	36%	79.0%	98.7%
ECO102637	BCE107013	72%	48.1%	93.8%
ECO102637	BFU114595	62%	99.3%	99.7%
ECO102637	BMA107024	62%	99.3%	99.7%
ECO102637	CJU100469	47%	97.9%	98.6%
ECO102637	CPN200957	41%	99.1%	99.3%
ECO102637	CTR200124	41%	99.1%	99.3%
ECO102637	CAC100475	42%	98.3%	98.2%
ECO102637	CBO102316	42%	98.4%	98.3%
ECO102637	CDF100894	44%	98.1%	98.0%
ECO102637	CDP100382	40%	99.2%	99.8%
ECO102637	EBC101519	91%	98.3%	100%
ECO102637	EFA202378	44%	99.2%	99.3%
ECO102637	EFM102001	41%	13.7%	100%
ECO102637	ECO102637	100%	100%	100%
ECO102637	HIN100794	69%	99.7%	99.9%
ECO102637	HPY101224	46%	98.4%	98.8%
ECO102637	KPN301584	91%	99.9%	100%
ECO102637	LPN103164	56%	98.6%	99.1%
ECO102637	LMO101358	43%	99.1%	99.0%
ECO102637	MCA100516	58%	99.2%	99.1%
ECO102637	MAV102135	39%	97.5%	99.1%
ECO102637	MBV100967	40%	99.1%	99.1%
ECO102637	MLP100309	38%	99.1%	99.4%
ECO102637	MTU202518	40%	99.1%	99.1%
ECO102637	MGE100298	31%	97.7%	98.4%
ECO102637	MPN100422	33%	91.0%	88.8%
ECO102637	NGO101407	61%	99.4%	99.7%
ECO102637	NME201646	61%	99.4%	99.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102637	PMU101287	70%	99.7%	99.9%
ECO102637	PRT101312	78%	99.9%	100%
ECO102637	PAE200902	65%	99.4%	99.8%
ECO102637	PPU106922	65%	98.3%	98.6%
ECO102637	PSY103114	64%	93.8%	98.8%
ECO102637	SPA101276	94%	99.4%	100%
ECO102637	STY102766	95%	100%	100%
ECO102637	SAU801618	45%	98.9%	99.0%
ECO102637	SEP201165	44%	98.9%	99.0%
ECO102637	SHA101190	45%	98.9%	98.6%
ECO102637	SMU100824	44%	98.6%	99.1%
ECO102637	SPN401239	42%	98.9%	99.3%
ECO102637	SPY201063	43%	98.6%	99.1%
ECO102637	TPA101007	40%	79.0%	97.4%
ECO102637	UUR100371	32%	99.1%	99.2%
ECO102637	VCH100535	68%	99.9%	100%
ECO102637	YPS003498	82%	99.9%	100%
ECO102638	ABA101317	32%	87.3%	83.1%
ECO102638	BFR105888	23%	86.7%	89.0%
ECO102638	BPT102831	29%	86.7%	70.2%
ECO102638	BCE103131	33%	90.4%	47.6%
ECO102638	CAC101416	25%	90.4%	67.8%
ECO102638	CDF104561	26%	90.4%	67.0%
ECO102638	EBC101520	84%	100%	100%
ECO102638	EFA200848	23%	69.9%	40.2%
ECO102638	EFM200848	25%	85.5%	50.9%
ECO102638	ECO102638	100%	100%	100%
ECO102638	HIN100578	28%	68.7%	92.1%
ECO102638	KPN301586	76%	100%	100%
ECO102638	LPN101898	32%	90.4%	93.3%
ECO102638	MCA103400	28%	89.2%	50.6%
ECO102638	NGO100458	29%	85.5%	84.3%
ECO102638	NME201548	30%	85.5%	84.3%
ECO102638	PMU101816	29%	65.7%	88.8%
ECO102638	PRT104789	37%	82.5%	97.9%
ECO102638	PAE203614	40%	89.8%	90.2%
ECO102638	PPU101132	36%	70.5%	75.9%
ECO102638	PSY107055	39%	84.3%	85.5%
ECO102638	SPA101275	86%	100%	100%
ECO102638	STY102769	87%	100%	100%
ECO102638	SPN401716	25%	81.3%	44.1%
ECO102638	SPY201239	29%	56.6%	36.8%
ECO102638	VCH100534	36%	84.9%	86.2%
ECO102638	YPS003500	44%	88.6%	95.2%
ECO102639	ABA101315	74%	92.9%	94.0%
ECO102639	BAN109036	49%	90.9%	95.2%
ECO102639	BAN107984	70%	56.9%	96.6%
ECO102639	BFR11938	63%	91.2%	92.8%
ECO102639	BPT102835	68%	95.8%	96.6%
ECO102639	BBU100130	54%	96.0%	95.1%
ECO102639	BCE109039	69%	96.9%	95.8%
ECO102639	BFU103521	68%	97.7%	96.1%
ECO102639	BMA106800	72%	91.2%	90.7%
ECO102639	CJU101578	62%	91.5%	94.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102639	CPN201091	56%	98.0%	98.6%
ECO102639	CTR200019	59%	90.9%	91.2%
ECO102639	CAC102599	65%	91.8%	92.8%
ECO102639	CBO100413	66%	91.8%	91.0%
ECO102639	CDF100868	64%	91.2%	91.0%
ECO102639	CDP100408	63%	90.7%	86.0%
ECO102639	EBC101521	92%	100%	100%
ECO102639	EFA201505	59%	97.5%	98.0%
ECO102639	EFM100436	61%	87.5%	96.9%
ECO102639	ECO102639	100%	100%	100%
ECO102639	HIN100579	73%	100%	99.7%
ECO102639	HPY100150	61%	95.2%	97.1%
ECO102639	KPN301587	93%	100%	100%
ECO102639	LPN100193	70%	99.2%	100%
ECO102639	LMO100506	63%	90.9%	92.2%
ECO102639	MCA103696	71%	96.9%	97.7%
ECO102639	MAV102772	62%	98.6%	98.6%
ECO102639	MBV102991	66%	98.6%	99.4%
ECO102639	MLP100604	65%	92.9%	97.5%
ECO102639	MTU202700	66%	98.6%	99.4%
ECO102639	MGE100348	46%	85.3%	88.5%
ECO102639	MPN100352	45%	85.8%	90.5%
ECO102639	NGO100154	69%	92.1%	86.9%
ECO102639	NME201518	69%	92.1%	93.7%
ECO102639	PMU101817	75%	99.4%	97.5%
ECO102639	PRT101313	84%	99.7%	100%
ECO102639	PAE203615	71%	99.2%	100%
ECO102639	PPU106715	73%	92.6%	92.1%
ECO102639	PSY104402	73%	93.2%	89.2%
ECO102639	SPA101274	88%	100%	100%
ECO102639	STY102772	97%	100%	100%
ECO102639	SAU801285	62%	92.4%	93.9%
ECO102639	SEP201588	59%	99.2%	97.4%
ECO102639	SHA101287	61%	92.4%	93.7%
ECO102639	SMU101217	62%	90.9%	84.9%
ECO102639	SPN401755	60%	98.0%	87.6%
ECO102639	SPY201616	62%	90.9%	86.0%
ECO102639	TPA100684	59%	91.8%	80.1%
ECO102639	UUR100082	40%	91.8%	97.0%
ECO102639	VCH100533	84%	93.8%	80.3%
ECO102639	YPS003502	87%	100%	100%
ECO102641	ABA105758	38%	84.2%	90.7%
ECO102641	BPT100211	34%	96.4%	96.3%
ECO102641	BCE110777	42%	83.7%	99.1%
ECO102641	BFU102083	39%	83.7%	76.8%
ECO102641	BMA101152	39%	83.7%	99.1%
ECO102641	EBC101821	88%	99.7%	100%
ECO102641	ECO102641	100%	100%	100%
ECO102641	KPN301585	87%	99.4%	100%
ECO102641	LPN102694	40%	83.1%	87.6%
ECO102641	MCA101336	34%	66.2%	51.0%
ECO102641	MAV106642	33%	16.3%	17.5%
ECO102641	MBV100885	33%	16.6%	15.7%
ECO102641	MTU201213	33%	16.6%	14.6%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102641	NGO101013	38%	83.7%	87.4%
ECO102641	NME201354	38%	83.7%	90.6%
ECO102641	PMU100513	27%	72.3%	68.7%
ECO102641	PRT105375	29%	98.6%	97.3%
ECO102641	PAE204442	67%	98.6%	97.5%
ECO102641	PPU108958	46%	85.3%	95.3%
ECO102641	PSY105088	46%	85.9%	94.7%
ECO102641	SPA100411	81%	98.1%	99.7%
ECO102641	STY102777	92%	100%	100%
ECO102641	VCH101926	27%	83.7%	94.1%
ECO102641	YPS000499	74%	99.2%	96.8%
ECO102645	CBO103413	46%	98.8%	97.7%
ECO102645	CDF102939	60%	99.6%	99.2%
ECO102645	EBC101896	95%	81.5%	99.1%
ECO102645	ECO102645	100%	100%	100%
ECO102645	KPN307029	91%	100%	100%
ECO102645	PMU101968	74%	100%	100%
ECO102645	PSY101670	33%	83.4%	94.0%
ECO102645	SPA101711	94%	100%	100%
ECO102645	STY102788	97%	100%	100%
ECO102645	STM103254	97%	100%	100%
ECO102646	CBO101041	31%	96.6%	82.7%
ECO102646	CDF104371	29%	96.6%	77.1%
ECO102646	EBC101897	70%	100%	100%
ECO102646	EFA200720	29%	88.2%	66.5%
ECO102646	EFM201620	27%	90.8%	67.5%
ECO102646	ECO102646	100%	100%	100%
ECO102646	KPN303732	73%	100%	100%
ECO102646	MAV103524	58%	20.2%	18.5%
ECO102646	MBV103369	45%	29.4%	27.8%
ECO102646	MLP100731	45%	29.4%	27.8%
ECO102646	MTU201326	45%	29.4%	27.8%
ECO102646	PMU101967	44%	92.4%	90.2%
ECO102646	SPA101712	82%	100%	100%
ECO102646	STY102790	83%	100%	100%
ECO102646	STM103595	83%	100%	100%
ECO102646	SMU100625	35%	59.7%	43.8%
ECO102646	SPY101903	32%	88.2%	70.4%
ECO102654	EBC103477	78%	98.5%	98.5%
ECO102654	ECO102654	100%	100%	100%
ECO102654	KPN303729	75%	98.8%	98.8%
ECO102654	SPA100711	39%	99.1%	99.1%
ECO102654	STY104055	40%	99.1%	97.6%
ECO102654	STM100084	41%	99.1%	97.6%
ECO102654	VCH101533	38%	99.1%	96.8%
ECO102654	YPS001725	36%	99.1%	98.8%
ECO102655	CDF100104	39%	36.9%	98.9%
ECO102655	CDF101686	37%	94.2%	97.0%
ECO102655	EBC103488	88%	99.0%	99.8%
ECO102655	EFM200442	36%	93.6%	99.6%
ECO102655	ECO102655	100%	100%	100%
ECO102655	KPN305684	88%	97.5%	98.5%
ECO102655	PPU110278	31%	19.2%	17.2%
ECO102655	SPN400505	37%	93.8%	72.9%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102655	SPY200412	38%	95.7%	73.7%
ECO102669	BFU102622	56%	100%	94.9%
ECO102669	CJU100586	41%	98.1%	98.6%
ECO102669	CAC102120	44%	98.1%	99.2%
ECO102669	CBO100979	38%	89.8%	93.6%
ECO102669	CDP100853	51%	98.1%	96.5%
ECO102669	EBC102590	86%	98.1%	79.9%
ECO102669	ECO102669	100%	100%	100%
ECO102669	HPY100884	43%	97.9%	99.2%
ECO102669	KPN303726	84%	99.7%	99.7%
ECO102669	LPN100627	46%	98.1%	98.4%
ECO102669	PRT101111	64%	98.9%	99.2%
ECO102669	SPA101915	93%	98.1%	80.6%
ECO102669	STY102830	94%	99.7%	99.7%
ECO102669	STM103675	94%	99.7%	99.7%
ECO102671	EBC107209	86%	88.0%	100%
ECO102671	ECO102671	100%	100%	100%
ECO102671	KPN303720	88%	77.7%	95.5%
ECO102671	SPA100903	89%	69.7%	98.6%
ECO102671	STY102834	89%	99.9%	99.9%
ECO102671	STM103679	90%	99.9%	99.9%
ECO102671	SAU802611	40%	5.3%	52.9%
ECO102690	BAN104917	36%	76.1%	80.8%
ECO102690	BAN109893	52%	97.0%	99.5%
ECO102690	BFR12076	51%	89.1%	89.1%
ECO102690	BCE101378	56%	75.1%	80.7%
ECO102690	BFU105924	51%	78.6%	87.7%
ECO102690	BMA103440	52%	87.6%	67.2%
ECO102690	CJU101334	28%	70.6%	81.8%
ECO102690	CAC100962	53%	96.0%	96.5%
ECO102690	EBC104331	89%	100%	100%
ECO102690	ECO102690	100%	100%	100%
ECO102690	KPN103912	92%	100%	100%
ECO102690	PRT103978	62%	99.5%	100%
ECO102690	PAE201392	58%	75.1%	77.0%
ECO102690	PSY108238	50%	94.0%	80.9%
ECO102690	PSY106624	50%	94.0%	80.9%
ECO102690	SPA104299	77%	17.4%	77.3%
ECO102690	STY103443	85%	100%	100%
ECO102690	SEP201659	52%	96.0%	97.5%
ECO102690	SHA102289	56%	96.0%	97.5%
ECO102690	VCH102521	67%	97.0%	91.2%
ECO102690	YPS000099	80%	98.0%	92.5%
ECO102705	ABA100092	27%	81.8%	51.5%
ECO102705	BAN110678	43%	73.6%	53.4%
ECO102705	BAN109471	43%	73.6%	53.4%
ECO102705	BFR105878	35%	86.8%	93.2%
ECO102705	BPT100447	31%	48.8%	40.8%
ECO102705	BCE115084	31%	52.1%	44.7%
ECO102705	BFU101022	28%	57.9%	50%
ECO102705	BMA106574	31%	52.1%	44.7%
ECO102705	CJU100148	28%	52.9%	33.2%
ECO102705	CAC100156	25%	85.1%	87.5%
ECO102705	CBO101681	43%	95.0%	98.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102705	EBC104323	94%	99.2%	100%
ECO102705	ECO102705	100%	100%	100%
ECO102705	HIN101163	27%	92.6%	95.7%
ECO102705	KPN303830	93%	100%	100%
ECO102705	MCA101606	27%	82.6%	52.0%
ECO102705	NGO101844	30%	69.4%	62.1%
ECO102705	NME200649	26%	94.2%	97.1%
ECO102705	PMU100185	29%	92.6%	95.7%
ECO102705	PRT102255	84%	100%	100%
ECO102705	PAE202664	76%	95.9%	98.3%
ECO102705	PPU111281	75%	95.9%	98.3%
ECO102705	PSY100460	72%	95.9%	98.3%
ECO102705	SPA104187	93%	100%	100%
ECO102705	STY103502	94%	99.2%	100%
ECO102705	STM104214	94%	99.2%	100%
ECO102705	SAU800711	35%	94.2%	84.9%
ECO102705	SEP200752	34%	94.2%	84.9%
ECO102705	SHA101448	37%	96.7%	87.1%
ECO102705	SMU100908	39%	74.4%	59.5%
ECO102705	VCH101280	79%	100%	99.2%
ECO102705	YPS000126	83%	98.3%	100%
ECO102706	ABA104102	26%	67.7%	56.5%
ECO102706	BPT101729	27%	74.8%	58.4%
ECO102706	BCE111382	26%	81.3%	67.3%
ECO102706	BCE104052	26%	81.3%	64.3%
ECO102706	BFU111756	34%	96.1%	97.7%
ECO102706	BMA109566	26%	75.3%	62.7%
ECO102706	CJU100383	37%	9.2%	7.0%
ECO102706	ECO101667	41%	97.5%	99.5%
ECO102706	ECO102706	100%	100%	100%
ECO102706	KPN303429	45%	10.9%	8.6%
ECO102706	LPN103326	26%	86.1%	74.7%
ECO102706	MCA100693	27%	85.2%	70.9%
ECO102706	MAV102272	27%	74.1%	76.0%
ECO102706	MBV104554	26%	74.6%	80.4%
ECO102706	MLP101354	27%	75.3%	77.2%
ECO102706	MTU200558	28%	75.8%	77.7%
ECO102706	NGO101376	27%	77.1%	58.8%
ECO102706	NME200707	27%	82.2%	65.3%
ECO102706	PAE202951	27%	84.1%	70.8%
ECO102706	PPU108891	27%	77.1%	66.1%
ECO102706	PSY104867	28%	74.8%	63.3%
ECO102714	ECO102714	100%	100%	100%
ECO102714	PAE204095	33%	87.8%	98.3%
ECO102714	SHA100148	34%	85.7%	95.1%
ECO102722	BAN100835	30%	63.1%	69.7%
ECO102722	BAN107688	32%	64.9%	67.2%
ECO102722	BFR104257	34%	73.0%	70.4%
ECO102722	CAC102158	26%	91.9%	87.7%
ECO102722	CBO100493	21%	94.6%	58.2%
ECO102722	CDF104542	30%	64.9%	61.4%
ECO102722	EFA200060	30%	73.0%	70%
ECO102722	EFM202176	30%	95.5%	91.2%
ECO102722	ECO102722	100%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102722	KPN301507	56%	96.4%	96.3%
ECO102722	LMO100551	30%	88.3%	85.2%
ECO102722	MBV101398	40%	65.8%	70.3%
ECO102722	MTU202763	40%	65.8%	70.3%
ECO102722	NGO101975	27%	95.5%	97.4%
ECO102722	NME200373	38%	64.9%	68.6%
ECO102722	SAU802068	25%	64.9%	65%
ECO102722	SEP201326	25%	64.9%	65%
ECO102722	SHA101049	23%	91.9%	88.4%
ECO102722	SMU101371	30%	90.1%	90.9%
ECO102736	BAN104134	38%	93.9%	96.9%
ECO102736	BAN100117	45%	93.0%	96.4%
ECO102736	BAN105510	51%	95.8%	93.6%
ECO102736	BAN111762	52%	95.8%	93.6%
ECO102736	CJU101531	49%	95.6%	98.6%
ECO102736	CDP101612	61%	97.2%	94.0%
ECO102736	EBC103670	93%	100%	99.5%
ECO102736	ECO102736	100%	100%	100%
ECO102736	HIN100275	59%	95.6%	97.8%
ECO102736	HPY100131	43%	94.9%	95.9%
ECO102736	KPN308636	92%	100%	100%
ECO102736	LPN103077	64%	99.5%	99.8%
ECO102736	PMU100037	58%	96.0%	98.3%
ECO102736	PRT103179	80%	99.5%	99.5%
ECO102736	PPU110333	64%	94.2%	100%
ECO102736	PSY103212	64%	93.7%	99.5%
ECO102736	SPA101480	94%	99.5%	100%
ECO102736	STY103893	95%	100%	100%
ECO102736	STM104294	95%	100%	100%
ECO102736	VCH101631	50%	99.5%	99.5%
ECO102736	YPS001136	82%	99.5%	98.8%
ECO102737	BCE106651	52%	99.6%	86.8%
ECO102737	BFU111678	51%	99.6%	93.7%
ECO102737	CDF102230	39%	99.8%	100%
ECO102737	EBC103668	94%	99.3%	100%
ECO102737	ECO102737	100%	100%	100%
ECO102737	KPN307371	92%	100%	100%
ECO102737	MLP101075	51%	99.6%	99.6%
ECO102737	NGO100729	51%	98.5%	96.3%
ECO102737	NME200054	49%	93.6%	96.1%
ECO102737	PRT100267	79%	100%	100%
ECO102737	PPU107497	54%	99.6%	99.6%
ECO102737	PSY104683	52%	99.6%	99.6%
ECO102737	STY103896	94%	100%	100%
ECO102737	STM104297	94%	100%	100%
ECO102737	SAU802530	33%	61.1%	92.0%
ECO102737	SEP201095	33%	61.1%	92.0%
ECO102737	SHA100506	33%	61.1%	92.3%
ECO102741	BFR10515	34%	92.7%	93.2%
ECO102741	BCE113397	39%	93.2%	89.3%
ECO102741	CJU100451	36%	88.8%	91.6%
ECO102741	CBO103139	22%	89.5%	94.7%
ECO102741	ECO102741	100%	100%	100%
ECO102741	HIN100590	34%	92.9%	96.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102741	HPY101157	35%	93.6%	97.3%
ECO102741	KPN309059	89%	100%	100%
ECO102741	NGO101858	31%	94.1%	93.2%
ECO102741	NME200657	31%	94.1%	97.5%
ECO102741	SPA104049	93%	94.1%	100%
ECO102741	STY103920	92%	100%	100%
ECO102744	BCE105647	36%	98.6%	96.0%
ECO102744	BFU109391	35%	98.6%	94.2%
ECO102744	BFU108766	36%	98.6%	89.5%
ECO102744	ECO102744	100%	100%	100%
ECO102744	HIN100592	61%	100%	98.6%
ECO102744	KPN307040	92%	100%	100%
ECO102744	SPA104052	91%	100%	100%
ECO102744	STY103924	91%	100%	100%
ECO102744	STM104325	91%	100%	100%
ECO102744	SPN401968	45%	98.6%	95.2%
ECO102749	EBC100951	86%	97.4%	98.7%
ECO102749	ECO102749	100%	100%	100%
ECO102749	KPN305190	84%	98.7%	97.4%
ECO102749	PMU101798	35%	71.1%	25.9%
ECO102749	PRT104389	44%	94.7%	97.4%
ECO102749	PSY107484	34%	57.9%	91.7%
ECO102749	SPA104038	93%	97.4%	98.7%
ECO102749	STY103939	93%	97.4%	98.7%
ECO102749	SEP203585	32%	94.7%	60.2%
ECO102763	EBC107113	56%	99.4%	93.3%
ECO102763	ECO102763	100%	100%	100%
ECO102763	KPN305145	49%	99.4%	84.2%
ECO102763	SPA106196	66%	99.4%	99.4%
ECO102763	STY104010	66%	99.4%	99.4%
ECO102763	VCH100842	22%	37.8%	32.1%
ECO102763	YPS004214	41%	29.5%	78.0%
ECO102764	ABA105245	60%	100%	100%
ECO102764	BAN100788	50%	99.2%	99.4%
ECO102764	BFR11837	66%	100%	100%
ECO102764	BPT100700	34%	100%	100%
ECO102764	BCE114856	33%	100%	95.3%
ECO102764	BFU101750	33%	100%	100%
ECO102764	BMA105484	35%	100%	100%
ECO102764	CAC100774	36%	99.6%	98.1%
ECO102764	CBO101177	21%	68.2%	54.6%
ECO102764	CDP100080	63%	98.9%	93.2%
ECO102764	EBC102732	95%	100%	100%
ECO102764	EFA201843	51%	98.9%	98.7%
ECO102764	EFM100074	44%	39.0%	97.5%
ECO102764	ECO102764	100%	100%	100%
ECO102764	HIN100884	33%	100%	100%
ECO102764	KPN305143	93%	100%	100%
ECO102764	LMO102901	50%	100%	100%
ECO102764	MCA101497	59%	100%	100%
ECO102764	MAV101962	67%	98.9%	97.7%
ECO102764	MBV103568	66%	98.9%	97.7%
ECO102764	MLP100936	66%	98.9%	97.7%
ECO102764	MTU202727	66%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102764	MGE100232	49%	100%	100%
ECO102764	MPN100516	49%	100%	87.5%
ECO102764	NGO100594	71%	100%	99.2%
ECO102764	NME201812	71%	100%	100%
ECO102764	PMU100079	33%	100%	100%
ECO102764	PRT100903	36%	100%	100%
ECO102764	PAE200341	69%	100%	100%
ECO102764	PPU102228	35%	100%	100%
ECO102764	PSY101984	35%	100%	100%
ECO102764	SPA102433	96%	100%	100%
ECO102764	STY104016	95%	100%	100%
ECO102764	SAU801427	51%	98.9%	97.5%
ECO102764	SEP200374	48%	98.9%	97.5%
ECO102764	SEP201188	48%	98.9%	97.5%
ECO102764	SHA101980	49%	98.9%	97.5%
ECO102764	SMU100950	29%	97.3%	96.1%
ECO102764	SPN400585	30%	95.1%	89.2%
ECO102764	SPY200657	30%	93.6%	92.1%
ECO102764	VCH100662	32%	100%	100%
ECO102764	YPS002874	88%	100%	100%
ECO102768	EBC103078	83%	97.8%	100%
ECO102768	ECO102768	100%	100%	100%
ECO102768	HIN100383	61%	92.6%	95.1%
ECO102768	KPN301609	84%	97.8%	97.0%
ECO102768	LPN100331	48%	93.9%	96.4%
ECO102768	PMU101067	58%	94.8%	97.7%
ECO102768	PRT100191	75%	94.3%	96%
ECO102768	SPA102493	86%	100%	100%
ECO102768	STY104040	88%	100%	99.1%
ECO102768	STM100058	88%	100%	99.1%
ECO102768	VCH100655	62%	94.3%	97.7%
ECO102768	YPS002878	72%	96.1%	96.5%
ECO102783	ECO102783	100%	100%	100%
ECO102783	SPA104199	38%	82.6%	92.6%
ECO102783	STY104456	39%	82.6%	92.7%
ECO102783	STM100042	39%	82.6%	92.7%
ECO102783	UUR100311	26%	38.3%	45.7%
ECO102787	CBO101785	24%	75.7%	47.3%
ECO102787	ECO102787	100%	100%	100%
ECO102788	BMA103545	36%	92.0%	87.1%
ECO102788	CPN201041	24%	50.9%	35.9%
ECO102788	CTR200854	21%	54.0%	35.8%
ECO102788	ECO102788	100%	100%	100%
ECO102788	PRT103050	35%	89.0%	83.7%
ECO102788	PAE201706	27%	70.6%	68.3%
ECO102788	SPA104004	37%	85.9%	84.2%
ECO102788	STY103261	37%	85.9%	84.2%
ECO102788	STM103969	20%	73.6%	78.3%
ECO102802	ABA100552	26%	97.6%	93.9%
ECO102802	BPT101760	31%	98.8%	95.3%
ECO102802	BMA108998	28%	96.4%	92.2%
ECO102802	CBO101375	46%	99.9%	98.3%
ECO102802	EFA201637	30%	97.9%	79.2%
ECO102802	ECO102802	100%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102802	MBV100418	29%	98.9%	95.4%
ECO102802	MTU200372	29%	98.9%	95.4%
ECO102802	TPA100078	20%	48.8%	46.9%
ECO102814	CBO103064	43%	98.3%	99.0%
ECO102814	EFA201627	44%	95.0%	95.3%
ECO102814	ECO102814	100%	100%	100%
ECO102815	BFU100618	24%	89.2%	92.8%
ECO102815	CBO101548	33%	89.4%	94.6%
ECO102815	CDF100946	24%	89.2%	95.0%
ECO102815	CDF102110	35%	89.7%	94.8%
ECO102815	EBC104972	22%	88.8%	81.8%
ECO102815	EFA201626	34%	89.9%	94.6%
ECO102815	ECO102815	100%	100%	100%
ECO102815	KPN304250	22%	94.4%	99.4%
ECO102815	PRT100066	23%	93.1%	91.2%
ECO102815	YPS002667	21%	77.8%	84.6%
ECO102817	CDF100372	31%	9.9%	89.7%
ECO102817	CDF100786	36%	78.9%	99.9%
ECO102817	CDF103342	34%	82.2%	98.7%
ECO102817	CDF100973	34%	82.5%	98.8%
ECO102817	ECO102817	100%	100%	100%
ECO102817	MAV104590	26%	8.9%	42.2%
ECO102817	PAE201522	26%	83.4%	96.2%
ECO102819	ABA105065	62%	97.5%	97.1%
ECO102819	BAN109973	25%	39.4%	94.4%
ECO102819	BAN108621	25%	51.5%	91.1%
ECO102819	BAN113546	25%	63.3%	87.3%
ECO102819	BFR102598	35%	16.2%	16.3%
ECO102819	BPT101914	23%	74.5%	72.6%
ECO102819	BCE107325	50%	94.5%	97.4%
ECO102819	BFU104800	47%	98.2%	95.8%
ECO102819	BMA103965	48%	94.8%	95.4%
ECO102819	CJU100060	23%	84.7%	91.9%
ECO102819	CAC102908	31%	99.1%	99.1%
ECO102819	CDF102112	32%	98.4%	99.5%
ECO102819	EBC101322	59%	97.3%	100%
ECO102819	EFA200357	30%	83.4%	83.7%
ECO102819	ECO102819	100%	100%	100%
ECO102819	HPY100263	20%	78.6%	84.6%
ECO102819	KPN301122	58%	97.3%	97.9%
ECO102819	LPN100461	28%	94.8%	97.5%
ECO102819	MCA101946	27%	26.7%	26.9%
ECO102819	MAV104895	37%	10.3%	8.2%
ECO102819	MBV100021	40%	10.3%	8.5%
ECO102819	MTU202019	40%	10.3%	8.2%
ECO102819	PAE201520	57%	96.1%	97.5%
ECO102819	PPU107264	55%	98.4%	99.3%
ECO102819	PSY103885	54%	99.5%	99.8%
ECO102819	SPN401213	25%	81.3%	72.3%
ECO102819	SPY201589	34%	11.4%	11.7%
ECO102827	ABA101939	69%	99.5%	100%
ECO102827	BAN110383	35%	98.6%	99.7%
ECO102827	BAN112271	45%	98.9%	99.2%
ECO102827	BFR11646	44%	96.4%	99.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102827	BPT101803	64%	98.9%	98.4%
ECO102827	BBU100074	48%	93.2%	96.8%
ECO102827	BCE103450	62%	99.2%	98.6%
ECO102827	BFU108643	64%	76.7%	100%
ECO102827	BMA102879	62%	99.2%	98.6%
ECO102827	CJU101373	49%	90.7%	90.4%
ECO102827	CPN300572	47%	93.4%	98%
ECO102827	CTR100183	44%	97.0%	96.7%
ECO102827	CAC100933	48%	86.8%	96.7%
ECO102827	CBO100813	47%	88.2%	99.1%
ECO102827	CDF101444	44%	98.6%	99.7%
ECO102827	CDP101706	45%	91.0%	79.4%
ECO102827	EBC102997	96%	100%	100%
ECO102827	EFA200592	48%	98.9%	99.2%
ECO102827	ECO102827	100%	100%	100%
ECO102827	HPY100168	49%	96.7%	97.0%
ECO102827	KPN303319	96%	87.7%	100%
ECO102827	LPN101389	73%	100%	100%
ECO102827	LMO101259	49%	87.7%	98.2%
ECO102827	MCA101198	63%	80%	100%
ECO102827	MAV104984	44%	92.6%	87.2%
ECO102827	MBV105866	44%	92.6%	90.2%
ECO102827	MLP100413	43%	92.6%	92.0%
ECO102827	MTU203065	44%	92.6%	90.2%
ECO102827	NGO100784	64%	99.2%	98.6%
ECO102827	NME200212	64%	99.2%	98.6%
ECO102827	PMU100190	82%	87.7%	100%
ECO102827	PRT100475	90%	87.7%	100%
ECO102827	PAE100476	68%	99.5%	100%
ECO102827	PPU100841	70%	99.5%	100%
ECO102827	PSY108064	65%	99.5%	100%
ECO102827	SPA102977	95%	100%	100%
ECO102827	STY104137	95%	100%	100%
ECO102827	SAU800754	45%	88.2%	98.2%
ECO102827	SEP201383	48%	88.2%	97.3%
ECO102827	SHA101268	47%	88.2%	97.6%
ECO102827	SMU100349	44%	88.2%	98.8%
ECO102827	SPN400665	46%	88.5%	97.9%
ECO102827	SPY200463	44%	91.0%	98.2%
ECO102827	TPA100569	46%	93.2%	92.4%
ECO102827	YPS000161	88%	100%	100%
ECO102828	ABA101961	44%	98.4%	98.8%
ECO102828	BAN104770	24%	89.4%	63.9%
ECO102828	BAN102480	32%	96.0%	68.9%
ECO102828	BFR100673	31%	90.8%	99.8%
ECO102828	BPT101805	46%	99.1%	99.1%
ECO102828	BBU100253	38%	80.2%	81.9%
ECO102828	BCE102975	34%	18.4%	97.0%
ECO102828	BFU108641	48%	95.7%	95.8%
ECO102828	BMA106924	48%	95.7%	95.9%
ECO102828	CJU100028	29%	90.3%	93.5%
ECO102828	CPN200184	28%	89.4%	86.2%
ECO102828	CTR200722	30%	95.7%	93.6%
ECO102828	CAC102562	30%	95.1%	95.6%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102828	CBO101432	30%	99.1%	97.8%
ECO102828	CDF100497	30%	99.5%	68.6%
ECO102828	EBC102952	87%	78.9%	100%
ECO102828	EFA201172	32%	95.5%	68.6%
ECO102828	EFM100083	33%	48.2%	92.7%
ECO102828	ECO102828	100%	100%	100%
ECO102828	HIN101186	58%	96.0%	96.3%
ECO102828	HPY100344	31%	79.7%	83.9%
ECO102828	KPN303321	88%	99.8%	99.8%
ECO102828	LPN103347	51%	98.8%	98.8%
ECO102828	LMO102252	33%	88.9%	62.7%
ECO102828	MCA101569	42%	95.1%	92.9%
ECO102828	NGO100971	48%	96.2%	95.9%
ECO102828	NME200968	48%	96.2%	95.9%
ECO102828	PMU100192	60%	96.0%	96.3%
ECO102828	PRT103507	62%	98.8%	98.6%
ECO102828	PAE203722	58%	99.1%	99.8%
ECO102828	PPU107844	56%	99.1%	99.8%
ECO102828	PSY104923	57%	99.1%	99.8%
ECO102828	SPA102978	84%	100%	100%
ECO102828	STY104138	91%	100%	100%
ECO102828	SAU801636	32%	96.0%	70.3%
ECO102828	SEP201590	31%	97.6%	71.5%
ECO102828	SHA101075	32%	97.6%	71.5%
ECO102828	SMU100405	32%	95.3%	71.8%
ECO102828	SPN400537	33%	95.7%	71.1%
ECO102828	SPY200696	31%	94.3%	70.8%
ECO102828	TPA100696	27%	2.1%	20.3%
ECO102828	VCH102382	63%	98.8%	98.5%
ECO102828	YPS000162	75%	99.8%	99.8%
ECO102832	EBC102958	80%	99.3%	99.3%
ECO102832	ECO102832	100%	100%	100%
ECO102832	KPN303342	72%	99.3%	99.3%
ECO102832	PRT102348	38%	96.3%	97.0%
ECO102832	SPA102982	83%	97.0%	95.6%
ECO102832	STY104152	80%	83.7%	98.3%
ECO102832	YPS000169	52%	94.8%	92.2%
ECO102833	ABA104232	34%	59.1%	52.5%
ECO102833	ABA100192	33%	70.5%	72.9%
ECO102833	BPT105896	32%	87.5%	89.5%
ECO102833	BCE102877	39%	71.6%	70.8%
ECO102833	BFU110742	32%	81.8%	84.4%
ECO102833	BMA108958	39%	71.6%	70%
ECO102833	EBC102960	89%	100%	100%
ECO102833	ECO102833	100%	100%	100%
ECO102833	HIN100608	56%	83.0%	85.9%
ECO102833	KPN303344	88%	100%	100%
ECO102833	LPN100900	41%	81.8%	91.1%
ECO102833	MCA102471	33%	75%	75%
ECO102833	NGO101277	33%	81.8%	87.8%
ECO102833	NME201059	33%	81.8%	87.8%
ECO102833	PMU101790	54%	83.0%	86.9%
ECO102833	PRT102346	78%	94.3%	89.2%
ECO102833	PAE200759	45%	81.8%	85.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102833	PPU107872	41%	81.8%	85.7%
ECO102833	PSY102332	44%	81.8%	85.7%
ECO102833	SPA102972	93%	100%	100%
ECO102833	STY104153	93%	100%	100%
ECO102833	VCH102435	57%	85.2%	87.2%
ECO102833	YPS000170	81%	100%	100%
ECO102834	ABA100533	24%	72.4%	75.4%
ECO102834	BPT101177	31%	89.3%	89.3%
ECO102834	BCE101423	24%	40.2%	97.8%
ECO102834	BFU101500	28%	92.9%	84.8%
ECO102834	BMA108730	28%	92.3%	87.4%
ECO102834	CDP100504	29%	31.9%	26.3%
ECO102834	EBC102962	85%	100%	100%
ECO102834	ECO102834	100%	100%	100%
ECO102834	HIN100446	37%	93.6%	98.6%
ECO102834	KPN303346	82%	100%	99.7%
ECO102834	LPN101317	24%	69.9%	63.6%
ECO102834	MCA102416	23%	92.9%	97.9%
ECO102834	NGO100033	24%	82.5%	86.8%
ECO102834	NME201332	23%	82.5%	86.8%
ECO102834	PMU101874	37%	92.3%	94.2%
ECO102834	PRT102360	59%	97.5%	97.3%
ECO102834	PAE200758	31%	91.1%	93.3%
ECO102834	PPU103341	31%	91.1%	93.3%
ECO102834	PSY102335	32%	92.9%	94.6%
ECO102834	SPA102974	84%	100%	100%
ECO102834	STY104154	85%	100%	100%
ECO102834	STM100447	85%	100%	100%
ECO102834	VCH102436	41%	94.5%	93.5%
ECO102834	YPS000171	68%	99.1%	98.2%
ECO102839	ABA101985	21%	15.0%	33.5%
ECO102839	BAN111848	37%	41.3%	81.6%
ECO102839	BAN103164	40%	43.8%	83.9%
ECO102839	BFR105629	61%	37.1%	100%
ECO102839	BPT101500	58%	98.5%	98.8%
ECO102839	BCE101816	65%	35.5%	99.7%
ECO102839	BFU113866	59%	99.7%	98.5%
ECO102839	BMA101641	59%	99.6%	98.4%
ECO102839	CBO103893	40%	14.5%	60.3%
ECO102839	CDF104582	40%	15.0%	56.9%
ECO102839	EBC102216	89%	62.8%	100%
ECO102839	ECO102839	100%	100%	100%
ECO102839	KPN302321	91%	100%	100%
ECO102839	LPN103285	43%	35.6%	89.4%
ECO102839	LMO101451	42%	18.6%	52.9%
ECO102839	MCA102219	58%	99.5%	99.4%
ECO102839	MAV102690	57%	6.5%	61.9%
ECO102839	MBV101231	54%	99.2%	99.9%
ECO102839	MLP101253	53%	98.5%	98.6%
ECO102839	MTU201799	54%	99.2%	99.9%
ECO102839	NGO100494	58%	99.6%	99.7%
ECO102839	NME201783	58%	99.6%	99.7%
ECO102839	PRT105559	78%	100%	100%
ECO102839	PAE205208	65%	99.9%	99.6%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102839	PPU102796	64%	99.7%	99.5%
ECO102839	PSY104260	60%	99.4%	99.3%
ECO102839	SPA102064	92%	69.9%	100%
ECO102839	STY104159	95%	100%	100%
ECO102839	SAU801535	40%	21.2%	47.6%
ECO102839	SEP200942	39%	46.5%	87.5%
ECO102839	SHA100981	40%	19.5%	50.6%
ECO102839	YPS000177	83%	100%	100%
ECO102842	ABA100860	36%	98%	97.3%
ECO102842	BAN109853	21%	78%	82.4%
ECO102842	BAN110803	22%	78%	82.5%
ECO102842	BCE103921	33%	97.2%	98.0%
ECO102842	BFU102513	34%	97.5%	98.7%
ECO102842	BMA106019	34%	97.5%	98.0%
ECO102842	EBC102213	82%	100%	100%
ECO102842	ECO102842	100%	100%	100%
ECO102842	KPN302315	86%	100%	100%
ECO102842	LPN101662	39%	97.8%	99.5%
ECO102842	MCA100913	33%	86.8%	84.3%
ECO102842	NGO101638	27%	96.8%	98.7%
ECO102842	NME202001	28%	96.8%	98.7%
ECO102842	PMU101726	52%	98%	100%
ECO102842	PRT102355	65%	100%	97.6%
ECO102842	PAE205216	45%	98%	98.0%
ECO102842	PPU102206	45%	98.2%	97.8%
ECO102842	PSY101343	45%	83.8%	98.8%
ECO102842	SPA100602	83%	94.2%	100%
ECO102842	STY104163	87%	100%	100%
ECO102842	VCH102438	56%	99.2%	97.1%
ECO102842	YPS000180	71%	99.8%	99.0%
ECO102847	ABA105202	47%	38.5%	60.9%
ECO102847	BAN105088	29%	95.6%	88.5%
ECO102847	BFR101447	32%	74.7%	97.7%
ECO102847	BPT105849	29%	96.2%	80.1%
ECO102847	BCE106510	29%	96.2%	87.6%
ECO102847	BFU103183	32%	80.2%	69.8%
ECO102847	BMA109897	32%	96.2%	86.9%
ECO102847	CJU101133	39%	18.1%	15.9%
ECO102847	CPN201090	27%	92.3%	88.3%
ECO102847	CTR200018	28%	91.2%	87.1%
ECO102847	CAC100796	25%	93.4%	91.2%
ECO102847	CBO101645	25%	92.9%	90.8%
ECO102847	CDF100385	31%	80.2%	76.2%
ECO102847	CDP100143	31%	45.6%	40.8%
ECO102847	EBC103700	85%	100%	91.9%
ECO102847	EFA200313	28%	87.9%	85.6%
ECO102847	EFM100240	33%	73.6%	70.6%
ECO102847	ECO102847	100%	100%	100%
ECO102847	HIN100838	53%	92.9%	90.4%
ECO102847	HPY100748	29%	51.1%	45.5%
ECO102847	KPN303078	80%	99.5%	91.4%
ECO102847	LPN101529	35%	98.4%	90.7%
ECO102847	LMO101273	27%	71.4%	71.5%
ECO102847	MCA102486	33%	47.3%	95.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102847	MAV101485	29%	81.3%	76.0%
ECO102847	MBV100624	28%	78.6%	64.6%
ECO102847	MLP100128	28%	79.7%	74.1%
ECO102847	MTU200981	28%	78.6%	73.1%
ECO102847	MGE100249	33%	35.7%	38.2%
ECO102847	MPN100488	35%	36.8%	39.6%
ECO102847	NGO100917	31%	78.6%	75.1%
ECO102847	NME200308	26%	97.8%	92.2%
ECO102847	PMU101721	53%	95.1%	91.1%
ECO102847	PRT100675	56%	99.5%	88.3%
ECO102847	PAE205223	39%	95.6%	87.7%
ECO102847	PPU102242	40%	96.2%	88.6%
ECO102847	PSY101332	37%	94.5%	96.2%
ECO102847	SPA101441	82%	100%	100%
ECO102847	STY104168	86%	100%	100%
ECO102847	STM100485	86%	100%	100%
ECO102847	SAU801550	29%	77.5%	74.3%
ECO102847	SEP200967	24%	95.1%	90.2%
ECO102847	SHA101021	30%	77.5%	74.9%
ECO102847	SMU100642	33%	59.9%	58.4%
ECO102847	SPN401902	35%	92.3%	88.4%
ECO102847	TPA100686	33%	37.4%	32%
ECO102847	VCH102443	57%	99.5%	94.3%
ECO102847	YPS000185	69%	99.5%	91.4%
ECO102852	BFR100860	60%	99.2%	97.2%
ECO102852	BFU115799	35%	95.0%	46.1%
ECO102852	CAC100955	27%	15.4%	61.0%
ECO102852	CDP100186	60%	96.5%	95.1%
ECO102852	ECO102852	100%	100%	100%
ECO102852	MAV101088	60%	96.8%	93.3%
ECO102852	MBV102766	60%	96.8%	93.3%
ECO102852	MLP101093	62%	94.7%	90.1%
ECO102852	MTU201472	60%	96.8%	93.3%
ECO102852	NGO101266	37%	7.3%	34.0%
ECO102857	ABA105537	20%	51.6%	53.6%
ECO102857	BAN102598	28%	49.2%	72.3%
ECO102857	BAN112147	24%	62.6%	69.7%
ECO102857	EBC103707	82%	100%	100%
ECO102857	ECO102857	100%	100%	100%
ECO102857	KPN303070	85%	99.2%	100%
ECO102857	MAV100904	29%	76.0%	79.5%
ECO102857	MBV102375	26%	50%	74.3%
ECO102857	MTU203571	26%	65.4%	68.8%
ECO102857	PRT101295	51%	94.7%	98.8%
ECO102857	SPA100221	86%	54.5%	98.5%
ECO102857	STY104484	88%	99.6%	99.2%
ECO102857	VCH100478	37%	85.0%	87.4%
ECO102857	YPS000189	63%	94.7%	92.7%
ECO102868	ABA103851	31%	14.3%	56.3%
ECO102868	ECO102868	100%	100%	100%
ECO102868	MBV106174	27%	18.4%	18.2%
ECO102868	MTU200037	27%	18.4%	17.7%
ECO102869	EFA202092	32%	96.6%	22.6%
ECO102869	EFM200261	38%	98.6%	21.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102869	ECO102869	100%	100%	100%
ECO102869	KPN201713	38%	96.6%	98.6%
ECO102869	LMO101172	37%	98.0%	98.0%
ECO102869	SAU800331	35%	95.2%	95.2%
ECO102869	SPN401937	34%	85.7%	18.8%
ECO102869	SPY201502	37%	97.3%	21.6%
ECO102870	ABA100381	68%	99.5%	98.9%
ECO102870	BAN111549	52%	49.5%	87.1%
ECO102870	BAN102492	50%	98.8%	96.5%
ECO102870	BPT100911	63%	99.1%	98.5%
ECO102870	BCE113404	63%	99.1%	96.1%
ECO102870	BFU111408	60%	98.9%	97.1%
ECO102870	BMA106204	63%	99.1%	96.1%
ECO102870	CJU101551	44%	98.3%	98.1%
ECO102870	CAC101106	49%	98.8%	98.2%
ECO102870	CAC102328	50%	98.8%	98.2%
ECO102870	CDF103784	37%	41.2%	95.3%
ECO102870	CDP100257	45%	99.2%	95.9%
ECO102870	EBC103706	95%	100%	100%
ECO102870	EFA201838	50%	97.7%	98.8%
ECO102870	EFM100121	60%	24.4%	98.8%
ECO102870	ECO102870	100%	100%	100%
ECO102870	HIN101002	77%	100%	100%
ECO102870	KPN303075	95%	100%	100%
ECO102870	LPN102231	75%	28.7%	99.5%
ECO102870	LPN102506	58%	94.6%	98.0%
ECO102870	LMO101021	47%	99.4%	98.1%
ECO102870	MCA100777	67%	99.7%	97.8%
ECO102870	MGE100068	32%	97.6%	98.0%
ECO102870	MPN100073	33%	98.5%	98.9%
ECO102870	NGO100398	64%	99.2%	99.7%
ECO102870	NME201529	64%	99.2%	99.7%
ECO102870	PMU101242	75%	100%	100%
ECO102870	PMU101638	76%	100%	100%
ECO102870	PRT102791	81%	100%	99.8%
ECO102870	PAE200547	72%	100%	99.7%
ECO102870	PPU104660	72%	100%	99.7%
ECO102870	PSY103014	72%	97.3%	99.7%
ECO102870	SPA101296	94%	100%	100%
ECO102870	STY104533	95%	100%	100%
ECO102870	SAU801342	45%	98.6%	98.5%
ECO102870	SEP202003	45%	98.6%	98.5%
ECO102870	SHA100154	54%	40.7%	96.4%
ECO102870	SMU101576	49%	98.6%	98.9%
ECO102870	SPN401839	49%	98.6%	98.9%
ECO102870	SPY201289	51%	98.6%	91.4%
ECO102870	UUR100593	33%	97.7%	98.3%
ECO102870	VCH103347	78%	99.7%	97.4%
ECO102870	VCH100468	78%	100%	95.7%
ECO102870	YPS000208	86%	100%	99.8%
ECO102872	ABA105768	24%	82.0%	84.0%
ECO102872	BAN107335	28%	66.7%	79.1%
ECO102872	BAN106751	36%	88.2%	92.8%
ECO102872	BPT102032	36%	86.9%	91.0%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102872	BCE104852	49%	97.1%	86.7%
ECO102872	BFU102304	50%	88.6%	84.8%
ECO102872	BMA100624	42%	91.5%	90.2%
ECO102872	CAC101176	27%	81.4%	93.3%
ECO102872	CDF103020	27%	95.1%	99.3%
ECO102872	EBC103712	97%	88.6%	100%
ECO102872	ECO102872	100%	100%	100%
ECO102872	KPN303054	98%	100%	100%
ECO102872	LPN100482	25%	81.7%	81.6%
ECO102872	MCA103142	28%	57.2%	65.2%
ECO102872	NGO101601	73%	99.0%	98.7%
ECO102872	NME201862	73%	99.0%	98.7%
ECO102872	PMU101381	71%	99.3%	99.3%
ECO102872	PRT101181	81%	98.7%	98.7%
ECO102872	PAE201420	40%	91.5%	90.6%
ECO102872	PPU106459	55%	88.2%	84.4%
ECO102872	SPA102479	94%	72.5%	100%
ECO102872	STY104539	98%	100%	100%
ECO102872	STM102066	23%	82.4%	79.9%
ECO102872	SAU802164	27%	63.1%	71.5%
ECO102872	SEP200453	22%	80.1%	78.5%
ECO102872	SHA102088	22%	80.1%	78.5%
ECO102872	SPY201597	24%	83.3%	80.2%
ECO102872	VCH103534	60%	99.3%	98.7%
ECO102878	CPN200131	30%	20.5%	18.7%
ECO102878	CTR100845	31%	18.1%	19.5%
ECO102878	EBC106015	95%	100%	100%
ECO102878	EFM201679	42%	43.8%	90.9%
ECO102878	ECO102878	100%	100%	100%
ECO102878	KPN201723	92%	97.6%	100%
ECO102878	MAV101739	36%	91.8%	94.4%
ECO102878	MBV105298	31%	87.3%	94.4%
ECO102878	MTU203288	32%	91.8%	84.5%
ECO102878	PSY104242	33%	87.3%	96.9%
ECO102878	SPA102475	97%	97.6%	100%
ECO102878	STY104560	97%	100%	100%
ECO102878	STM100573	97%	100%	100%
ECO102878	SEP202196	39%	94.8%	97.8%
ECO102880	BAN108721	29%	27.7%	28.1%
ECO102880	BAN109561	30%	46.8%	45.1%
ECO102880	BPT100275	46%	94.5%	94.2%
ECO102880	EBC106749	85%	100%	100%
ECO102880	ECO102880	100%	100%	100%
ECO102880	KPN302103	85%	100%	100%
ECO102880	MBV105139	32%	26.4%	22.8%
ECO102880	MTU202934	32%	26.4%	22.8%
ECO102880	PRT101790	54%	87.2%	65.5%
ECO102880	PAE202747	50%	94.9%	91.1%
ECO102880	PPU106584	56%	82.1%	68.4%
ECO102880	PSY102563	52%	95.7%	95.3%
ECO102880	SPA102539	83%	100%	100%
ECO102880	STY104564	87%	100%	100%
ECO102880	STM100577	87%	100%	100%
ECO102880	VCH100465	61%	97.9%	98.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102880	YPS000219	79%	91.1%	91.1%
ECO102885	ABA100701	46%	95.0%	88.4%
ECO102885	BMA106277	36%	81.8%	76.6%
ECO102885	CAC102187	43%	92.1%	90.3%
ECO102885	CBO103281	43%	93.8%	89.9%
ECO102885	CDF101037	39%	95.6%	91.7%
ECO102885	EBC103404	72%	95.6%	100%
ECO102885	ECO102885	100%	100%	100%
ECO102885	KPN302118	71%	100%	100%
ECO102885	LPN103418	45%	92.4%	92.4%
ECO102885	MCA102746	46%	95.3%	95.1%
ECO102885	MBV104192	30%	48.7%	43.2%
ECO102885	MTU203605	30%	48.7%	47.4%
ECO102885	NGO101966	47%	95.0%	94.5%
ECO102885	NME200207	48%	95.0%	94.5%
ECO102885	PRT105772	51%	95.6%	97.6%
ECO102885	PAE200394	46%	95.0%	95.1%
ECO102885	PPU102683	46%	92.1%	95.5%
ECO102885	PSY103723	47%	95.0%	95.1%
ECO102885	SPA102545	78%	100%	100%
ECO102885	STY104579	78%	95.6%	100%
ECO102885	VCH100457	49%	95.0%	94.8%
ECO102885	YPS000233	56%	93.8%	90.5%
ECO102920	ECO102918	34%	93.9%	87.3%
ECO102920	ECO102919	36%	92.6%	91.6%
ECO102920	ECO102920	100%	100%	100%
ECO102921	ABA103557	42%	98.6%	89.0%
ECO102921	BAN112240	37%	28.5%	5.3%
ECO102921	BAN111707	34%	89.6%	86.5%
ECO102921	BFR102762	30%	17.8%	21.1%
ECO102921	BPT100941	54%	99.8%	99.6%
ECO102921	BCE106620	41%	97.2%	89.2%
ECO102921	BFU103359	50%	47.9%	59.9%
ECO102921	BMA109810	41%	96.2%	88.6%
ECO102921	CJU101119	25%	24.4%	86.0%
ECO102921	CPN200065	33%	93.2%	34.0%
ECO102921	CTR200064	37%	42.7%	24.4%
ECO102921	CAC101744	33%	96.6%	95.8%
ECO102921	CDP101483	36%	22.8%	38.6%
ECO102921	EBC103757	79%	100%	100%
ECO102921	EFA200337	30%	94.0%	94.4%
ECO102921	EFM100784	27%	22.6%	43.0%
ECO102921	ECO103416	80%	100%	100%
ECO102921	ECO102921	100%	100%	100%
ECO102921	HIN101571	30%	43.3%	35%
ECO102921	HPY101470	27%	28.5%	72.8%
ECO102921	KPN304763	80%	61.1%	100%
ECO102921	LPN103150	31%	32.1%	96.7%
ECO102921	LMO102163	35%	97.4%	97.0%
ECO102921	MCA100847	26%	31.3%	89.3%
ECO102921	MAV103930	28%	96.2%	78.0%
ECO102921	MBV104571	33%	94.2%	74.8%
ECO102921	MLP101343	29%	96.2%	77.8%
ECO102921	MTU200542	33%	94.2%	74.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102921	NGO100709	32%	46.7%	17.7%
ECO102921	NME201949	32%	39.9%	24.0%
ECO102921	PMU100249	32%	23.0%	32.4%
ECO102921	PRT103145	68%	100%	100%
ECO102921	PAE204290	52%	100%	100%
ECO102921	PPU103316	53%	100%	99.8%
ECO102921	PSY103947	52%	99.2%	99.0%
ECO102921	SPA101797	80%	100%	100%
ECO102921	STY100867	81%	100%	100%
ECO102921	STM103553	81%	100%	100%
ECO102921	SAU800664	35%	97.0%	97.9%
ECO102921	SEP200699	34%	96.2%	97.3%
ECO102921	SHA102241	33%	97.0%	97.9%
ECO102921	VCH102406	30%	97.6%	37.9%
ECO102921	YPS002478	70%	100%	100%
ECO102922	CAC100107	29%	20.4%	58.1%
ECO102922	EBC103186	82%	99.8%	99.5%
ECO102922	ECO102922	100%	100%	100%
ECO102922	KPN308954	84%	99.8%	99.5%
ECO102922	PRT100650	70%	98.2%	97.3%
ECO102922	SPA103864	86%	98.9%	98.4%
ECO102922	STY100405	90%	99.8%	99.8%
ECO102922	SHA102036	40%	9.9%	9.9%
ECO102922	VCH101551	29%	13.1%	56.6%
ECO102928	CBO100990	28%	100%	99.8%
ECO102928	ECO102928	100%	100%	100%
ECO102928	PRT101527	72%	100%	100%
ECO102928	SPA103628	90%	90.1%	98.8%
ECO102928	STY100430	93%	100%	100%
ECO102929	ECO102929	100%	100%	100%
ECO102929	LMO101092	25%	38.3%	97.1%
ECO102929	PRT105241	71%	95.9%	95.4%
ECO102929	SPA103626	93%	91.6%	100%
ECO102929	STY100431	96%	100%	100%
ECO102935	BFR12116	56%	94.5%	97.3%
ECO102935	BCE112705	66%	99.4%	98.6%
ECO102935	BFU106872	66%	99.4%	98.6%
ECO102935	BMA107444	67%	99.4%	92.7%
ECO102935	CDP100172	56%	97.4%	94.2%
ECO102935	EBC103723	87%	100%	100%
ECO102935	EFM201542	56%	95.1%	99.1%
ECO102935	ECO102935	100%	100%	100%
ECO102935	KPN301761	59%	96.2%	99.7%
ECO102935	PSY103084	66%	99.4%	99.1%
ECO102935	SPA100617	70%	49.1%	89.5%
ECO102935	STY101139	60%	95.1%	97.9%
ECO102935	STM100906	60%	95.1%	97.9%
ECO102935	SMU100710	25%	77.7%	91.9%
ECO102935	YPS000578	55%	96.2%	100%
ECO102949	ABA105590	62%	98.5%	55.0%
ECO102949	BFR103517	42%	80.9%	54.7%
ECO102949	BFU107731	35%	10.2%	8.2%
ECO102949	CBO100864	42%	85.0%	53.7%
ECO102949	CDF100913	39%	96.1%	61.2%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102949	EBC103718	92%	79.4%	96.5%
ECO102949	ECO102949	100%	100%	100%
ECO102949	KPN306892	92%	98.8%	54.3%
ECO102949	PAE204923	64%	96.9%	56.1%
ECO102949	PPU107577	62%	99.3%	57.6%
ECO102949	PSY101911	64%	98.8%	100%
ECO102949	SPA105251	92%	94.4%	54.8%
ECO102949	STY100457	93%	96.1%	54.9%
ECO102949	VCH101683	64%	99.8%	52.3%
ECO102950	CPN200382	36%	17.8%	13.9%
ECO102950	EBC102780	93%	98.5%	100%
ECO102950	ECO102950	100%	100%	100%
ECO102950	NME300608	27%	21.2%	89.6%
ECO102950	PSY108481	65%	96.6%	100%
ECO102966	ABA103592	36%	94.2%	94.8%
ECO102966	BAN108519	21%	72%	24.7%
ECO102966	BPT102066	40%	94.5%	87.7%
ECO102966	BCE110576	31%	76.4%	80.5%
ECO102966	BFU110089	27%	76.4%	76.4%
ECO102966	BMA100363	29%	66.5%	52.5%
ECO102966	CPN200952	28%	54.5%	54.9%
ECO102966	CTR200130	28%	57.1%	58.6%
ECO102966	EBC103928	85%	100%	100%
ECO102966	EFM201047	24%	74.9%	76.0%
ECO102966	ECO102966	100%	100%	100%
ECO102966	HIN100379	53%	94.9%	95.3%
ECO102966	KPN309045	83%	100%	100%
ECO102966	MCA103602	31%	90.2%	92.8%
ECO102966	MAV105050	21%	72%	68.5%
ECO102966	MBV103054	33%	61.1%	60.9%
ECO102966	MLP101322	30%	75.6%	66.9%
ECO102966	MTU200799	31%	75.6%	67.0%
ECO102966	PMU101019	54%	94.5%	94.9%
ECO102966	PRT100350	62%	100%	100%
ECO102966	PAE204964	43%	96.7%	97.1%
ECO102966	PPU104681	42%	94.9%	96.6%
ECO102966	PSY101033	45%	97.8%	94.7%
ECO102966	SPA103721	91%	100%	100%
ECO102966	STY100734	92%	100%	100%
ECO102966	SHA102882	31%	20%	20.6%
ECO102966	VCH102398	53%	96%	97.1%
ECO102966	YPS001992	70%	100%	100%
ECO102967	EBC103926	95%	99.3%	99.3%
ECO102967	ECO102967	100%	100%	100%
ECO102967	KPN309071	92%	99.3%	99.3%
ECO102967	PAE204965	37%	98.6%	93.4%
ECO102967	PPU104679	35%	94.3%	91.9%
ECO102967	PSY101043	36%	94.3%	84.0%
ECO102967	SPA103719	95%	100%	100%
ECO102967	STY100736	95%	100%	100%
ECO102967	VCH102399	50%	98.6%	92.6%
ECO102967	YPS001991	79%	98.6%	97.9%
ECO102986	BPT100204	51%	62.7%	95.2%
ECO102986	BCE105324	49%	63.3%	95.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102986	BFU103929	53%	68.8%	98.2%
ECO102986	BMA102492	48%	64.2%	93.0%
ECO102986	CJU101075	42%	97.9%	98.5%
ECO102986	EBC103920	94%	99.8%	100%
ECO102986	ECO102986	100%	100%	100%
ECO102986	HIN101495	71%	97.7%	97.9%
ECO102986	HPY100845	40%	96.6%	98.5%
ECO102986	KPN308271	92%	99.4%	99.4%
ECO102986	LMO101198	33%	26.6%	95.3%
ECO102986	MAV104245	46%	26.6%	93.4%
ECO102986	MLP100531	25%	52.8%	76.5%
ECO102986	NGO100932	50%	64.6%	95.9%
ECO102986	NME200956	50%	64.8%	95.4%
ECO102986	PMU100884	69%	98.3%	98.5%
ECO102986	PRT102176	82%	99.2%	99.8%
ECO102986	PAE204991	57%	99.2%	99.6%
ECO102986	PPU104725	56%	98.5%	100%
ECO102986	PSY101063	58%	99.0%	99.4%
ECO102986	SPA102480	93%	97.5%	100%
ECO102986	STY100790	93%	99.8%	99.8%
ECO102986	SAU800641	30%	27.5%	94.7%
ECO102986	SEP200670	31%	27.5%	94.7%
ECO102986	YPS001982	86%	99.6%	99.8%
ECO102990	ABA100117	56%	90.5%	98.2%
ECO102990	BFR104611	31%	74.0%	65.5%
ECO102990	BPT100463	45%	82.0%	81.6%
ECO102990	BCE100277	53%	97.3%	98.3%
ECO102990	BFU103175	54%	97.1%	98.8%
ECO102990	BMA101052	53%	97.3%	98.3%
ECO102990	CJU100728	35%	50%	54.0%
ECO102990	CAC103726	23%	74.0%	68.8%
ECO102990	CDP101606	30%	75.2%	64.6%
ECO102990	EBC101436	87%	97.6%	100%
ECO102990	ECO102990	100%	100%	100%
ECO102990	HIN101573	58%	98.1%	98.6%
ECO102990	KPN304100	86%	100%	99.8%
ECO102990	LPN102504	55%	98.1%	99.0%
ECO102990	MCA100227	40%	90.5%	89.5%
ECO102990	MAV103429	30%	75.2%	66.7%
ECO102990	MBV106184	30%	72.8%	64.8%
ECO102990	MLP101592	28%	88.8%	84.8%
ECO102990	MTU203852	30%	72.8%	64.8%
ECO102990	NGO100210	54%	97.3%	97.8%
ECO102990	NME201288	54%	97.3%	96.2%
ECO102990	PMU100247	59%	99.5%	98.8%
ECO102990	PRT100516	68%	98.5%	99.8%
ECO102990	PAE200583	60%	98.8%	99.3%
ECO102990	PPU100635	49%	98.1%	99.5%
ECO102990	PSY103399	56%	98.1%	98.8%
ECO102990	SPA101468	85%	98.3%	100%
ECO102990	STY100798	89%	99.8%	99.5%
ECO102990	STM101254	90%	99.8%	99.5%
ECO102990	VCH102410	61%	97.1%	99.3%
ECO102990	YPS001978	72%	98.3%	98.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO102999	BAN101878	64%	54.9%	86.7%
ECO102999	BAN111500	60%	70.4%	87.7%
ECO102999	BFR101607	39%	74.6%	67.9%
ECO102999	BPT103142	60%	100%	100%
ECO102999	BBU100255	37%	97.2%	100%
ECO102999	BCE106500	61%	100%	100%
ECO102999	BFU102600	68%	84.5%	85.7%
ECO102999	BMA102838	68%	84.5%	85.7%
ECO102999	CJU100338	44%	98.6%	100%
ECO102999	CPN200733	40%	83.1%	100%
ECO102999	CTR200610	42%	78.9%	94.8%
ECO102999	CAC101256	58%	81.7%	100%
ECO102999	CBO102486	55%	81.7%	100%
ECO102999	CDF100846	50%	83.1%	100%
ECO102999	EBC104303	100%	90.1%	98.5%
ECO102999	EFA200381	62%	70.4%	86.2%
ECO102999	EFM103017	55%	40.8%	90.6%
ECO102999	ECO102999	100%	100%	100%
ECO102999	HIN100510	83%	100%	100%
ECO102999	HPY100555	44%	98.6%	100%
ECO102999	KPN204459	100%	100%	100%
ECO102999	LPN101208	68%	63.4%	78.9%
ECO102999	LMO101512	56%	70.4%	87.7%
ECO102999	MCA101455	67%	100%	100%
ECO102999	NGO103576	68%	63.4%	81.8%
ECO102999	NME200467	70%	84.5%	85.7%
ECO102999	PMU101239	83%	100%	100%
ECO102999	PRT103336	95%	100%	100%
ECO102999	PAE200578	81%	100%	100%
ECO102999	PSY102551	80%	100%	100%
ECO102999	SPA100115	100%	100%	100%
ECO102999	STY100808	100%	100%	100%
ECO102999	STM101264	100%	100%	100%
ECO102999	SAU801575	56%	74.6%	91.4%
ECO102999	SEP203226	56%	74.6%	91.4%
ECO102999	SHA101643	56%	74.6%	91.4%
ECO102999	SMU102404	64%	70.4%	75.8%
ECO102999	SPN401270	62%	70.4%	75.8%
ECO102999	SPY200574	64%	70.4%	86.2%
ECO102999	TPA100750	40%	100%	100%
ECO102999	VCH100511	88%	100%	100%
ECO102999	YPS001963	100%	100%	100%
ECO103000	ABA100135	40%	71.8%	74.4%
ECO103000	BAN108415	46%	10.8%	100%
ECO103000	BAN103625	38%	66.8%	64.9%
ECO103000	BFR100350	32%	75.6%	66.4%
ECO103000	BPT103140	46%	75.7%	65.1%
ECO103000	BBU100709	29%	70.9%	78.8%
ECO103000	BCE103536	49%	40.4%	94.3%
ECO103000	BFU102598	46%	77.6%	75.7%
ECO103000	BMA106679	41%	95.4%	91.7%
ECO103000	CJU101544	33%	64.2%	59.8%
ECO103000	CPN200902	31%	75.0%	72.6%
ECO103000	CTR200170	33%	64.4%	61.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103000	CAC100870	37%	72.5%	69.1%
ECO103000	CBO101827	39%	61.8%	59.2%
ECO103000	CDF100203	34%	70.9%	66.9%
ECO103000	CDP100521	31%	85.0%	77.8%
ECO103000	EBC100341	90%	66.6%	99.7%
ECO103000	BFA201925	40%	61.8%	58.2%
ECO103000	EFM102089	36%	24.3%	90%
ECO103000	ECO103000	100%	100%	100%
ECO103000	HIN100511	56%	98.3%	97.0%
ECO103000	HPY100011	35%	64.7%	64.9%
ECO103000	KPN301044	90%	100%	100%
ECO103000	LPN100532	43%	99.3%	98.4%
ECO103000	LMO101045	40%	65.2%	61.3%
ECO103000	MCA102484	41%	3.3%	14.0%
ECO103000	MAV100979	33%	73.1%	88.5%
ECO103000	MBV105699	32%	85.7%	78.2%
ECO103000	MLP100501	31%	85.7%	78.3%
ECO103000	MTU202309	32%	85.7%	78.2%
ECO103000	MGE100254	27%	54.0%	53.7%
ECO103000	MPN100483	28%	59.6%	57.6%
ECO103000	NGO100326	44%	88.6%	88.6%
ECO103000	NME201595	45%	88.6%	88.6%
ECO103000	PMU101240	57%	100%	99.3%
ECO103000	PRT100374	73%	79.7%	99.4%
ECO103000	PAE200576	55%	72.5%	64.0%
ECO103000	PPU100647	54%	98.8%	97.7%
ECO103000	PSY103379	54%	98.3%	97.2%
ECO103000	SPA101806	85%	98.5%	99.7%
ECO103000	STY100820	86%	100%	100%
ECO103000	STM101266	86%	100%	100%
ECO103000	SAU801562	37%	61.1%	58.7%
ECO103000	SEP200998	35%	65.9%	63.9%
ECO103000	SHA101656	36%	61.1%	62.0%
ECO103000	SMU100153	27%	71.4%	95.5%
ECO103000	SPN400978	31%	75.7%	75.0%
ECO103000	SPY200576	32%	73.1%	70.7%
ECO103000	TPA100488	28%	80.0%	79.0%
ECO103000	UUR100499	27%	63.3%	58.5%
ECO103000	YPS001962	76%	100%	99.8%
ECO103001	ABA104769	62%	99.5%	99.0%
ECO103001	BAN102742	65%	39.0%	96.0%
ECO103001	BAN100470	62%	34.1%	9.4%
ECO103001	BFR11674	41%	43.7%	92.3%
ECO103001	BPT103127	55%	99.0%	81.9%
ECO103001	BBU100711	30%	100%	99.2%
ECO103001	BCE113968	66%	6.9%	23.5%
ECO103001	BCE107290	55%	98.7%	90.5%
ECO103001	BFU102597	55%	99.0%	90.6%
ECO103001	BMA103953	55%	99.0%	90.6%
ECO103001	CJU100929	36%	92.7%	91.3%
ECO103001	CPN201097	61%	44.5%	46.2%
ECO103001	CTR200894	37%	99.7%	94.4%
ECO103001	CAC102729	63%	34.1%	9.3%
ECO103001	CBO103068	64%	34.1%	9.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103001	CDF103183	66%	38.8%	1.5%
ECO103001	CDP100305	54%	34.9%	0.6%
ECO103001	EBC101192	97%	15.8%	16.1%
ECO103001	EFA201924	63%	34.1%	9.5%
ECO103001	EFM100355	61%	34.1%	10.5%
ECO103001	ECO103001	100%	100%	100%
ECO103001	HIN100512	67%	100%	100%
ECO103001	HPY100086	38%	85.2%	77.2%
ECO103001	KPN301045	95%	100%	100%
ECO103001	LPN102321	62%	99.7%	98.2%
ECO103001	LMO101276	61%	34.1%	9.4%
ECO103001	MCA100749	60%	99.0%	97.4%
ECO103001	MAV103013	41%	6.7%	26.5%
ECO103001	MBV101368	60%	35.6%	2.3%
ECO103001	MLP100627	60%	39.8%	5.2%
ECO103001	MTU202666	60%	35.6%	2.3%
ECO103001	MGE100253	37%	65.6%	96.2%
ECO103001	MPN100484	44%	44.7%	62.7%
ECO103001	NGO100336	52%	99.5%	96.1%
ECO103001	NME201596	53%	99.5%	96.1%
ECO103001	PMU101241	72%	100%	100%
ECO103001	PRT100575	87%	100%	100%
ECO103001	PAE200575	66%	99.2%	98.9%
ECO103001	PPU100648	63%	99.0%	99.3%
ECO103001	PSY101423	66%	99.2%	98.9%
ECO103001	SPA101807	79%	98.4%	100%
ECO103001	STY100822	97%	100%	93.2%
ECO103001	STM101268	97%	100%	93.2%
ECO103001	SAU801561	61%	34.1%	9.5%
ECO103001	SEP200997	55%	27.1%	19.8%
ECO103001	SHA100172	61%	34.1%	10.6%
ECO103001	SMU100154	65%	35.6%	7.0%
ECO103001	SPN400979	64%	35.6%	7.0%
ECO103001	SPY200577	65%	35.6%	7.0%
ECO103001	TPA100489	35%	99.8%	99.7%
ECO103001	UUR100351	45%	44.2%	62.1%
ECO103001	VCH100509	77%	100%	100%
ECO103001	YPS001961	91%	100%	100%
ECO103020	BCE109431	28%	62.6%	90.6%
ECO103020	BFU102845	30%	62.6%	58.0%
ECO103020	BMA103254	28%	74.0%	70.3%
ECO103020	CAC100416	44%	96.7%	98.2%
ECO103020	CDF101374	43%	97.3%	98.8%
ECO103020	EBC102580	84%	97.6%	98.2%
ECO103020	EFA202154	38%	97.0%	99.7%
ECO103020	EFM200659	38%	97.3%	98.8%
ECO103020	ECO103020	100%	100%	100%
ECO103020	KPN303709	80%	98.2%	99.7%
ECO103020	LPN100369	24%	74.9%	71.1%
ECO103020	LMO100582	40%	96.7%	99.7%
ECO103020	SPA108751	80%	97.0%	100%
ECO103020	STY100856	83%	97.6%	94.8%
ECO103020	STM101299	83%	97.6%	98.2%
ECO103020	SMU100226	32%	97.0%	99.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103020	SPN401334	34%	97.0%	91.8%
ECO103020	SPY200315	31%	87.1%	91.8%
ECO103020	YPS001888	73%	97.3%	98.2%
ECO103021	ABA105571	53%	99.4%	99.4%
ECO103021	CAC102504	28%	73.2%	82.5%
ECO103021	CDP100423	35%	89.7%	90.7%
ECO103021	EBC102581	85%	99.4%	99.1%
ECO103021	EFM103205	22%	44.9%	42.5%
ECO103021	ECO103021	100%	100%	100%
ECO103021	HPY200518	42%	13.7%	19.4%
ECO103021	KPN303711	87%	99.4%	98.8%
ECO103021	LPN102662	52%	96.6%	97.8%
ECO103021	MCA101267	21%	61.1%	53.1%
ECO103021	MAV100595	27%	28.3%	27.3%
ECO103021	MBV102718	32%	94.4%	79.1%
ECO103021	MLP100145	22%	34.0%	31.2%
ECO103021	MTU202686	32%	94.4%	79.1%
ECO103021	NGO102022	55%	92.8%	92.9%
ECO103021	NME200243	55%	92.8%	92.9%
ECO103021	PRT101901	34%	90.0%	92.4%
ECO103021	PAE202547	46%	91.0%	83.6%
ECO103021	PPU111253	46%	93.5%	89.0%
ECO103021	PSY105168	34%	93.5%	92.7%
ECO103021	SPA108753	85%	99.1%	98.8%
ECO103021	STY100858	86%	99.1%	98.8%
ECO103021	STM101302	87%	99.1%	98.8%
ECO103021	SPN401382	25%	35.5%	20%
ECO103021	VCH103270	40%	91.0%	91.2%
ECO103021	YPS002741	33%	94.4%	94.2%
ECO103024	BMA106155	28%	94.9%	97.3%
ECO103024	CJU100448	35%	76.4%	96.9%
ECO103024	CAC101727	58%	99.4%	99.2%
ECO103024	CDF101611	34%	76.4%	96.9%
ECO103024	EBC104084	85%	79.2%	100%
ECO103024	EFM200772	55%	99.4%	98.4%
ECO103024	ECO103024	100%	100%	100%
ECO103024	KPN306321	87%	100%	100%
ECO103024	YPS001858	79%	99.4%	99.2%
ECO103029	EBC104070	63%	100%	100%
ECO103029	ECO103029	100%	100%	100%
ECO103029	KPN301952	60%	100%	92.0%
ECO103029	SPA101871	68%	97.6%	97.6%
ECO103029	STY100864	68%	97.6%	97.6%
ECO103029	STM101311	68%	97.6%	97.6%
ECO103029	YPS001848	39%	87.4%	84.5%
ECO103030	CJU101325	29%	83.5%	94.8%
ECO103030	CPN200721	29%	42.5%	12.0%
ECO103030	EBC104087	70%	100%	100%
ECO103030	ECO103030	100%	100%	100%
ECO103030	KPN301954	68%	100%	100%
ECO103030	PRT103868	42%	89.0%	87.7%
ECO103030	PAE200541	36%	88.2%	82.7%
ECO103030	PPU102582	41%	74.8%	72.3%
ECO103030	PSY106182	40%	88.2%	81.6%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103030	SPA101872	84%	96.1%	100%
ECO103030	STY100866	84%	96.1%	100%
ECO103030	STM101314	84%	96.1%	100%
ECO103030	YPS001846	42%	96.9%	97.6%
ECO103047	EBC104067	90%	99.3%	97.0%
ECO103047	ECO103047	100%	100%	100%
ECO103047	KPN302949	87%	99.3%	97.0%
ECO103047	SPA101135	92%	98.7%	97.0%
ECO103047	STY100910	93%	99.3%	97.0%
ECO103049	CDF100099	22%	23.5%	36.5%
ECO103049	EBC104077	88%	100%	100%
ECO103049	ECO103049	100%	100%	100%
ECO103049	KPN302952	90%	100%	100%
ECO103049	SPA102422	94%	100%	100%
ECO103054	CAC103652	22%	48.9%	45.8%
ECO103054	CBO100821	23%	56.2%	28.7%
ECO103054	ECO103054	100%	100%	100%
ECO103054	LMO101991	21%	22.3%	55.8%
ECO103054	SEP100701	22%	44.3%	46.5%
ECO103055	ECO103055	100%	100%	100%
ECO103059	ECO103059	100%	100%	100%
ECO103059	KPN301970	86%	100%	100%
ECO103059	MAV101420	22%	91.7%	85.0%
ECO103059	PAE202208	31%	93.0%	90.9%
ECO103059	SAU802512	26%	96.4%	96.7%
ECO103059	SEP201038	27%	96.4%	96.9%
ECO103059	SHA101788	27%	96.6%	96.7%
ECO103064	BCE109317	51%	91.8%	100%
ECO103064	BMA108844	47%	99.3%	100%
ECO103064	CDF103015	23%	73.7%	73.6%
ECO103064	EBC100019	86%	8.9%	100%
ECO103064	EBC100022	86%	8.9%	100%
ECO103064	EBC103089	90%	9.4%	97.6%
ECO103064	EBC104063	84%	68.5%	100%
ECO103064	ECO103064	100%	100%	100%
ECO103064	PRT102737	62%	99.3%	99.3%
ECO103064	YPS002910	63%	99.3%	97.9%
ECO103069	ABA100914	33%	98.3%	94.5%
ECO103069	BFR11934	34%	99.7%	97.9%
ECO103069	BPT102002	33%	99.7%	93.2%
ECO103069	BFU111409	34%	99.7%	93.0%
ECO103069	CAC102554	53%	98.3%	99.3%
ECO103069	CBO101667	56%	97.2%	97.6%
ECO103069	CDF100408	46%	99.3%	100%
ECO103069	CDF101639	47%	99.0%	97.6%
ECO103069	EBC103878	91%	99.3%	97.9%
ECO103069	EFA201312	37%	99.0%	99.7%
ECO103069	EFM201347	38%	99.0%	99.0%
ECO103069	ECO103069	100%	100%	100%
ECO103069	HPY100173	37%	98.6%	99.7%
ECO103069	KPN100140	40%	40.9%	93.7%
ECO103069	LMO100774	38%	97.9%	98.6%
ECO103069	MCA100353	31%	99.7%	95.7%
ECO103069	MAV102852	34%	31.8%	24.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103069	MAV103638	34%	31.8%	31.4%
ECO103069	MPN100129	34%	98.3%	99.3%
ECO103069	PAE200554	34%	99.7%	93.2%
ECO103069	PPU104672	33%	99.7%	94.6%
ECO103069	SMU101408	38%	99.0%	99.7%
ECO103069	SPN400530	38%	99.0%	99.7%
ECO103069	SPY201455	37%	99.0%	99.7%
ECO103069	TPA100654	36%	99.0%	97.9%
ECO103069	UUR100603	35%	98.6%	98.6%
ECO103069	YPS000084	59%	99.0%	99.6%
ECO103074	ECO103074	100%	100%	100%
ECO103075	EBC102522	42%	96.5%	85.8%
ECO103075	ECO103075	100%	100%	100%
ECO103075	KPN306854	41%	96.5%	97.7%
ECO103075	PAE202130	34%	96.1%	97.5%
ECO103076	EBC102524	47%	96.4%	96.0%
ECO103076	ECO103076	100%	100%	100%
ECO103076	KPN203709	39%	97.3%	97.8%
ECO103076	SPA103706	40%	93.2%	99.9%
ECO103094	BAN102211	37%	73.4%	99.6%
ECO103094	BAN103847	45%	95.5%	96.2%
ECO103094	BFR10255	33%	94.7%	93.6%
ECO103094	CAC103020	36%	85.4%	97.5%
ECO103094	CBO102910	35%	83.0%	99.0%
ECO103094	CDF103369	38%	85.6%	98.1%
ECO103094	CDP101075	52%	85.3%	97.0%
ECO103094	EBC103897	91%	96.9%	99.7%
ECO103094	EFA200476	43%	71.1%	88.7%
ECO103094	EFM201829	41%	73.5%	93.9%
ECO103094	ECO103094	100%	100%	100%
ECO103094	HIN100222	62%	93.8%	98.5%
ECO103094	KPN300133	97%	22.8%	100%
ECO103094	KPN301427	94%	97.4%	100%
ECO103094	LPN103085	43%	86.4%	99.2%
ECO103094	LMO100391	43%	72.0%	87.7%
ECO103094	MAV100272	48%	88.9%	97.7%
ECO103094	MBV105490	46%	89.5%	97.9%
ECO103094	MLP100490	42%	56.7%	69.9%
ECO103094	MTU201236	46%	89.5%	97.9%
ECO103094	MGE100435	30%	58.0%	85.1%
ECO103094	MPN100219	33%	54.3%	79.6%
ECO103094	PMU101112	61%	94.4%	99.5%
ECO103094	PRT102432	79%	95.7%	99.0%
ECO103094	PAE202838	48%	86.4%	97.2%
ECO103094	PPU101891	46%	85.3%	96.0%
ECO103094	PSY103180	47%	85.3%	95.8%
ECO103094	SPA101061	91%	72.3%	100%
ECO103094	STY100977	97%	100%	100%
ECO103094	SAU802081	39%	73.2%	92.5%
ECO103094	SEP201342	39%	73.8%	92.5%
ECO103094	SHA100953	40%	73.8%	96.6%
ECO103094	SMU100751	42%	74.8%	92.6%
ECO103094	SPN401439	40%	73.5%	95.2%
ECO103094	SPY201084	38%	95.7%	93.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103094	TPA100762	44%	56.2%	55.9%
ECO103094	UUR100589	30%	58.8%	86.2%
ECO103094	VCH103524	45%	96.7%	93.2%
ECO103094	YPS001037	80%	96.6%	99.2%
ECO103097	ABA104153	69%	100%	100%
ECO103097	BAN112139	56%	100%	100%
ECO103097	BAN112261	56%	100%	100%
ECO103097	BFR101219	58%	34.8%	96.9%
ECO103097	BPT102559	65%	100%	100%
ECO103097	BBU100803	55%	89.9%	90.9%
ECO103097	BCE114521	66%	100%	100%
ECO103097	BFU106341	65%	98.9%	97.8%
ECO103097	BMA104593	67%	100%	100%
ECO103097	CJU100816	54%	98.9%	97.8%
ECO103097	CPN200838	46%	100%	100%
ECO103097	CTR200226	46%	100%	100%
ECO103097	CAC101338	53%	89.9%	92.0%
ECO103097	CBO102464	58%	89.9%	76.9%
ECO103097	CDF100875	62%	91.0%	95.3%
ECO103097	CDP100449	57%	100%	100%
ECO103097	EBC103888	93%	100%	100%
ECO103097	EFA202022	52%	100%	100%
ECO103097	EFM202414	56%	100%	100%
ECO103097	ECO103097	100%	100%	100%
ECO103097	HIN101437	80%	100%	100%
ECO103097	HIN101294	80%	100%	100%
ECO103097	HPY101023	51%	98.9%	97.8%
ECO103097	KPN301430	92%	100%	100%
ECO103097	LPN100705	59%	69.7%	95.4%
ECO103097	LMO101938	57%	100%	100%
ECO103097	MCA100389	65%	100%	100%
ECO103097	MAV100300	53%	100%	100%
ECO103097	MBV101245	52%	100%	100%
ECO103097	MLP100514	56%	100%	100%
ECO103097	MTU202747	52%	100%	100%
ECO103097	MGE100434	47%	77.5%	80.2%
ECO103097	MPN100220	50%	76.4%	79.1%
ECO103097	NGO100722	60%	100%	100%
ECO103097	NME200754	60%	100%	100%
ECO103097	PMU100301	78%	100%	100%
ECO103097	PRT102435	88%	100%	100%
ECO103097	PAE204737	69%	100%	100%
ECO103097	PPU105055	70%	100%	100%
ECO103097	PSY104828	77%	70.8%	100%
ECO103097	SPA101259	95%	100%	100%
ECO103097	STY101470	97%	100%	100%
ECO103097	SAU801273	55%	100%	100%
ECO103097	SEP201566	53%	100%	100%
ECO103097	SHA100171	55%	100%	100%
ECO103097	SMU101327	52%	100%	100%
ECO103097	SPN401466	51%	100%	100%
ECO103097	SPY201503	52%	100%	100%
ECO103097	TPA100877	46%	100%	100%
ECO103097	UUR100204	48%	98.9%	98.9%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103097	VCH100634	74%	100%	100%
ECO103097	YPS006344	86%	100%	100%
ECO103098	ABA100464	48%	95.9%	96.0%
ECO103098	BAN111627	34%	81.8%	84.0%
ECO103098	BAN109916	38%	81.8%	83.4%
ECO103098	BFR100430	32%	68.2%	94.8%
ECO103098	BPT100250	46%	73.9%	98.0%
ECO103098	BBU100802	36%	66.2%	74.5%
ECO103098	BCE108686	46%	98.1%	96.8%
ECO103098	BFU101157	45%	98.1%	97.1%
ECO103098	BMA109950	45%	96.2%	98.0%
ECO103098	CJU101028	30%	66.9%	77.2%
ECO103098	CPN200432	41%	64.3%	86.0%
ECO103098	CTR200363	42%	67.2%	87.6%
ECO103098	CAC102432	36%	92.7%	97.2%
ECO103098	CBO100717	35%	90.8%	95.2%
ECO103098	CDF100873	35%	91.4%	94.7%
ECO103098	CDP100454	39%	66.9%	72.7%
ECO103098	EBC101433	90%	99.7%	100%
ECO103098	EFA200593	38%	83.1%	84.6%
ECO103098	EFM202633	36%	83.8%	78.4%
ECO103098	ECO103098	100%	100%	100%
ECO103098	HIN101257	60%	93.6%	92.3%
ECO103098	KPN301431	89%	100%	100%
ECO103098	LPN102640	43%	95.2%	95.7%
ECO103098	LMO102138	38%	83.8%	85.5%
ECO103098	MCA100805	37%	98.4%	98.7%
ECO103098	MAV100285	38%	66.6%	71.8%
ECO103098	MBV101244	42%	66.6%	71.8%
ECO103098	MLP100948	35%	92.0%	87.5%
ECO103098	MTU202755	42%	66.6%	71.8%
ECO103098	NGO101078	42%	93.0%	92.2%
ECO103098	NME201447	42%	93.0%	92.2%
ECO103098	PMU100756	57%	99.0%	99.3%
ECO103098	PRT102436	70%	98.7%	97.5%
ECO103098	PAE204738	50%	98.4%	99.3%
ECO103098	PPU107161	50%	98.4%	99.0%
ECO103098	PSY104829	49%	98.4%	99.0%
ECO103098	SPA101258	93%	100%	100%
ECO103098	STY101471	93%	100%	100%
ECO103098	SAU801271	37%	69.7%	74.4%
ECO103098	SEP201564	39%	67.8%	72.5%
ECO103098	SHA100169	34%	53.8%	73.0%
ECO103098	SMU100957	38%	74.5%	82.5%
ECO103098	SPN401091	38%	75.2%	84.9%
ECO103098	SPY200961	33%	95.5%	99.7%
ECO103098	TPA100879	29%	64.0%	61.2%
ECO103098	UUR100356	33%	65.6%	92.1%
ECO103098	VCH100633	66%	97.5%	98.1%
ECO103098	YPS001049	72%	99.0%	96.0%
ECO103100	ABA104593	51%	99.9%	100%
ECO103100	BAN113310	37%	72.8%	94.4%
ECO103100	BAN110029	49%	74.3%	96.4%
ECO103100	BFR11714	43%	91.1%	81.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103100	BPT100248	50%	89.3%	95.4%
ECO103100	BBU100800	45%	69.9%	71.3%
ECO103100	BCE101969	56%	79.8%	100%
ECO103100	BFU100867	49%	99.9%	100%
ECO103100	BMA109716	50%	99.3%	100%
ECO103100	CJU100125	38%	99.9%	100%
ECO103100	CPN200434	33%	98.7%	97.9%
ECO103100	CTR200365	33%	98.7%	97.9%
ECO103100	CAC100425	53%	64.9%	84.4%
ECO103100	CBO103185	48%	74.3%	94.1%
ECO103100	CDF102888	53%	65.2%	90.6%
ECO103100	CDP100479	50%	64.3%	96.5%
ECO103100	EBC101431	93%	19.4%	32.3%
ECO103100	EFA200621	44%	82.6%	95.1%
ECO103100	EFM201052	45%	80.3%	99.0%
ECO103100	ECO103100	100%	100%	100%
ECO103100	HIN101252	70%	94.2%	99.4%
ECO103100	HPY101031	37%	94.5%	90.9%
ECO103100	KPN301426	95%	93.7%	99.9%
ECO103100	LPN102343	71%	49.0%	100%
ECO103100	LMO100282	47%	83.0%	92.8%
ECO103100	MCA100802	50%	92.9%	98.3%
ECO103100	MAV100286	48%	64.7%	97.5%
ECO103100	MBV104310	50%	48.8%	99.8%
ECO103100	MLP100953	44%	71.5%	71.9%
ECO103100	MTU202801	45%	71.8%	72.9%
ECO103100	MGE100144	42%	63.6%	91.4%
ECO103100	MPN100676	41%	67.5%	97.6%
ECO103100	NGO101494	51%	89.2%	99.9%
ECO103100	NME201748	47%	99.9%	100%
ECO103100	PMU100759	71%	93.9%	98.8%
ECO103100	PRT102425	78%	99.9%	99.9%
ECO103100	PAE204740	57%	99.9%	100%
ECO103100	PPU108488	55%	99.9%	100%
ECO103100	PSY104832	68%	62.2%	100%
ECO103100	SPA101256	93%	52.0%	100%
ECO103100	STY101473	96%	100%	100%
ECO103100	SAU801269	48%	77.3%	99.6%
ECO103100	SEP201562	47%	81.3%	99.9%
ECO103100	SHA100514	47%	77.9%	93.8%
ECO103100	SMU100784	40%	88.9%	89.0%
ECO103100	SPN400481	39%	96.7%	96.2%
ECO103100	SPY201321	41%	90%	81.3%
ECO103100	TPA100881	47%	72.0%	80.8%
ECO103100	UUR100322	44%	64.5%	93.3%
ECO103100	VCH100631	71%	99.9%	99.9%
ECO103100	YPS001051	82%	100%	100%
ECO103101	ABA103925	53%	99.2%	99.8%
ECO103101	BAN104708	34%	67.7%	94.9%
ECO103101	BAN102313	37%	69.3%	92.9%
ECO103101	BFR10840	30%	67.9%	89.5%
ECO103101	BPT100246	51%	99.8%	100%
ECO103101	BBU100799	25%	96.6%	94.8%
ECO103101	BCE107342	49%	99.2%	99.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103101	BFU100866	50%	99.2%	99.8%
ECO103101	BMA107734	50%	99.2%	99.8%
ECO103101	CJU100425	30%	69.3%	94.2%
ECO103101	CPN200435	30%	95.2%	99.8%
ECO103101	CTR200366	31%	92.5%	98.6%
ECO103101	CAC100279	36%	71.3%	99.7%
ECO103101	CBO102108	36%	72.1%	77.7%
ECO103101	CDF102471	36%	77.4%	98.4%
ECO103101	CDP100481	33%	54.9%	83.4%
ECO103101	EBC101239	93%	99.2%	100%
ECO103101	EFA200624	35%	79.0%	100%
ECO103101	EFM201833	36%	77.4%	99.0%
ECO103101	ECO103101	100%	100%	100%
ECO103101	HIN101251	73%	99.8%	100%
ECO103101	HPY101493	26%	70.7%	95.2%
ECO103101	KPN300994	95%	100%	100%
ECO103101	LPN100039	60%	99.2%	99.8%
ECO103101	LMO100131	39%	68.3%	90.6%
ECO103101	MCA100801	47%	99.2%	99.8%
ECO103101	MAV103287	27%	39.4%	97.8%
ECO103101	MBV103220	34%	67.3%	91.9%
ECO103101	MLP100955	32%	70.7%	96.8%
ECO103101	MTU202803	34%	67.3%	91.9%
ECO103101	MGE100143	29%	71.3%	67.6%
ECO103101	MPN100677	28%	70.1%	65.4%
ECO103101	NGO101492	48%	99.0%	99.8%
ECO103101	NME201747	47%	99.8%	98.8%
ECO103101	PMU100760	74%	99.6%	100%
ECO103101	PRT102427	85%	100%	100%
ECO103101	PAE204741	64%	99.2%	99.8%
ECO103101	PPU108490	63%	89.9%	99.8%
ECO103101	PSY104834	63%	99.2%	99.8%
ECO103101	SPA101734	89%	100%	100%
ECO103101	STY101474	93%	100%	100%
ECO103101	SAU801266	38%	69.1%	87.2%
ECO103101	SEP201559	37%	77.6%	94.8%
ECO103101	SHA101153	38%	69.1%	90.2%
ECO103101	SMU100777	33%	69.7%	90.4%
ECO103101	SPN400478	32%	70.7%	96.3%
ECO103101	SPY201324	32%	70.7%	95.3%
ECO103101	TPA100882	29%	91.5%	94.4%
ECO103101	UUR100320	27%	66.3%	77.1%
ECO103101	VCH100630	78%	100%	100%
ECO103101	YPS001052	88%	100%	100%
ECO103104	BPT101520	35%	85.6%	100%
ECO103104	ECO103104	100%	100%	100%
ECO103104	HPY201308	25%	77.9%	79.6%
ECO103104	PRT105681	32%	92.9%	94.7%
ECO103115	ABA101804	72%	97.6%	97.6%
ECO103115	BAN102544	58%	95.3%	83.3%
ECO103115	BAN111062	58%	95.3%	85.1%
ECO103115	BFR10883	63%	96.5%	91.0%
ECO103115	BPT102470	71%	98.8%	97.7%
ECO103115	BBU100779	65%	96.5%	98.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103115	BCE103036	65%	96.5%	94.3%
ECO103115	BFU106480	63%	96.5%	94.3%
ECO103115	BMA101618	65%	96.5%	94.3%
ECO103115	CJU100084	65%	96.5%	96.4%
ECO103115	CPN200204	56%	100%	97.6%
ECO103115	CTR200690	56%	96.5%	95.2%
ECO103115	CAC103330	70%	95.3%	80%
ECO103115	CBO102962	66%	90.6%	77%
ECO103115	CDF101911	66%	91.8%	81.2%
ECO103115	CDP101220	64%	96.5%	90.9%
ECO103115	EBC100461	95%	100%	100%
ECO103115	EFA202214	61%	95.3%	81.6%
ECO103115	EFM200824	64%	95.3%	82.5%
ECO103115	ECO103115	100%	100%	100%
ECO103115	HIN100859	87%	100%	100%
ECO103115	HPY100293	63%	100%	95.5%
ECO103115	KPN300596	94%	100%	100%
ECO103115	LPN100139	70%	100%	92.4%
ECO103115	LMO100798	60%	98.8%	86.5%
ECO103115	MCA101440	69%	100%	100%
ECO103115	MAV104122	64%	98.8%	93.2%
ECO103115	MBV104431	64%	96.5%	93.0%
ECO103115	MLP100903	64%	98.8%	93.2%
ECO103115	MTU202405	64%	96.5%	93.0%
ECO103115	MGE100239	55%	90.6%	74.0%
ECO103115	MPN100509	57%	90.6%	74.0%
ECO103115	NGO101635	76%	96.5%	91.1%
ECO103115	NME202000	76%	96.5%	91.1%
ECO103115	PMU100348	90%	100%	100%
ECO103115	PRT100790	95%	100%	100%
ECO103115	PAE204565	76%	98.8%	98.8%
ECO103115	PPU109793	69%	98.8%	98.8%
ECO103115	PSY102707	70%	96.5%	90.1%
ECO103115	SPA100460	95%	100%	100%
ECO103115	STY101487	95%	100%	100%
ECO103115	SAU801645	60%	97.6%	82.8%
ECO103115	SEP201610	60%	97.6%	82.8%
ECO103115	SHA100024	59%	97.6%	82.8%
ECO103115	SMU100757	60%	95.3%	82.5%
ECO103115	SPN401014	59%	95.3%	89.9%
ECO103115	SPY200612	59%	95.3%	82.5%
ECO103115	TPA100735	52%	100%	95.4%
ECO103115	UUR100211	58%	80%	68%
ECO103115	VCH100431	89%	97.6%	96.5%
ECO103115	YPS002142	94%	100%	100%
ECO103116	ABA105440	61%	99.0%	99.0%
ECO103116	BAN107763	44%	100%	100%
ECO103116	BAN108298	44%	100%	100%
ECO103116	BFR10884	37%	100%	86.8%
ECO103116	BPT104764	47%	100%	42.0%
ECO103116	BBU100777	32%	98.1%	98.1%
ECO103116	BCE111959	44%	100%	100%
ECO103116	BFU106477	43%	100%	83.1%
ECO103116	BMA107479	43%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103116	CJU100083	40%	100%	100%
ECO103116	CPN200203	38%	97.1%	95.3%
ECO103116	CTR200691	43%	94.2%	92.5%
ECO103116	CAC100327	38%	100%	100%
ECO103116	CBO100385	44%	100%	78.2%
ECO103116	CDF101910	41%	100%	97.2%
ECO103116	CDP101222	38%	98.1%	99.0%
ECO103116	EBC100460	100%	31.1%	100%
ECO103116	EFA202217	41%	100%	96.2%
ECO103116	EFM200259	43%	100%	100%
ECO103116	ECO103116	100%	100%	100%
ECO103116	HIN100860	79%	100%	100%
ECO103116	HPY100292	46%	99.0%	98.1%
ECO103116	KPN300595	96%	87.4%	100%
ECO103116	LPN100481	53%	98.1%	98.1%
ECO103116	LMO101855	42%	100%	100%
ECO103116	MCA101422	62%	100%	100%
ECO103116	MAV102387	39%	97.1%	96.1%
ECO103116	MBV104430	37%	98.1%	96.2%
ECO103116	MLP100904	37%	97.1%	96.1%
ECO103116	MTU202406	37%	98.1%	96.2%
ECO103116	MGE100237	32%	95.1%	94%
ECO103116	MPN100511	34%	95.1%	94%
ECO103116	NGO101632	54%	99.0%	89.5%
ECO103116	NME201999	54%	99.0%	100%
ECO103116	PMU100347	83%	100%	100%
ECO103116	PRT100789	78%	99.0%	100%
ECO103116	PAE204566	64%	100%	100%
ECO103116	PPU108773	60%	99.0%	65.0%
ECO103116	PSY108282	56%	100%	64.8%
ECO103116	SPA100461	97%	69.9%	100%
ECO103116	STY101488	99%	100%	100%
ECO103116	SAU801647	41%	100%	100%
ECO103116	SEP201612	39%	100%	100%
ECO103116	SMU100215	36%	99.0%	97.1%
ECO103116	SPN401012	39%	99.0%	97.1%
ECO103116	SPY200610	37%	99.0%	97.1%
ECO103116	TPA100737	32%	98.1%	97.1%
ECO103116	UUR100213	42%	99.0%	98%
ECO103116	VCH100430	78%	100%	100%
ECO103116	YPS002148	88%	100%	100%
ECO103159	ABA100671	35%	96.7%	95.4%
ECO103159	BPT102294	42%	93.9%	99.5%
ECO103159	BCE101468	44%	93.9%	99.5%
ECO103159	BFU100537	39%	56.6%	99.2%
ECO103159	BMA107004	44%	93.9%	99.5%
ECO103159	EBC102178	95%	99.5%	99.5%
ECO103159	ECO103159	100%	100%	100%
ECO103159	HIN101410	62%	95.8%	95.8%
ECO103159	KPN302003	93%	99.5%	99.5%
ECO103159	LPN101126	63%	98.1%	99.0%
ECO103159	MCA100934	40%	87.3%	90.8%
ECO103159	NGO101309	44%	93.9%	99.5%
ECO103159	NME200463	45%	93.9%	99.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103159	PMU100522	67%	94.3%	94.3%
ECO103159	PRT100887	81%	98.6%	98.1%
ECO103159	PAE204426	53%	93.4%	97.1%
ECO103159	PPU111756	56%	93.4%	96.1%
ECO103159	PSY103836	57%	93.4%	97.1%
ECO103159	SPA100956	97%	99.1%	100%
ECO103159	STY101557	97%	99.5%	99.5%
ECO103159	VCH100566	72%	99.5%	100%
ECO103159	YPS002273	83%	98.6%	98.1%
ECO103160	ABA100673	76%	100%	100%
ECO103160	BAN112009	53%	100%	100%
ECO103160	BAN109246	55%	100%	100%
ECO103160	BFR11427	50%	93.1%	94.5%
ECO103160	BPT102858	64%	100%	100%
ECO103160	BBU100337	56%	97.7%	93.4%
ECO103160	BCE104886	63%	100%	100%
ECO103160	BFU103523	65%	100%	100%
ECO103160	BMA104857	63%	100%	100%
ECO103160	CJU101395	49%	95.4%	96.9%
ECO103160	CPN200506	47%	93.8%	91.8%
ECO103160	CTR200396	47%	93.8%	91.7%
ECO103160	CAC102494	63%	100%	100%
ECO103160	CBO103462	59%	100%	100%
ECO103160	CDF100063	60%	100%	100%
ECO103160	CDP100047	50%	93.1%	68.4%
ECO103160	EBC102179	99%	100%	100%
ECO103160	EFA200812	52%	100%	100%
ECO103160	EFM201820	52%	100%	100%
ECO103160	ECO103160	100%	100%	100%
ECO103160	HIN101411	86%	100%	100%
ECO103160	HPY100081	51%	95.4%	96.9%
ECO103160	KPN302005	100%	100%	100%
ECO103160	LPN102542	61%	100%	100%
ECO103160	LMO100441	55%	100%	100%
ECO103160	MCA100086	73%	95.4%	96.9%
ECO103160	MAV103416	51%	93.1%	72.9%
ECO103160	MBV101153	52%	93.1%	80.1%
ECO103160	MLP100233	46%	98.5%	83.7%
ECO103160	MTU203395	52%	93.1%	80.1%
ECO103160	MGE100427	46%	100%	100%
ECO103160	MPN100226	47%	100%	100%
ECO103160	NGO102668	64%	96.2%	96.2%
ECO103160	NME200353	64%	96.2%	96.2%
ECO103160	PMU100521	89%	100%	100%
ECO103160	PRT100490	91%	100%	100%
ECO103160	PAE204430	76%	100%	100%
ECO103160	PPU105982	75%	100%	100%
ECO103160	PSY108021	76%	100%	100%
ECO103160	SPA100957	99%	100%	100%
ECO103160	STY101559	99%	100%	100%
ECO103160	SAU802217	50%	100%	100%
ECO103160	SEP202046	50%	100%	100%
ECO103160	SHA100041	50%	100%	100%
ECO103160	SMU101370	52%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103160	SPN400272	50%	100%	100%
ECO103160	SPY201485	50%	100%	100%
ECO103160	TPA101014	49%	98.5%	99.2%
ECO103160	UUR100583	55%	96.9%	94.7%
ECO103160	VCH100561	90%	100%	100%
ECO103160	YPS002276	92%	100%	100%
ECO103161	ABA100676	71%	100%	100%
ECO103161	BAN101291	58%	98.6%	96.6%
ECO103161	BAN111521	58%	98.6%	96.6%
ECO103161	BFR11426	48%	99.3%	93.5%
ECO103161	BPT102861	65%	99.3%	99.3%
ECO103161	BBU100338	51%	95.1%	92.5%
ECO103161	BCE107311	64%	100%	80.7%
ECO103161	BFU103522	65%	100%	100%
ECO103161	BMA107182	64%	100%	79.3%
ECO103161	CJU101396	52%	93.7%	95.0%
ECO103161	CPN200505	47%	99.3%	95.3%
ECO103161	CTR200395	52%	98.6%	94.7%
ECO103161	CAC102148	52%	100%	98.6%
ECO103161	CBO103121	54%	100%	97.9%
ECO103161	CDF100062	54%	99.3%	98.6%
ECO103161	CDP100045	47%	99.3%	95.9%
ECO103161	EBC102180	98%	100%	100%
ECO103161	EFA200811	58%	98.6%	95.9%
ECO103161	EFM201491	60%	98.6%	79.5%
ECO103161	ECO103161	100%	100%	100%
ECO103161	HIN101412	91%	100%	100%
ECO103161	HPY100082	51%	93.7%	94.3%
ECO103161	KPN301994	96%	100%	100%
ECO103161	LPN102178	71%	100%	98.6%
ECO103161	LMO100177	55%	98.6%	96.6%
ECO103161	MCA103453	68%	98.6%	97.9%
ECO103161	MAV103415	51%	96.5%	93.2%
ECO103161	MBV101152	52%	95.1%	69.2%
ECO103161	MLP100232	49%	100%	96.6%
ECO103161	MTU203396	52%	96.5%	93.2%
ECO103161	MGE100428	43%	95.1%	93.2%
ECO103161	MPN100225	42%	96.5%	93.8%
ECO103161	NGO101071	68%	100%	99.3%
ECO103161	NME200352	67%	100%	99.3%
ECO103161	PMU100520	90%	100%	100%
ECO103161	PRT100489	93%	100%	100%
ECO103161	PAE204431	74%	100%	100%
ECO103161	PPU105984	73%	100%	100%
ECO103161	PSY103838	74%	96.5%	96.5%
ECO103161	SPA100958	100%	100%	100%
ECO103161	STY101563	100%	100%	100%
ECO103161	SAU802218	58%	96.5%	94.5%
ECO103161	SEP202048	54%	96.5%	94.5%
ECO103161	SHA100040	56%	72.5%	92.0%
ECO103161	SMU101369	55%	98.6%	94.6%
ECO103161	SPN400271	58%	98.6%	94.6%
ECO103161	SPY201486	57%	98.6%	94.6%
ECO103161	TPA101015	48%	96.5%	96.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103161	UUR100584	46%	92.3%	88.5%
ECO103161	VCH100560	77%	100%	100%
ECO103161	YPS002279	95%	100%	100%
ECO103163	EBC102436	90%	98.5%	100%
ECO103163	ECO103163	100%	100%	100%
ECO103163	HIN101594	37%	92.5%	89.6%
ECO103163	KPN301998	92%	100%	100%
ECO103163	PMU100688	40%	92.5%	92.0%
ECO103163	PRT100487	68%	98.5%	99.3%
ECO103163	PAE204439	24%	86.6%	81.8%
ECO103163	PPU111785	23%	90.3%	86.2%
ECO103163	PSY103846	25%	82.1%	85.0%
ECO103163	SPA100846	93%	99.3%	96.4%
ECO103163	STY101569	96%	100%	100%
ECO103163	STM101859	97%	100%	100%
ECO103163	VCH100557	44%	94.0%	87.6%
ECO103163	YPS002289	80%	94.0%	94.8%
ECO103164	ABA102114	35%	90.3%	93.0%
ECO103164	BPT102616	37%	96.7%	96.4%
ECO103164	BCE114751	42%	75.6%	86.3%
ECO103164	BFU102903	42%	75.4%	84.8%
ECO103164	BMA102577	42%	75.6%	86.1%
ECO103164	CPN200861	36%	97.8%	76.2%
ECO103164	CAC101858	40%	75.2%	69.0%
ECO103164	CDF103193	41%	79.6%	73.8%
ECO103164	CDP100135	36%	73.6%	74.8%
ECO103164	EBC102437	84%	100%	100%
ECO103164	ECO103164	100%	100%	100%
ECO103164	HIN101231	57%	100%	100%
ECO103164	KPN302000	81%	100%	100%
ECO103164	MBV100623	35%	73.4%	88.2%
ECO103164	MTU200972	34%	73.4%	69.2%
ECO103164	NGO101854	34%	91.4%	88.8%
ECO103164	NME200654	35%	91.4%	88.8%
ECO103164	PMU100734	58%	100%	100%
ECO103164	PRT100486	65%	99.8%	98.5%
ECO103164	SPA100847	89%	100%	100%
ECO103164	STY101572	90%	100%	100%
ECO103164	STM101862	89%	100%	100%
ECO103164	SPN402042	35%	71.9%	84.1%
ECO103164	YPS002292	72%	100%	100%
ECO103175	BPT105606	23%	76.4%	67.2%
ECO103175	BCE100520	30%	22.5%	47.3%
ECO103175	BFU102649	21%	86.1%	63.6%
ECO103175	BMA106473	22%	86.1%	64.6%
ECO103175	EBC100005	73%	9.5%	59.1%
ECO103175	EBC103540	75%	99.2%	77.8%
ECO103175	ECO103175	100%	100%	100%
ECO103175	KPN302541	71%	98.5%	100%
ECO103175	LPN102990	21%	98.4%	75.6%
ECO103175	PRT101519	38%	99.9%	77.7%
ECO103175	PAE204474	21%	97.9%	75.7%
ECO103175	PPU109810	20%	98.7%	76.1%
ECO103175	PSY104777	22%	93.3%	72.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103175	SPA100160	74%	34.4%	100%
ECO103175	STY101629	79%	100%	78.0%
ECO103175	VCH100415	27%	97.9%	75.1%
ECO103175	YPS003182	48%	99.9%	78.5%
ECO103176	BCE109237	27%	24.5%	68.0%
ECO103176	ECO103176	100%	100%	100%
ECO103176	KPN305789	74%	100%	100%
ECO103176	SPA101850	81%	99.3%	100%
ECO103181	ABA101202	68%	93.5%	98.6%
ECO103181	BAN111944	44%	89.1%	96.8%
ECO103181	BAN102999	58%	90.5%	97.1%
ECO103181	BFR10062	45%	89.6%	96.5%
ECO103181	BPT102509	73%	91.3%	96.8%
ECO103181	BBU100714	52%	87.7%	89.2%
ECO103181	BCE109815	71%	93.2%	98.6%
ECO103181	BFU108081	70%	91.6%	97.1%
ECO103181	BFU113174	71%	93.2%	98.6%
ECO103181	BMA103717	71%	93.2%	98.6%
ECO103181	CJU100248	55%	92.1%	97.4%
ECO103181	CPN201000	55%	95.1%	94.3%
ECO103181	CTR200082	54%	95.1%	94.3%
ECO103181	CAC102861	58%	88.6%	95.8%
ECO103181	CBO101490	59%	89.4%	96.1%
ECO103181	CDF101880	57%	90.5%	94.1%
ECO103181	EBC103541	100%	94.6%	100%
ECO103181	ECO103181	100%	100%	100%
ECO103181	HIN100036	78%	96.5%	93.9%
ECO103181	HPY101353	51%	94.3%	99.7%
ECO103181	KPN302551	99%	94.6%	100%
ECO103181	LMO102883	57%	90.7%	97.6%
ECO103181	PMU101955	80%	94.6%	99.4%
ECO103181	PRT101213	95%	94.6%	100%
ECO103181	PAE204479	79%	94.6%	100%
ECO103181	PPU108925	79%	97.8%	100%
ECO103181	PSY104799	81%	57.2%	100%
ECO103181	SPA101315	91%	78.2%	100%
ECO103181	STY101647	100%	94.6%	100%
ECO103181	TPA100493	52%	92.1%	96.8%
ECO103181	VCH100410	90%	94.6%	100%
ECO103181	YPS003161	99%	94.6%	100%
ECO103182	BPT101055	23%	63.5%	65.3%
ECO103182	EBC103543	76%	100%	100%
ECO103182	ECO103182	100%	100%	100%
ECO103182	KPN302547	73%	100%	100%
ECO103182	LPN102746	22%	75.1%	78.2%
ECO103182	PAE201432	22%	81.1%	79.2%
ECO103182	PPU107473	21%	81.1%	79.6%
ECO103182	SPA101314	83%	99.2%	100%
ECO103182	STY101649	84%	100%	100%
ECO103182	VCH100393	32%	100%	96.9%
ECO103182	YPS003159	50%	99.2%	100%
ECO103185	ABA100121	43%	97.4%	96.4%
ECO103185	BAN102691	32%	100%	95.4%
ECO103185	BAN100195	35%	98.7%	97.6%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103185	BFR12359	33%	91.0%	86.0%
ECO103185	BPT102941	56%	99.4%	99.3%
ECO103185	BCE100976	55%	64.1%	97.8%
ECO103185	BFU107829	54%	99.4%	99.4%
ECO103185	BMA104958	52%	99.4%	99.4%
ECO103185	CJU101215	37%	100%	98.7%
ECO103185	CPN200574	29%	97.4%	95.2%
ECO103185	CTR200393	31%	97.4%	96.3%
ECO103185	CAC102521	33%	99.4%	98.1%
ECO103185	CBO102046	31%	100%	98.7%
ECO103185	CDF101397	32%	100%	98.7%
ECO103185	EBC103552	91%	100%	100%
ECO103185	EFA203429	32%	97.4%	95.7%
ECO103185	EFM200558	31%	100%	93.4%
ECO103185	ECO103185	100%	100%	100%
ECO103185	HIN100950	69%	100%	100%
ECO103185	HPY100367	29%	100%	98.7%
ECO103185	KPN307946	88%	100%	100%
ECO103185	LPN101729	51%	100%	100%
ECO103185	LMO100213	39%	97.4%	95.5%
ECO103185	MCA103068	38%	98.1%	97.1%
ECO103185	NGO101619	61%	99.4%	99.3%
ECO103185	NME200553	60%	99.4%	99.3%
ECO103185	PMU101092	65%	100%	100%
ECO103185	PRT101210	69%	100%	100%
ECO103185	PAE204842	64%	99.4%	99.4%
ECO103185	PPU108140	66%	99.4%	99.3%
ECO103185	PSY100848	61%	99.4%	99.3%
ECO103185	SPA101602	92%	100%	100%
ECO103185	STY101662	92%	100%	100%
ECO103185	STM102306	92%	100%	100%
ECO103185	SAU801527	34%	100%	100%
ECO103185	SEP200910	34%	100%	100%
ECO103185	SHA101871	35%	100%	100%
ECO103185	SMU100535	34%	100%	100%
ECO103185	SPN400383	37%	100%	100%
ECO103185	SPY201346	34%	100%	100%
ECO103185	VCH100292	72%	100%	78.1%
ECO103185	YPS003132	82%	100%	100%
ECO103186	ABA100122	64%	98.9%	97.1%
ECO103186	BAN102154	47%	97.8%	99.8%
ECO103186	BAN113444	53%	98.4%	98.7%
ECO103186	BFR11898	48%	99.8%	89.1%
ECO103186	BFR11613	50%	98.4%	87.9%
ECO103186	BPT102938	67%	98.9%	99.1%
ECO103186	BCE104481	66%	100%	98.7%
ECO103186	BFU115826	65%	100%	98.7%
ECO103186	BMA101045	66%	98.9%	97.6%
ECO103186	CJU101214	53%	98.2%	99.3%
ECO103186	CPN200575	49%	98.7%	97.8%
ECO103186	CTR200394	51%	98.7%	97.2%
ECO103186	CAC103617	57%	98.9%	99.6%
ECO103186	CBO103874	55%	98.9%	99.3%
ECO103186	CDF101399	53%	98.2%	97.6%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103186	CDP100823	46%	96.0%	38.1%
ECO103186	EBC102634	93%	70.2%	100%
ECO103186	EFA200245	52%	98.4%	97.4%
ECO103186	EFM201807	52%	98.7%	96.9%
ECO103186	ECO103186	100%	100%	100%
ECO103186	HIN100951	82%	99.8%	100%
ECO103186	HPY100366	51%	98.2%	96.3%
ECO103186	KPN308876	96%	100%	100%
ECO103186	LPN102993	74%	98.9%	99.3%
ECO103186	LMO101165	53%	98.4%	97.8%
ECO103186	MCA102208	62%	98.2%	98.4%
ECO103186	MAV103606	47%	98.9%	62.9%
ECO103186	MBV101167	45%	98.7%	68.2%
ECO103186	MLP100439	45%	94.4%	70.9%
ECO103186	MTU202464	45%	98.7%	68.2%
ECO103186	NGO101616	68%	98.2%	97.4%
ECO103186	NME200552	69%	98.2%	97.4%
ECO103186	PMU101091	83%	99.8%	100%
ECO103186	PRT100504	86%	99.8%	100%
ECO103186	PAE204843	71%	99.8%	99.8%
ECO103186	PPU108141	70%	99.6%	99.1%
ECO103186	PSY108097	69%	99.6%	100%
ECO103186	SPA101601	95%	98.9%	100%
ECO103186	STY101665	96%	100%	100%
ECO103186	STM102307	96%	100%	100%
ECO103186	SAU801526	53%	98.2%	98.2%
ECO103186	SEP200908	52%	98.2%	98.0%
ECO103186	SHA100988	52%	98.2%	98.2%
ECO103186	SMU100533	51%	96.9%	97.1%
ECO103186	SPN400385	53%	98.0%	97.4%
ECO103186	SPY201344	52%	98.0%	97.6%
ECO103186	VCH100291	85%	99.6%	100%
ECO103186	YPS003128	92%	99.8%	99.8%
ECO103188	BAN108690	42%	96.3%	98.7%
ECO103188	BAN112300	47%	96.3%	97.9%
ECO103188	BFR12375	25%	89.1%	87.4%
ECO103188	BPT101875	22%	89.5%	67.2%
ECO103188	BBU100813	33%	90.1%	97.7%
ECO103188	CPN200265	25%	71.1%	72.5%
ECO103188	CBO103269	26%	88.2%	90.9%
ECO103188	CDF103913	25%	94.8%	98.5%
ECO103188	EBC102639	92%	99.6%	100%
ECO103188	ECO103188	100%	100%	100%
ECO103188	HIN100955	64%	96.9%	97.1%
ECO103188	KPN302542	89%	99.6%	100%
ECO103188	LMO101454	24%	30.3%	53.2%
ECO103188	PMU101089	59%	96.9%	98.7%
ECO103188	PRT100502	78%	98.8%	99.8%
ECO103188	SPA101599	91%	98.8%	100%
ECO103188	STY101671	93%	99.6%	100%
ECO103188	STM102309	93%	99.6%	100%
ECO103188	SMU101245	32%	20.8%	47.3%
ECO103188	YPS003121	82%	96.9%	97.1%
ECO103195	BFR10437	32%	90.9%	94.9%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103195	CJU100335	30%	91.9%	94.3%
ECO103195	ECO103195	100%	100%	100%
ECO103195	KPN308332	75%	98.7%	100%
ECO103195	LPN101631	30%	89.1%	89.3%
ECO103195	STM102321	88%	98.7%	98.7%
ECO103212	ABA105502	40%	98.6%	97.0%
ECO103212	BAN107407	30%	90.4%	89.1%
ECO103212	BAN101826	32%	99.3%	99.5%
ECO103212	BPT100805	36%	97.9%	89.7%
ECO103212	BCE107697	37%	97.7%	86.0%
ECO103212	BFU101027	39%	90.7%	82.5%
ECO103212	BMA101603	36%	97.7%	92.1%
ECO103212	CPN200071	27%	61.5%	66.5%
ECO103212	CTR200830	28%	60.6%	64.9%
ECO103212	CAC100526	31%	92.1%	92.3%
ECO103212	CBO102152	30%	98.6%	99.3%
ECO103212	CDF102436	30%	95.1%	96.1%
ECO103212	CDP100308	32%	86.0%	100%
ECO103212	EBC103645	86%	100%	97.7%
ECO103212	EFA201559	31%	93.0%	89.3%
ECO103212	EFM201913	31%	83.4%	98.4%
ECO103212	ECO103212	100%	100%	100%
ECO103212	HIN100605	51%	98.4%	94.7%
ECO103212	KPN301222	86%	100%	99.5%
ECO103212	LMO100111	31%	99.8%	99.3%
ECO103212	MCA102831	37%	99.8%	98.4%
ECO103212	MAV100826	30%	87.4%	84.5%
ECO103212	MBV102144	30%	86.0%	82.9%
ECO103212	MTU201388	30%	86.0%	82.9%
ECO103212	NGO101723	40%	98.1%	98.3%
ECO103212	NME200155	40%	98.1%	98.3%
ECO103212	PMU101561	53%	99.8%	97.8%
ECO103212	PRT105024	68%	100%	100%
ECO103212	PAE200017	50%	98.6%	98.8%
ECO103212	PPU103623	49%	98.6%	98.4%
ECO103212	PSY103506	48%	98.6%	96.9%
ECO103212	SPA104301	88%	84.4%	99.7%
ECO103212	STY101845	88%	100%	100%
ECO103212	STM102354	88%	100%	100%
ECO103212	SAU801217	28%	98.8%	93.3%
ECO103212	SEP201495	28%	99.1%	99.1%
ECO103212	SMU101505	31%	85.1%	82.7%
ECO103212	SPN401577	33%	92.1%	90.4%
ECO103212	SPY201253	30%	90.4%	88.9%
ECO103212	VCH100044	62%	98.8%	97.7%
ECO103212	YPS002538	73%	100%	100%
ECO103216	BAN110095	31%	75.4%	78.6%
ECO103216	BAN104882	38%	75.4%	74.0%
ECO103216	BCE107484	37%	97.5%	88.7%
ECO103216	BFU103220	36%	99.2%	71.0%
ECO103216	BMA101250	50%	62.3%	57.1%
ECO103216	EBC103642	74%	99.2%	99.2%
ECO103216	ECO103216	100%	100%	100%
ECO103216	KPN300812	79%	98.4%	98.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103216	PRT100263	51%	97.5%	95.2%
ECO103216	SPA104310	86%	100%	100%
ECO103216	STY101840	86%	100%	100%
ECO103217	ABA100130	70%	97.6%	99.2%
ECO103217	BAN103288	47%	85.8%	97.5%
ECO103217	BAN102478	47%	85.8%	97.5%
ECO103217	BFR100896	51%	94.5%	74.5%
ECO103217	BPT100897	68%	100%	96.9%
ECO103217	BBU100502	44%	96.9%	100%
ECO103217	BCE109774	70%	96.9%	93.9%
ECO103217	BFU101597	66%	100%	97.7%
ECO103217	BMA104335	71%	96.9%	93.9%
ECO103217	CJU101502	49%	91.3%	99.1%
ECO103217	CPN200120	43%	91.3%	98.6%
ECO103217	CTR200782	41%	91.3%	98.6%
ECO103217	CAC100809	43%	85.8%	95.6%
ECO103217	CBO102497	43%	85.8%	96.5%
ECO103217	CDF102169	48%	85.8%	96.5%
ECO103217	CDP100024	52%	94.5%	77.1%
ECO103217	EBC103646	100%	100%	100%
ECO103217	EFA201974	48%	87.4%	98.4%
ECO103217	EFM201685	44%	87.4%	99.2%
ECO103217	ECO103217	100%	100%	100%
ECO103217	HIN100784	89%	100%	99.2%
ECO103217	HPY101274	43%	91.3%	100%
ECO103217	KPN300813	98%	100%	100%
ECO103217	LMO100340	42%	85.8%	97.8%
ECO103217	MCA100427	75%	92.9%	99.2%
ECO103217	MAV101006	53%	86.6%	75.3%
ECO103217	MBV100492	52%	86.6%	61.1%
ECO103217	MLP101193	47%	94.5%	75.9%
ECO103217	MTU203409	52%	86.6%	61.1%
ECO103217	MGE100181	35%	83.5%	91.1%
ECO103217	MPN100639	34%	86.6%	93.5%
ECO103217	NGO100883	70%	92.9%	96.7%
ECO103217	NME200096	71%	92.9%	96.7%
ECO103217	PMU101389	89%	100%	100%
ECO103217	PRT101773	93%	100%	100%
ECO103217	PAE204235	75%	98.4%	99.2%
ECO103217	PPU104535	79%	92.9%	92.2%
ECO103217	PSY105785	80%	92.9%	92.2%
ECO103217	SPA104312	96%	100%	100%
ECO103217	STY101829	99%	100%	100%
ECO103217	SAU802223	47%	85.8%	97.5%
ECO103217	SEP202058	47%	85.8%	97.5%
ECO103217	SHA100503	48%	86.6%	97.6%
ECO103217	SMU100584	47%	85.8%	97.7%
ECO103217	SPN400216	46%	85.8%	97.7%
ECO103217	SPY101855	46%	85.8%	97.7%
ECO103217	TPA100211	50%	92.1%	71.3%
ECO103217	UUR100260	45%	78.7%	89.1%
ECO103217	VCH102533	91%	100%	100%
ECO103217	YPS002494	94%	99.2%	98.4%
ECO103218	ABA100129	66%	99.1%	96.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103218	BAN107601	34%	92.7%	97.5%
ECO103218	BAN108468	45%	93.6%	98.1%
ECO103218	BFR10426	39%	96.7%	98.2%
ECO103218	BPT100896	61%	98.2%	98.8%
ECO103218	BBU100501	35%	95.4%	91.3%
ECO103218	BCE103299	59%	97.6%	98.8%
ECO103218	BFU101596	61%	97.6%	98.8%
ECO103218	BMA100053	60%	97.6%	98.8%
ECO103218	CJU101501	33%	95.7%	92.9%
ECO103218	CPN200119	38%	90.0%	80.6%
ECO103218	CTR200783	38%	90.6%	80.5%
ECO103218	CAC100456	44%	95.1%	99.4%
ECO103218	CBO100600	44%	93.6%	97.8%
ECO103218	CDF104551	45%	94.5%	98.1%
ECO103218	CDP100022	42%	96.4%	92.9%
ECO103218	EBC103650	99%	100%	100%
ECO103218	EFA201975	45%	95.4%	99.4%
ECO103218	EFM200465	45%	95.4%	99.4%
ECO103218	ECO103218	100%	100%	100%
ECO103218	HIN100783	91%	100%	100%
ECO103218	HPY101275	29%	94.2%	91.3%
ECO103218	KPN300703	99%	76.9%	100%
ECO103218	LMO100649	45%	93.6%	98.1%
ECO103218	MCA100426	64%	98.2%	96.1%
ECO103218	MAV101008	43%	94.5%	89.3%
ECO103218	MBV100494	44%	93.9%	88.8%
ECO103218	MLP101194	44%	93.9%	88.8%
ECO103218	MTU203410	44%	93.9%	88.8%
ECO103218	MGE100180	31%	86.0%	89.9%
ECO103218	MPN100640	31%	86.6%	90.8%
ECO103218	NGO100885	62%	99.1%	99.1%
ECO103218	NME200097	62%	99.1%	99.1%
ECO103218	PMU101390	92%	100%	100%
ECO103218	PRT101775	97%	100%	100%
ECO103218	PAE204236	73%	99.1%	97.6%
ECO103218	PPU104534	73%	99.1%	97.6%
ECO103218	PSY100281	80%	46.8%	93.9%
ECO103218	SPA104314	100%	100%	100%
ECO103218	STY101828	100%	100%	100%
ECO103218	SAU802224	42%	93.6%	98.1%
ECO103218	SEP202059	42%	93.6%	98.1%
ECO103218	SHA100502	42%	93.6%	98.1%
ECO103218	SMU100586	45%	93.6%	98.1%
ECO103218	SPN400215	45%	93.6%	98.4%
ECO103218	SPY200063	45%	93.6%	98.1%
ECO103218	TPA100210	37%	93.9%	91.2%
ECO103218	UUR100259	36%	93.6%	98.5%
ECO103218	VCH102534	90%	100%	100%
ECO103218	YPS002493	99%	100%	100%
ECO103219	ABA100128	71%	100%	100%
ECO103219	BAN103804	49%	100%	100%
ECO103219	BFR10425	49%	100%	100%
ECO103219	BPT100895	64%	100%	100%
ECO103219	BBU100614	44%	96.6%	95.2%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103219	BCE103241	70%	100%	100%
ECO103219	BFU101595	71%	100%	100%
ECO103219	BMA100015	71%	100%	100%
ECO103219	CJU101500	50%	100%	100%
ECO103219	CPN200012	39%	94.7%	91.9%
ECO103219	CTR200903	38%	99.5%	98.6%
ECO103219	CAC102218	50%	100%	100%
ECO103219	CBO101434	54%	100%	100%
ECO103219	CDF103315	50%	91.3%	99.0%
ECO103219	CDP100020	47%	100%	100%
ECO103219	EBC103653	97%	100%	100%
ECO103219	EFA202012	45%	100%	99.0%
ECO103219	ECO103219	100%	100%	100%
ECO103219	HIN100782	89%	100%	100%
ECO103219	HPY101276	49%	100%	100%
ECO103219	KPN300702	98%	100%	100%
ECO103219	LMO100680	48%	100%	100%
ECO103219	MCA100425	67%	100%	100%
ECO103219	MAV101010	46%	100%	100%
ECO103219	MBV100325	47%	100%	100%
ECO103219	MLP101195	46%	100%	100%
ECO103219	MTU203411	47%	100%	100%
ECO103219	MGE100317	38%	99.0%	98.0%
ECO103219	MPN100395	39%	99.0%	98.0%
ECO103219	NGO100887	73%	100%	100%
ECO103219	NME200098	73%	100%	100%
ECO103219	PMU101391	89%	100%	100%
ECO103219	PRT104446	94%	100%	100%
ECO103219	PAE204237	74%	100%	100%
ECO103219	PPU108168	73%	100%	100%
ECO103219	PSY107923	73%	100%	100%
ECO103219	SPA104316	99%	100%	100%
ECO103219	STY101827	99%	100%	100%
ECO103219	SAU801719	47%	100%	100%
ECO103219	SEP201745	47%	100%	100%
ECO103219	SHA100142	47%	100%	100%
ECO103219	SMU101344	45%	100%	99.0%
ECO103219	SPN400078	45%	100%	99.0%
ECO103219	SPY201664	45%	100%	99.0%
ECO103219	TPA100303	39%	95.6%	96.1%
ECO103219	UUR100503	40%	100%	99.0%
ECO103219	VCH102535	87%	100%	100%
ECO103219	YPS002492	96%	100%	100%
ECO103220	ABA100127	78%	95.3%	96.1%
ECO103220	BAN102381	62%	100%	100%
ECO103220	BAN110714	65%	100%	100%
ECO103220	BFR10424	51%	100%	100%
ECO103220	BPT100894	70%	100%	100%
ECO103220	BBU100500	52%	99.2%	95.5%
ECO103220	BCE109619	71%	95.3%	92.5%
ECO103220	BFU101594	71%	95.3%	91.8%
ECO103220	BMA109746	72%	95.3%	92.5%
ECO103220	CJU101499	51%	100%	100%
ECO103220	CPN200118	51%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103220	CTR200784	55%	93.8%	90.9%
ECO103220	CAC100574	63%	93.8%	92.4%
ECO103220	CBO101814	67%	93.8%	91.7%
ECO103220	CDF101597	62%	98.4%	96.2%
ECO103220	CDP100018	58%	93.8%	90.3%
ECO103220	EBC103656	97%	100%	100%
ECO103220	EFA201976	59%	100%	100%
ECO103220	EFM200112	58%	100%	100%
ECO103220	ECO103220	100%	100%	100%
ECO103220	HIN100781	92%	100%	100%
ECO103220	HPY101277	52%	100%	100%
ECO103220	KPN300701	99%	100%	100%
ECO103220	LMO102707	62%	100%	100%
ECO103220	MCA100424	75%	95.3%	96.2%
ECO103220	MAV101012	60%	95.3%	89.1%
ECO103220	MBV100327	58%	95.3%	88.5%
ECO103220	MLP101196	60%	95.3%	89.1%
ECO103220	MTU203412	59%	95.3%	88.5%
ECO103220	MGE100179	47%	87.6%	86.3%
ECO103220	MPN100641	48%	92.2%	98.3%
ECO103220	NGO100889	74%	100%	100%
ECO103220	NME200099	74%	100%	100%
ECO103220	PMU101392	93%	100%	100%
ECO103220	PRT105644	99%	100%	100%
ECO103220	PAE204238	79%	100%	100%
ECO103220	PPU104532	78%	100%	100%
ECO103220	PSY106472	79%	100%	100%
ECO103220	SPA104318	96%	99.2%	100%
ECO103220	STY101826	98%	100%	100%
ECO103220	SAU802225	62%	100%	100%
ECO103220	SEP200240	62%	100%	100%
ECO103220	SHA100501	62%	100%	100%
ECO103220	SMU100588	66%	100%	100%
ECO103220	SPN400214	65%	100%	100%
ECO103220	SPY200062	67%	100%	100%
ECO103220	TPA100209	53%	96.1%	98.4%
ECO103220	UUR100258	52%	92.2%	98.3%
ECO103220	VCH102536	91%	100%	100%
ECO103220	YPS002491	98%	100%	100%
ECO103221	ABA100126	75%	100%	99.2%
ECO103221	BAN113421	75%	30.5%	87.8%
ECO103221	BAN112977	57%	98.3%	95.9%
ECO103221	BFR10423	52%	96.6%	91.3%
ECO103221	BPT100893	60%	96.6%	94.2%
ECO103221	BBU100499	53%	98.3%	93.6%
ECO103221	BCE106205	65%	96.6%	94.2%
ECO103221	BFU100384	66%	96.6%	94.2%
ECO103221	BMA110016	64%	96.6%	94.2%
ECO103221	CJU101498	55%	98.3%	96.7%
ECO103221	CPN200117	49%	98.3%	95.9%
ECO103221	CTR200785	49%	98.3%	95.9%
ECO103221	CAC101837	56%	98.3%	95.1%
ECO103221	CBO102219	58%	98.3%	95.1%
ECO103221	CDF103596	59%	100%	96.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103221	CDP100016	54%	98.3%	95.9%
ECO103221	EBC103659	98%	100%	100%
ECO103221	EFA201977	58%	98.3%	95.9%
ECO103221	EFM200415	62%	98.3%	95.9%
ECO103221	ECO103221	100%	100%	100%
ECO103221	HEN100780	86%	93.2%	90.2%
ECO103221	HPY101278	53%	98.3%	97.5%
ECO103221	KPN300700	86%	85.6%	100%
ECO103221	LMO102428	56%	98.3%	95.9%
ECO103221	MCA100423	73%	100%	100%
ECO103221	MAV101014	59%	98.3%	94.4%
ECO103221	MBV100329	57%	98.3%	94.4%
ECO103221	MLP101197	57%	98.3%	94.4%
ECO103221	MTU203413	57%	98.3%	94.4%
ECO103221	MGE100178	52%	98.3%	93.5%
ECO103221	MPN100642	55%	98.3%	93.5%
ECO103221	NGO100891	70%	98.3%	96.7%
ECO103221	NME200100	70%	98.3%	96.7%
ECO103221	PMU101393	86%	100%	100%
ECO103221	PRT100020	86%	92.4%	100%
ECO103221	PAE204239	75%	100%	100%
ECO103221	PPU104531	74%	100%	100%
ECO103221	PSY105783	82%	64.4%	100%
ECO103221	SPA104321	97%	100%	100%
ECO103221	STY101825	96%	100%	100%
ECO103221	SAU802226	53%	98.3%	95.9%
ECO103221	SEP200241	51%	98.3%	95.9%
ECO103221	SHA100500	52%	98.3%	95.9%
ECO103221	SMU100590	61%	94.1%	91.7%
ECO103221	SPN400213	63%	94.1%	91.7%
ECO103221	SPY200061	63%	94.1%	91.7%
ECO103221	TPA100208	52%	98.3%	95.9%
ECO103221	UUR100257	55%	98.3%	93.9%
ECO103221	VCH102537	87%	100%	100%
ECO103221	YPS002490	85%	100%	100%
ECO103222	ABA100104	76%	100%	100%
ECO103222	BPT104512	71%	100%	100%
ECO103222	BBU100498	62%	97.4%	92.3%
ECO103222	BCE112105	76%	100%	100%
ECO103222	BFU103878	76%	100%	100%
ECO103222	BMA103855	76%	100%	100%
ECO103222	CJU101497	68%	100%	100%
ECO103222	CPN200908	44%	97.4%	84.4%
ECO103222	CAC101480	60%	100%	100%
ECO103222	CBO103541	57%	100%	97.4%
ECO103222	CDF103770	60%	100%	100%
ECO103222	CDP102780	40%	100%	100%
ECO103222	EBC103975	45%	86.8%	71.7%
ECO103222	EFA203137	63%	100%	100%
ECO103222	EFM202440	63%	100%	100%
ECO103222	ECO103222	100%	100%	100%
ECO103222	HIN100779	84%	100%	100%
ECO103222	HPY101279	81%	100%	100%
ECO103222	KPN202806	42%	86.8%	71.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103222	LMO101459	57%	100%	100%
ECO103222	MCA102164	42%	86.8%	71.7%
ECO103222	MBV104764	55%	100%	100%
ECO103222	MLP101198	50%	100%	100%
ECO103222	MTU203414	55%	100%	100%
ECO103222	MGE100177	65%	100%	100%
ECO103222	MPN100643	65%	100%	100%
ECO103222	NGO101308	43%	84.2%	78.0%
ECO103222	NME200101	63%	100%	100%
ECO103222	PMU101394	86%	100%	100%
ECO103222	PRT103159	81%	100%	100%
ECO103222	PAE204240	86%	100%	100%
ECO103222	PSY103480	86%	100%	67.9%
ECO103222	SPA100818	50%	68.4%	56.5%
ECO103222	STY104823	100%	100%	100%
ECO103222	STM104443	50%	68.4%	56.5%
ECO103222	SAU802227	63%	100%	100%
ECO103222	SEP202480	63%	100%	100%
ECO103222	SHA100499	63%	100%	100%
ECO103222	SMU100592	60%	100%	100%
ECO103222	SPN400212	63%	100%	100%
ECO103222	SPY200060	60%	100%	100%
ECO103222	TPA100207	65%	100%	100%
ECO103222	UUR100256	76%	100%	100%
ECO103222	VCH102538	84%	100%	100%
ECO103222	YPS003891	94%	100%	100%
ECO103223	ABA100105	58%	93.5%	91.8%
ECO103223	BAN100422	41%	50.1%	95.7%
ECO103223	BAN100831	34%	90.1%	92.7%
ECO103223	BAN109756	41%	95.3%	97.7%
ECO103223	BAN106840	43%	94.8%	97.7%
ECO103223	BFR12413	39%	95.5%	94.6%
ECO103223	BPT100873	66%	99.8%	99.1%
ECO103223	BBU100497	35%	94.4%	95.4%
ECO103223	BCE109015	67%	94.1%	98.6%
ECO103223	BFU100380	64%	99.8%	99.1%
ECO103223	BMA107419	66%	94.1%	98.6%
ECO103223	CJU101592	41%	93.2%	97.6%
ECO103223	CPN200116	38%	95.5%	96.1%
ECO103223	CTR200786	38%	95.9%	97.6%
ECO103223	CAC102097	36%	94.4%	97.2%
ECO103223	CBO103220	39%	94.1%	97.2%
ECO103223	CDF103985	40%	93.9%	96.9%
ECO103223	CDP100001	45%	94.1%	97.5%
ECO103223	EBC103637	98%	100%	100%
ECO103223	EFA201979	40%	94.4%	97.2%
ECO103223	EFM200235	41%	93.0%	96.1%
ECO103223	ECO103223	100%	100%	100%
ECO103223	HIN100778	74%	100%	100%
ECO103223	HPY101282	40%	92.6%	96.9%
ECO103223	KPN300616	90%	80.4%	100%
ECO103223	LPN101432	57%	83.7%	100%
ECO103223	LMO101544	41%	94.6%	97.7%
ECO103223	MCA100141	54%	93.0%	92.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103223	MAV102070	42%	94.1%	94.7%
ECO103223	MBV101627	42%	94.1%	97.3%
ECO103223	MLP101115	41%	94.1%	97.3%
ECO103223	MTU200729	42%	94.1%	97.3%
ECO103223	MGE100173	35%	92.1%	86.9%
ECO103223	MPN100647	35%	91.9%	86.4%
ECO103223	NGO100896	56%	97.7%	98.2%
ECO103223	NME200103	56%	97.7%	98.2%
ECO103223	PMU101395	77%	100%	100%
ECO103223	PRT100105	94%	48.3%	100%
ECO103223	PAE204241	65%	99.8%	98.9%
ECO103223	PPU112340	64%	99.8%	98.6%
ECO103223	PSY100299	64%	99.8%	98.4%
ECO103223	SPA104324	99%	96.6%	100%
ECO103223	STY101824	99%	100%	100%
ECO103223	SAU802230	41%	93.2%	96.0%
ECO103223	SEP200245	41%	93.2%	96.0%
ECO103223	SHA100178	40%	81.7%	98.4%
ECO103223	SMU100598	37%	92.8%	94.9%
ECO103223	SPN400209	38%	93.0%	95.2%
ECO103223	SPY200057	38%	94.4%	96.5%
ECO103223	TPA100206	38%	93.2%	91.8%
ECO103223	UUR100252	32%	91.9%	89.0%
ECO103223	VCH102539	81%	100%	100%
ECO103223	YPS002488	97%	100%	100%
ECO103224	ABA100106	65%	100%	98.6%
ECO103224	BAN100388	39%	99.3%	98.6%
ECO103224	BAN101282	50%	99.3%	98.6%
ECO103224	BFR100671	47%	98.6%	98.0%
ECO103224	BPT100871	61%	98.6%	97.3%
ECO103224	BBU100496	40%	97.2%	97.2%
ECO103224	BCE108533	59%	100%	100%
ECO103224	BFU100391	62%	100%	100%
ECO103224	BMA101533	61%	100%	100%
ECO103224	CJU101593	60%	44.4%	49.2%
ECO103224	CPN200115	44%	80.6%	82.6%
ECO103224	CTR200787	38%	94.4%	97.9%
ECO103224	CAC101804	49%	99.3%	98.6%
ECO103224	CBO103582	51%	99.3%	98.6%
ECO103224	CDF100735	46%	99.3%	96.7%
ECO103224	CDP101730	38%	100%	96.6%
ECO103224	EBC103640	98%	100%	100%
ECO103224	EFA201980	52%	99.3%	98.6%
ECO103224	EFM201975	51%	99.3%	98.6%
ECO103224	ECO103224	100%	100%	100%
ECO103224	HIN100777	82%	100%	100%
ECO103224	HPY101283	45%	77.1%	82.2%
ECO103224	KPN300615	90%	96.5%	100%
ECO103224	LPN100259	58%	100%	100%
ECO103224	LMO102003	49%	99.3%	98.6%
ECO103224	MCA100140	64%	100%	98.6%
ECO103224	MAV102081	39%	100%	97.9%
ECO103224	MBV101609	40%	100%	97.9%
ECO103224	MLP101118	39%	100%	97.9%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103224	MTU200720	40%	100%	97.9%
ECO103224	MGE100172	37%	99.3%	98%
ECO103224	MPN100648	41%	99.3%	97.4%
ECO103224	NGO100899	58%	99.3%	99.3%
ECO103224	NME200104	60%	99.3%	99.3%
ECO103224	PMU101396	81%	100%	100%
ECO103224	PRT103332	85%	100%	100%
ECO103224	PAE204242	64%	100%	100%
ECO103224	PPU104529	66%	100%	100%
ECO103224	PSY107337	65%	100%	100%
ECO103224	SPA104326	99%	100%	100%
ECO103224	STY101823	99%	100%	100%
ECO103224	SAU802231	46%	99.3%	98.6%
ECO103224	SEP200247	43%	99.3%	98.6%
ECO103224	SHA100093	66%	47.2%	79.1%
ECO103224	SMU100599	48%	99.3%	98.6%
ECO103224	SPN400208	50%	99.3%	98.6%
ECO103224	SPY200056	50%	99.3%	98.6%
ECO103224	TPA100205	37%	93.1%	89.5%
ECO103224	UUR100251	39%	99.3%	98.0%
ECO103224	VCH102540	77%	100%	100%
ECO103224	YPS002485	85%	100%	100%
ECO103225	ABA100108	68%	96.6%	98.3%
ECO103225	BAN104365	54%	100%	98.3%
ECO103225	BFR100963	46%	91.5%	93.1%
ECO103225	BPT104115	49%	96.6%	93.4%
ECO103225	BBU100495	32%	93.2%	54.5%
ECO103225	BFU104042	54%	93.2%	87.3%
ECO103225	BMA107387	54%	93.2%	87.3%
ECO103225	CAC103086	55%	98.3%	100%
ECO103225	CBO100965	54%	100%	98.3%
ECO103225	CDF102795	44%	100%	95.1%
ECO103225	CDP102962	47%	93.2%	90.2%
ECO103225	EBC103644	94%	100%	100%
ECO103225	EFA205229	45%	93.2%	93.2%
ECO103225	EFM200795	45%	93.2%	93.2%
ECO103225	ECO103225	100%	100%	100%
ECO103225	HIN100776	79%	100%	100%
ECO103225	KPN300492	96%	96.6%	100%
ECO103225	LPN102267	49%	100%	96.7%
ECO103225	LMO100063	49%	100%	98.3%
ECO103225	MCA102911	66%	96.6%	96.6%
ECO103225	MAV102080	54%	89.8%	74.6%
ECO103225	MBV101607	53%	91.5%	83.1%
ECO103225	MLP101119	50%	93.2%	77.5%
ECO103225	MTU200719	53%	91.5%	83.1%
ECO103225	NGO102470	51%	94.9%	91.8%
ECO103225	NME200105	53%	94.9%	91.8%
ECO103225	PMU101397	77%	100%	100%
ECO103225	PRT100559	89%	100%	96.7%
ECO103225	PAE204243	56%	93.2%	94.8%
ECO103225	PPU108173	61%	93.2%	94.8%
ECO103225	PSY107474	56%	93.2%	94.8%
ECO103225	SPA106249	96%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103225	STY105107	96%	100%	100%
ECO103225	SAU802232	50%	100%	98.3%
ECO103225	SEP202555	47%	100%	96.7%
ECO103225	SHA100092	49%	100%	98.3%
ECO103225	SMU102834	52%	93.2%	91.7%
ECO103225	SPN400207	54%	93.2%	91.7%
ECO103225	SPY200055	49%	93.2%	91.7%
ECO103225	VCH102541	78%	94.9%	96.6%
ECO103225	YPS004281	86%	100%	100%
ECO103226	ABA100109	76%	99.4%	100%
ECO103226	BAN111381	52%	98.8%	100%
ECO103226	BAN112822	54%	99.4%	100%
ECO103226	BFR10783	52%	92.8%	90.1%
ECO103226	BPT100869	67%	93.4%	91.2%
ECO103226	BBU100494	49%	92.2%	93.3%
ECO103226	BCE102110	66%	71.9%	88.2%
ECO103226	BFU100390	66%	93.4%	90.7%
ECO103226	BMA101481	67%	93.4%	92.3%
ECO103226	CJU101594	50%	80.8%	91.8%
ECO103226	CPN200114	44%	92.2%	93.3%
ECO103226	CTR200788	43%	88.6%	90.3%
ECO103226	CAC100146	53%	97.6%	98.8%
ECO103226	CBO100463	50%	97.6%	98.8%
ECO103226	CDF100733	54%	94.0%	92.9%
ECO103226	CDP101728	59%	91.0%	73.1%
ECO103226	EBC103648	100%	99.4%	100%
ECO103226	EFA201981	54%	99.4%	100%
ECO103226	EFM200438	53%	99.4%	100%
ECO103226	ECO103226	100%	100%	100%
ECO103226	HIN100775	92%	99.4%	100%
ECO103226	HPY101284	50%	83.8%	91.5%
ECO103226	KPN300491	97%	100%	100%
ECO103226	LPN100995	62%	92.2%	91.7%
ECO103226	LMO101368	55%	94.0%	94.0%
ECO103226	MCA100160	75%	99.4%	100%
ECO103226	MAV102079	59%	91.0%	67.6%
ECO103226	MBV101605	59%	91.0%	69.1%
ECO103226	MLP101120	58%	91.0%	70.0%
ECO103226	MTU200718	59%	91.0%	69.1%
ECO103226	MGE100171	42%	97.0%	76.8%
ECO103226	MPN100649	43%	92.8%	70.8%
ECO103226	NGO100919	60%	97.6%	94.8%
ECO103226	NME200106	60%	97.6%	94.8%
ECO103226	PMU101398	92%	99.4%	100%
ECO103226	PRT100558	92%	99.4%	100%
ECO103226	PAE204244	77%	98.8%	100%
ECO103226	PPU104527	78%	91.0%	91.6%
ECO103226	PSY105833	74%	97.6%	98.2%
ECO103226	SPA104328	98%	100%	100%
ECO103226	STY101822	100%	100%	100%
ECO103226	SAU802233	55%	98.2%	98.8%
ECO103226	SEP200249	55%	98.2%	98.8%
ECO103226	SHA100091	55%	98.2%	98.8%
ECO103226	SMU100600	54%	94.0%	95.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103226	SPN400206	52%	94.0%	95.7%
ECO103226	SPY200054	54%	94.0%	95.7%
ECO103226	TPA100204	51%	94.0%	91.3%
ECO103226	UUR100250	47%	95.8%	79.3%
ECO103226	VCH102542	84%	94.6%	94.6%
ECO103226	YPS002482	95%	100%	100%
ECO103227	ABA100110	56%	99.1%	98.3%
ECO103227	BAN106991	53%	99.1%	95.8%
ECO103227	BFR100058	44%	76.9%	97.7%
ECO103227	BPT100868	57%	100%	100%
ECO103227	BBU100493	32%	95.7%	95.0%
ECO103227	BCE113907	54%	100%	100%
ECO103227	BFU100389	56%	100%	100%
ECO103227	BMA109275	55%	100%	100%
ECO103227	CJU101595	31%	97.4%	92.4%
ECO103227	CPN200113	37%	98.3%	94.3%
ECO103227	CTR200789	37%	98.3%	94.3%
ECO103227	CAC102283	48%	100%	99.1%
ECO103227	CBO100811	49%	99.1%	93.4%
ECO103227	CDF103929	48%	99.1%	95.9%
ECO103227	CDP101725	49%	98.3%	84.4%
ECO103227	EBC103652	96%	100%	100%
ECO103227	EFA201982	50%	99.1%	95.8%
ECO103227	EFM200146	50%	99.1%	95.8%
ECO103227	ECO103227	100%	100%	100%
ECO103227	HIN100774	84%	100%	100%
ECO103227	HPY101285	32%	96.6%	90.8%
ECO103227	KPN300490	100%	100%	100%
ECO103227	LPN101342	44%	100%	100%
ECO103227	LMO102391	44%	100%	96.6%
ECO103227	MCA100159	58%	99.1%	98.3%
ECO103227	MAV102077	42%	98.3%	84.4%
ECO103227	MBV101604	45%	98.3%	93.4%
ECO103227	MLP101121	40%	98.3%	94.2%
ECO103227	MTU200717	45%	98.3%	93.4%
ECO103227	MGE100170	31%	99.1%	96.5%
ECO103227	MPN100650	37%	97.4%	99.1%
ECO103227	NGO100921	53%	100%	100%
ECO103227	NME200107	53%	100%	100%
ECO103227	PMU101399	83%	100%	100%
ECO103227	PRT100557	92%	100%	100%
ECO103227	PAE204245	59%	98.3%	97.4%
ECO103227	PPU104526	59%	99.1%	98.3%
ECO103227	PSY105780	60%	85.5%	100%
ECO103227	SPA104494	89%	100%	100%
ECO103227	STY101821	99%	100%	100%
ECO103227	SAU802234	45%	100%	96.6%
ECO103227	SEP200251	45%	100%	96.7%
ECO103227	SHA100055	47%	100%	96.7%
ECO103227	SMU100601	47%	99.1%	95.8%
ECO103227	SPN400205	49%	99.1%	95.8%
ECO103227	SPY200053	48%	99.1%	95.8%
ECO103227	TPA100203	35%	99.1%	95%
ECO103227	UUR100249	43%	93.2%	91.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103227	VCH102543	83%	100%	100%
ECO103227	YPS002455	92%	100%	100%
ECO103228	ABA100111	62%	100%	100%
ECO103228	BAN102950	47%	98.9%	99.4%
ECO103228	BAN110172	50%	98.9%	98.3%
ECO103228	BFR10781	41%	98.9%	97.4%
ECO103228	BPT100867	58%	100%	100%
ECO103228	BBU100492	37%	98.9%	97.2%
ECO103228	BCE105068	57%	100%	100%
ECO103228	BFU100388	57%	100%	100%
ECO103228	BMA103347	58%	100%	100%
ECO103228	CJU101596	48%	98.9%	97.8%
ECO103228	CPN200112	42%	98.9%	96.2%
ECO103228	CTR200790	43%	98.9%	96.2%
ECO103228	CAC101071	47%	98.9%	98.3%
ECO103228	CBO102597	46%	98.9%	97.8%
ECO103228	CDF100753	48%	98.9%	97.8%
ECO103228	CDP101722	44%	98.9%	98.3%
ECO103228	EBC103655	92%	100%	100%
ECO103228	EFA201983	48%	98.9%	98.3%
ECO103228	EFM201241	46%	98.9%	98.3%
ECO103228	ECO103228	100%	100%	100%
ECO103228	HIN100773	75%	100%	100%
ECO103228	HPY101286	42%	98.9%	97.8%
ECO103228	KPN300489	100%	19.8%	100%
ECO103228	LPN100869	56%	100%	100%
ECO103228	LMO102101	46%	98.9%	98.3%
ECO103228	MCA100158	58%	100%	100%
ECO103228	MAV102075	43%	98.9%	98.3%
ECO103228	MBV101643	43%	98.9%	98.3%
ECO103228	MLP101122	42%	98.9%	98.3%
ECO103228	MTU200716	43%	98.9%	98.3%
ECO103228	MGE100169	40%	98.9%	96.7%
ECO103228	MPN100651	40%	98.9%	96.7%
ECO103228	NGO100923	59%	100%	100%
ECO103228	NME200108	59%	100%	100%
ECO103228	PMU101400	79%	100%	100%
ECO103228	PRT100556	85%	100%	100%
ECO103228	PAE204246	62%	100%	100%
ECO103228	PPU104525	62%	100%	100%
ECO103228	PSY100295	61%	100%	100%
ECO103228	SPA104330	98%	100%	100%
ECO103228	STY101820	98%	100%	100%
ECO103228	SAU802235	44%	98.9%	98.3%
ECO103228	SEP200253	45%	98.9%	98.3%
ECO103228	SHA100054	49%	58.8%	97.2%
ECO103228	SMU100602	49%	98.9%	98.3%
ECO103228	SPN400204	46%	98.9%	98.3%
ECO103228	SPY200052	45%	98.9%	98.3%
ECO103228	TPA100202	38%	98.9%	97.8%
ECO103228	UUR100248	39%	98.9%	96.7%
ECO103228	VCH102544	73%	100%	100%
ECO103228	YPS002454	89%	100%	100%
ECO103229	ABA100112	65%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103229	BAN113611	50%	98.5%	95.6%
ECO103229	BAN101892	51%	99.2%	99.2%
ECO103229	BFR10780	43%	97.7%	99.2%
ECO103229	BPT100866	67%	100%	100%
ECO103229	BBU100491	35%	99.2%	99.2%
ECO103229	BCE101537	62%	100%	100%
ECO103229	BFU100387	64%	100%	100%
ECO103229	BMA101128	64%	100%	100%
ECO103229	CJU101597	41%	97.7%	98.5%
ECO103229	CPN200111	40%	96.2%	95.5%
ECO103229	CTR200791	37%	96.2%	95.5%
ECO103229	CAC102421	53%	99.2%	99.2%
ECO103229	CBO102964	52%	99.2%	99.2%
ECO103229	CDF100752	48%	99.2%	99.2%
ECO103229	CDP101719	52%	99.2%	99.2%
ECO103229	EBC103658	97%	100%	100%
ECO103229	EFA201984	48%	99.2%	99.2%
ECO103229	EFM200970	48%	99.2%	99.2%
ECO103229	ECO103229	100%	100%	100%
ECO103229	HIN100772	86%	100%	100%
ECO103229	HPY101287	39%	97.7%	98.5%
ECO103229	KPN300573	98%	86.9%	98.3%
ECO103229	LPN100471	56%	100%	100%
ECO103229	LMO100791	48%	99.2%	99.2%
ECO103229	MCA100157	59%	100%	100%
ECO103229	MAV102073	48%	99.2%	99.2%
ECO103229	MBV101642	47%	99.2%	99.2%
ECO103229	MLP101123	45%	99.2%	99.2%
ECO103229	MTU200715	47%	99.2%	99.2%
ECO103229	MGE100168	44%	96.2%	91.5%
ECO103229	MPN100652	45%	96.2%	90.8%
ECO103229	NGO100925	71%	100%	100%
ECO103229	NME200109	71%	100%	100%
ECO103229	PMU101401	88%	100%	100%
ECO103229	PRT100555	95%	100%	100%
ECO103229	PAE204247	64%	99.2%	99.2%
ECO103229	PPU108197	63%	99.2%	99.2%
ECO103229	PSY108276	63%	99.2%	99.2%
ECO103229	SPA104332	100%	100%	100%
ECO103229	STY101809	100%	100%	100%
ECO103229	SAU802236	51%	99.2%	99.2%
ECO103229	SEP200255	50%	99.2%	99.2%
ECO103229	SHA101609	43%	72.3%	100%
ECO103229	SMU100603	51%	99.2%	99.2%
ECO103229	SPN400203	48%	99.2%	99.2%
ECO103229	SPY200051	47%	99.2%	99.2%
ECO103229	TPA100201	46%	99.2%	99.2%
ECO103229	UUR100247	46%	96.2%	97.0%
ECO103229	VCH102545	80%	100%	100%
ECO103229	YPS002453	94%	100%	100%
ECO103230	ABA100113	63%	100%	100%
ECO103230	BAN104895	55%	42.6%	70.5%
ECO103230	BAN100258	55%	42.6%	70.5%
ECO103230	BFR103418	53%	95.0%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103230	BPT104100	64%	100%	100%
ECO103230	BBU100490	44%	53.5%	73.0%
ECO103230	BCE114286	59%	100%	100%
ECO103230	BFU100386	63%	100%	100%
ECO103230	BMA106945	63%	100%	100%
ECO103230	CJU101598	51%	42.6%	70.5%
ECO103230	CPN200907	50%	100%	100%
ECO103230	CTR200165	52%	100%	100%
ECO103230	CAC102855	54%	43.6%	72.1%
ECO103230	CBO101206	48%	61.4%	88.5%
ECO103230	CDF102552	54%	43.6%	72.1%
ECO103230	CDP100129	52%	100%	100%
ECO103230	EBC103661	93%	100%	100%
ECO103230	EFA201445	44%	100%	100%
ECO103230	EFA203574	50%	100%	100%
ECO103230	EFM201806	61%	38.6%	63.9%
ECO103230	ECO103230	100%	100%	100%
ECO103230	HIN100771	91%	100%	100%
ECO103230	HPY101288	53%	42.6%	70.5%
ECO103230	KPN300574	98%	100%	100%
ECO103230	LPN101663	46%	100%	100%
ECO103230	LMO102736	50%	100%	100%
ECO103230	MCA100105	61%	100%	100%
ECO103230	MAV102072	53%	42.6%	70.5%
ECO103230	MBV100099	46%	100%	100%
ECO103230	MLP101124	53%	42.6%	70.5%
ECO103230	MTU202023	46%	100%	100%
ECO103230	MGE100167	48%	42.6%	70.5%
ECO103230	MPN100653	48%	42.6%	70.5%
ECO103230	NGO100927	60%	100%	100%
ECO103230	NME200110	60%	100%	100%
ECO103230	PMU101402	93%	100%	100%
ECO103230	PRT100554	91%	100%	100%
ECO103230	PAE204248	69%	100%	100%
ECO103230	PPU109128	63%	100%	100%
ECO103230	PSY100242	67%	100%	100%
ECO103230	SPA104333	95%	100%	100%
ECO103230	STY101808	98%	100%	100%
ECO103230	SAU801336	51%	100%	100%
ECO103230	SEP201993	51%	100%	100%
ECO103230	SHA100036	50%	100%	100%
ECO103230	SMU102003	56%	38.6%	63.9%
ECO103230	SPN400202	54%	100%	100%
ECO103230	SPY201440	42%	100%	100%
ECO103230	TPA100200	47%	43.6%	72.1%
ECO103230	UUR100246	53%	42.6%	70.5%
ECO103230	VCH102546	83%	100%	100%
ECO103230	YPS002452	89%	100%	100%
ECO103231	ABA100107	73%	85.5%	100%
ECO103231	BAN113536	53%	98.9%	98.9%
ECO103231	BAN110693	59%	100%	100%
ECO103231	BFR10778	49%	98.9%	95.1%
ECO103231	BPT100865	64%	99.4%	99.4%
ECO103231	BBU100489	59%	97.8%	96.2%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103231	BCE101479	66%	99.4%	99.4%
ECO103231	BFU100385	66%	99.4%	99.4%
ECO103231	BMA102975	65%	99.4%	99.4%
ECO103231	CJU101599	47%	100%	98.9%
ECO103231	CPN200110	51%	100%	98.9%
ECO103231	CTR200792	50%	100%	98.9%
ECO103231	CAC100782	56%	97.8%	97.2%
ECO103231	CBO103765	56%	100%	99.4%
ECO103231	CDF100751	53%	99.4%	98.9%
ECO103231	CDP101582	57%	98.9%	94.7%
ECO103231	EBC103664	98%	100%	100%
ECO103231	EFA201985	60%	100%	100%
ECO103231	EFM200921	59%	100%	100%
ECO103231	ECO103231	100%	100%	100%
ECO103231	HIN100770	90%	100%	100%
ECO103231	HPY101289	46%	100%	98.9%
ECO103231	KPN300575	100%	79.3%	100%
ECO103231	LPN102846	67%	41.3%	93.7%
ECO103231	LMO101852	60%	100%	100%
ECO103231	MCA100155	66%	99.4%	100%
ECO103231	MAV102069	57%	98.9%	94.7%
ECO103231	MBV101640	57%	98.9%	94.7%
ECO103231	MLP101125	57%	98.9%	94.7%
ECO103231	MTU200713	57%	98.9%	94.7%
ECO103231	MGE100166	54%	100%	99.4%
ECO103231	MPN100654	55%	100%	99.4%
ECO103231	NGO100929	68%	99.4%	99.4%
ECO103231	NME200111	69%	99.4%	99.4%
ECO103231	PMU101403	92%	100%	100%
ECO103231	PRT100553	95%	100%	94.2%
ECO103231	PAE204249	68%	99.4%	99.4%
ECO103231	PPU104523	67%	99.4%	99.4%
ECO103231	PSY100243	78%	46.4%	98.8%
ECO103231	SPA104334	98%	100%	100%
ECO103231	STY101807	98%	100%	100%
ECO103231	SAU802238	60%	100%	100%
ECO103231	SEP200260	60%	100%	100%
ECO103231	SHA100780	60%	100%	100%
ECO103231	SMU100604	61%	98.9%	98.3%
ECO103231	SPN400201	61%	98.9%	98.3%
ECO103231	SPY200049	61%	98.9%	98.3%
ECO103231	TPA100199	55%	96.1%	93.0%
ECO103231	UUR100245	55%	100%	97.3%
ECO103231	VCH102547	84%	100%	100%
ECO103231	YPS002451	95%	100%	100%
ECO103232	ABA102168	56%	87.5%	98.9%
ECO103232	BAN110382	53%	91.3%	92.2%
ECO103232	BAN104944	52%	95.2%	96.1%
ECO103232	BFR103505	48%	96.2%	95.3%
ECO103232	BPT104094	58%	95.2%	93.4%
ECO103232	BBU100488	42%	99.0%	100%
ECO103232	BCE110380	55%	96.2%	96.1%
ECO103232	BFU100383	60%	91.3%	91.2%
ECO103232	BMA108868	56%	96.2%	96.1%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103232	CJU101600	47%	65.4%	88.3%
ECO103232	CPN200109	44%	65.4%	59.5%
ECO103232	CTR200793	45%	61.5%	55.9%
ECO103232	CAC102906	38%	94.2%	93.4%
ECO103232	CBO100250	46%	94.2%	94.3%
ECO103232	CDF103678	51%	87.5%	89.2%
ECO103232	CDP101580	45%	96.2%	99.0%
ECO103232	EBC103629	98%	100%	100%
ECO103232	EFA205255	50%	95.2%	96.1%
ECO103232	EFM201757	53%	95.2%	96.1%
ECO103232	ECO103232	100%	100%	100%
ECO103232	HIN100769	76%	99.0%	100%
ECO103232	HPY101290	43%	67.3%	95.9%
ECO103232	KPN305017	100%	100%	100%
ECO103232	LMO101665	47%	95.2%	96.1%
ECO103232	MCA100154	51%	97.1%	96.2%
ECO103232	MAV102067	45%	96.2%	99.0%
ECO103232	MBV101639	41%	96.2%	99.0%
ECO103232	MLP101126	42%	96.2%	99.0%
ECO103232	MTU200712	41%	96.2%	99.0%
ECO103232	MGE100165	33%	96.2%	98.1%
ECO103232	MPN100655	32%	96.2%	98.2%
ECO103232	NGO100931	52%	96.2%	96.3%
ECO103232	NME200112	51%	96.2%	96.3%
ECO103232	PMU101404	76%	99.0%	100%
ECO103232	PRT103501	92%	37.5%	100%
ECO103232	PAE204250	65%	97.1%	97.1%
ECO103232	PPU104522	62%	96.2%	96.2%
ECO103232	PSY100105	65%	96.2%	96.2%
ECO103232	SPA104335	97%	100%	100%
ECO103232	STY101806	99%	100%	100%
ECO103232	SAU802239	53%	96.2%	95.2%
ECO103232	SEP200261	51%	96.2%	95.2%
ECO103232	SHA101599	53%	66.3%	95.8%
ECO103232	SMU100605	47%	95.2%	97.0%
ECO103232	SPN400200	52%	95.2%	97.0%
ECO103232	SPY200048	47%	95.2%	97.0%
ECO103232	TPA100198	45%	96.2%	95.1%
ECO103232	UUR100244	38%	94.2%	92.7%
ECO103232	VCH102548	80%	99.0%	98.1%
ECO103232	YPS002450	96%	100%	100%
ECO103233	ABA102167	83%	91.1%	96.5%
ECO103233	BAN108009	66%	100%	100%
ECO103233	BFR100659	63%	100%	100%
ECO103233	BPT100864	76%	100%	100%
ECO103233	BBU100487	60%	100%	98.4%
ECO103233	BCE113728	76%	100%	100%
ECO103233	BFU100381	77%	100%	100%
ECO103233	BMA101057	76%	100%	100%
ECO103233	CJU101601	68%	100%	100%
ECO103233	CPN200108	55%	100%	100%
ECO103233	CTR200794	57%	100%	100%
ECO103233	CAC101685	64%	100%	100%
ECO103233	CBO100636	61%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103233	CDF102312	62%	100%	100%
ECO103233	CDP101578	65%	100%	100%
ECO103233	EBC103643	98%	100%	100%
ECO103233	EFA201986	62%	100%	100%
ECO103233	EFM201996	63%	100%	100%
ECO103233	ECO103233	100%	100%	100%
ECO103233	HIN100768	94%	100%	100%
ECO103233	HPY101291	65%	100%	100%
ECO103233	KPN305016	97%	67.5%	100%
ECO103233	LMO100716	62%	100%	100%
ECO103233	MCA100153	84%	100%	100%
ECO103233	MAV102065	65%	100%	100%
ECO103233	MBV101638	65%	100%	100%
ECO103233	MLP101127	65%	92.7%	100%
ECO103233	MTU200711	65%	100%	100%
ECO103233	MGE100164	56%	100%	100%
ECO103233	MPN100656	56%	100%	100%
ECO103233	NGO100934	78%	100%	100%
ECO103233	NME200113	78%	100%	100%
ECO103233	PMU101405	94%	100%	100%
ECO103233	PRT103251	96%	97.6%	100%
ECO103233	PAE204251	85%	100%	100%
ECO103233	PPU108200	84%	100%	100%
ECO103233	PSY100106	84%	100%	100%
ECO103233	SPA104303	98%	100%	100%
ECO103233	STY101805	98%	100%	100%
ECO103233	SAU802240	66%	100%	100%
ECO103233	SEP200262	68%	100%	100%
ECO103233	SHA100778	67%	100%	85.3%
ECO103233	SMU100606	62%	100%	100%
ECO103233	SPN400199	63%	100%	100%
ECO103233	SPY200047	63%	100%	100%
ECO103233	TPA100197	64%	100%	100%
ECO103233	UUR100243	58%	100%	100%
ECO103233	VCH102549	90%	100%	100%
ECO103233	YPS002449	97%	100%	100%
ECO103234	BAN105005	52%	89.3%	86.2%
ECO103234	BFR100428	60%	86.9%	85.9%
ECO103234	BPT104067	57%	91.7%	82.8%
ECO103234	BBU100486	51%	90.5%	90.5%
ECO103234	BCE100913	61%	91.7%	85.6%
ECO103234	BFU103897	60%	41.7%	77.8%
ECO103234	BMA102592	57%	91.7%	85.6%
ECO103234	CJU101602	48%	92.9%	94.0%
ECO103234	CPN200107	45%	83.3%	80.2%
ECO103234	CTR200795	47%	84.5%	84.3%
ECO103234	CAC101333	59%	91.7%	91.7%
ECO103234	CBO101908	62%	91.7%	91.7%
ECO103234	CDF102812	65%	85.7%	85.7%
ECO103234	CDP102662	54%	94.0%	83.7%
ECO103234	EBC103647	97%	100%	100%
ECO103234	EFA205257	54%	94.0%	83.2%
ECO103234	EFM201704	55%	94.0%	89.8%
ECO103234	ECO103234	100%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103234	HIN100766	85%	100%	98.8%
ECO103234	HPY101292	50%	88.1%	86.0%
ECO103234	KPN204999	96%	100%	100%
ECO103234	LMO101712	56%	89.3%	86.2%
ECO103234	MCA101811	56%	97.6%	91.1%
ECO103234	MAV102052	57%	91.7%	65.8%
ECO103234	MBV101010	54%	91.7%	56.6%
ECO103234	MLP101128	57%	86.9%	57.5%
ECO103234	MTU200707	54%	91.7%	56.6%
ECO103234	MGE100163	41%	91.7%	91.8%
ECO103234	MPN100657	38%	91.7%	91.8%
ECO103234	NGO102122	64%	96.4%	93.1%
ECO103234	NME200114	65%	96.4%	93.1%
ECO103234	PMU101406	83%	100%	98.8%
ECO103234	PRT103498	79%	81.0%	100%
ECO103234	PAE204252	70%	94.0%	89.8%
ECO103234	PPU104520	72%	94.0%	87.8%
ECO103234	PSY107655	69%	94.0%	89.8%
ECO103234	SPA104305	82%	100%	100%
ECO103234	STY101804	98%	100%	100%
ECO103234	SAU802241	49%	89.3%	86.2%
ECO103234	SEP200263	50%	89.3%	86.2%
ECO103234	SHA100777	49%	89.3%	86.2%
ECO103234	SMU100607	56%	94.0%	91.9%
ECO103234	SPN400198	54%	94.0%	91.9%
ECO103234	SPY200046	56%	94.0%	91.9%
ECO103234	TPA100196	49%	91.7%	91.7%
ECO103234	UUR100242	48%	91.7%	91.7%
ECO103234	VCH102550	86%	97.6%	97.6%
ECO103234	YPS002447	94%	100%	100%
ECO103235	BAN110808	40%	95.2%	90.9%
ECO103235	BFR105960	29%	95.2%	92.3%
ECO103235	BPT104063	59%	98.4%	98.4%
ECO103235	BBU100485	26%	88.9%	84.8%
ECO103235	BCE113660	54%	96.8%	95.3%
ECO103235	BFU103895	57%	96.8%	93.8%
ECO103235	BMA106564	55%	96.8%	95.3%
ECO103235	CJU101603	32%	92.1%	95.1%
ECO103235	CTR200796	35%	88.9%	79.2%
ECO103235	CAC100885	51%	95.2%	89.6%
ECO103235	CBO100087	42%	95.2%	90%
ECO103235	CDF101032	48%	95.2%	84.5%
ECO103235	CDP102152	50%	92.1%	76.3%
ECO103235	EBC103651	92%	100%	100%
ECO103235	EFA205258	45%	96.8%	98.4%
ECO103235	EFM200524	45%	96.8%	98.4%
ECO103235	ECO103235	100%	100%	100%
ECO103235	HIN100765	75%	98.4%	98.4%
ECO103235	HPY101293	37%	92.1%	87.9%
ECO103235	KPN205610	93%	100%	100%
ECO103235	LMO100756	40%	95.2%	95.2%
ECO103235	MCA100557	50%	95.2%	92.3%
ECO103235	MAV108778	46%	88.9%	72.7%
ECO103235	MBV101011	46%	88.9%	72.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103235	MLP101129	48%	88.9%	69.1%
ECO103235	MTU200706	46%	88.9%	72.7%
ECO103235	MGE100162	41%	92.1%	29%
ECO103235	MPN100658	43%	92.1%	52.3%
ECO103235	NGO103266	63%	95.2%	95.2%
ECO103235	NME200115	63%	95.2%	95.2%
ECO103235	PMU101407	77%	98.4%	98.4%
ECO103235	PRT104948	91%	73.0%	100%
ECO103235	PAE204253	75%	98.4%	98.4%
ECO103235	PPU108202	72%	98.4%	96.9%
ECO103235	PSY103398	72%	98.4%	96.9%
ECO103235	SPA104959	100%	47.6%	71.4%
ECO103235	STY107537	98%	100%	100%
ECO103235	SAU802242	40%	95.2%	87.0%
ECO103235	SEP202582	40%	95.2%	87.0%
ECO103235	SHA103379	40%	95.2%	87.0%
ECO103235	SMU102853	50%	88.9%	81.2%
ECO103235	SPN400197	50%	88.9%	82.4%
ECO103235	SPY200045	48%	88.9%	82.4%
ECO103235	UUR100241	36%	92.1%	77.3%
ECO103235	VCH102551	82%	100%	100%
ECO103235	YPS005126	93%	100%	100%
ECO103236	ABA100087	75%	85.3%	98.3%
ECO103236	BAN105442	58%	97.8%	93.1%
ECO103236	BFR12478	59%	97.8%	93.1%
ECO103236	BPT104060	75%	99.3%	98.6%
ECO103236	BBU100484	55%	97.8%	97.1%
ECO103236	BCE110254	75%	97.8%	97.1%
ECO103236	BFU100274	76%	97.8%	97.1%
ECO103236	BMA108797	76%	97.8%	97.1%
ECO103236	CJU101604	67%	97.8%	95.0%
ECO103236	CPN200105	53%	97.8%	97.1%
ECO103236	CTR200797	55%	97.8%	97.1%
ECO103236	CAC102622	56%	97.8%	91.2%
ECO103236	CBO103643	56%	97.8%	91.2%
ECO103236	CDF100749	55%	97.8%	93.7%
ECO103236	CDP101572	54%	52.2%	94.7%
ECO103236	EBC103654	97%	100%	100%
ECO103236	EFA201987	53%	100%	95.1%
ECO103236	BFM200770	54%	100%	95.1%
ECO103236	ECO103236	100%	100%	100%
ECO103236	HIN100764	89%	100%	100%
ECO103236	HPY101294	62%	97.1%	94.3%
ECO103236	KPN300638	95%	91.2%	100%
ECO103236	LMO101423	55%	97.8%	93.1%
ECO103236	MCA100019	77%	100%	100%
ECO103236	MAV102093	50%	97.8%	97.1%
ECO103236	MBV101012	48%	94.9%	94.2%
ECO103236	MLP101130	49%	97.8%	97.1%
ECO103236	MTU200705	49%	97.8%	97.1%
ECO103236	MGE100161	45%	92.6%	92.0%
ECO103236	MPN100659	47%	92.6%	91.4%
ECO103236	NGO100936	79%	99.3%	98.6%
ECO103236	NME200116	79%	99.3%	98.6%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103236	PMU101408	92%	100%	100%
ECO103236	PRT100078	94%	100%	100%
ECO103236	PAE204254	77%	100%	100%
ECO103236	PPU104518	78%	100%	100%
ECO103236	PSY103397	78%	100%	100%
ECO103236	SPA104307	98%	100%	100%
ECO103236	STY101803	98%	100%	100%
ECO103236	SAU802243	54%	97.8%	93.1%
ECO103236	SEP200265	53%	97.8%	93.1%
ECO103236	SHA100775	53%	97.8%	93.1%
ECO103236	SMU100608	53%	97.8%	97.8%
ECO103236	SPN400196	53%	97.8%	97.8%
ECO103236	SPY200044	54%	97.8%	97.8%
ECO103236	TPA100194	54%	97.1%	95.7%
ECO103236	UUR100240	52%	97.8%	97.1%
ECO103236	VCH102552	87%	100%	100%
ECO103236	YPS002443	91%	100%	100%
ECO103237	ABA100086	68%	98.3%	99.1%
ECO103237	BAN112122	55%	78.1%	100%
ECO103237	BAN102487	57%	89.3%	94.5%
ECO103237	BFR10672	54%	89.7%	85.2%
ECO103237	BPT100851	61%	100%	87.1%
ECO103237	BBU100483	47%	89.7%	72.4%
ECO103237	BCE110191	62%	99.1%	87.2%
ECO103237	BFU100273	60%	100%	99.1%
ECO103237	BMA108753	62%	99.1%	87.2%
ECO103237	CJU101605	57%	98.3%	99.1%
ECO103237	CPN200104	53%	95.3%	97.8%
ECO103237	CTR200798	55%	88.4%	92.0%
ECO103237	CAC103109	55%	89.3%	94.1%
ECO103237	CBO100517	54%	95.3%	100%
ECO103237	CDF100748	51%	98.7%	82.3%
ECO103237	CDP101570	53%	98.3%	89.8%
ECO103237	EBC103657	100%	100%	100%
ECO103237	EFA201993	59%	89.3%	95.0%
ECO103237	EFM201332	57%	89.3%	95.0%
ECO103237	ECO103237	100%	100%	100%
ECO103237	HIN100763	87%	100%	100%
ECO103237	HPY101295	55%	100%	98.7%
ECO103237	KPN300639	99%	100%	100%
ECO103237	LMO101810	59%	89.3%	95.0%
ECO103237	MCA100254	63%	100%	97.9%
ECO103237	MAV102092	49%	99.1%	85.4%
ECO103237	MBV101013	49%	100%	85.4%
ECO103237	MLP101131	50%	98.3%	81.5%
ECO103237	MTU200704	49%	100%	85.4%
ECO103237	MGE100160	41%	98.7%	86.2%
ECO103237	MPN100660	41%	99.6%	87.2%
ECO103237	NGO100939	59%	98.3%	97.8%
ECO103237	NME200117	60%	98.3%	97.8%
ECO103237	PMU101409	88%	100%	100%
ECO103237	PRT103066	97%	100%	100%
ECO103237	PAE204255	73%	96.6%	98.7%
ECO103237	PPU104517	72%	98.7%	96.2%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103237	PSY103396	71%	98.7%	100%
ECO103237	SPA104309	100%	100%	100%
ECO103237	STY101802	100%	100%	100%
ECO103237	SAU802244	55%	89.3%	95.4%
ECO103237	SEP200267	53%	89.3%	95.4%
ECO103237	SHA100774	54%	89.3%	95.4%
ECO103237	SMU100609	57%	89.3%	95.4%
ECO103237	SPN400195	57%	89.3%	95.4%
ECO103237	SPY200043	57%	89.3%	95.4%
ECO103237	TPA100193	48%	89.7%	85.4%
ECO103237	UUR100239	43%	89.7%	82.5%
ECO103237	VCH102553	87%	100%	100%
ECO103237	YPS002439	98%	100%	100%
ECO103238	ABA100085	74%	97.3%	97.3%
ECO103238	BAN109858	53%	100%	97.4%
ECO103238	BAN111310	60%	100%	97.3%
ECO103238	BFR102815	46%	96.4%	91.5%
ECO103238	BPT104052	70%	97.3%	98.2%
ECO103238	BBU100482	42%	96.4%	89.2%
ECO103238	BCE103775	61%	99.1%	100%
ECO103238	BFU100272	61%	99.1%	100%
ECO103238	BMA104499	61%	99.1%	100%
ECO103238	CJU101606	35%	89.1%	66.7%
ECO103238	CPN200103	41%	96.4%	95.5%
ECO103238	CTR200799	41%	96.4%	95.5%
ECO103238	CAC102305	50%	100%	99.1%
ECO103238	CBO100872	49%	100%	99.1%
ECO103238	CDF103249	48%	100%	92.4%
ECO103238	CDP102437	52%	96.4%	88.3%
ECO103238	EBC103660	97%	100%	100%
ECO103238	EFA201995	54%	96.4%	90.6%
ECO103238	EFM202159	55%	96.4%	92.2%
ECO103238	ECO103238	100%	100%	100%
ECO103238	HIN100762	91%	100%	100%
ECO103238	HPY101296	40%	92.7%	80.3%
ECO103238	KPN300640	97%	44.5%	100%
ECO103238	LMO100543	59%	90%	83.9%
ECO103238	MCA100253	70%	99.1%	100%
ECO103238	MAV102091	54%	97.3%	59.4%
ECO103238	MBV101014	53%	97.3%	54.3%
ECO103238	MLP101132	52%	97.3%	61.1%
ECO103238	MTU200703	53%	97.3%	54.3%
ECO103238	MGE100159	44%	99.1%	75.7%
ECO103238	MPN100661	50%	99.1%	59.2%
ECO103238	NGO102695	66%	99.1%	100%
ECO103238	NME200118	66%	99.1%	100%
ECO103238	PMU101410	90%	100%	100%
ECO103238	PRT103067	95%	100%	100%
ECO103238	PAE204256	69%	100%	100%
ECO103238	PPU104507	69%	100%	100%
ECO103238	PSY107686	69%	83.6%	100%
ECO103238	SPA104311	100%	100%	100%
ECO103238	STY101801	100%	100%	100%
ECO103238	SAU802245	54%	99.1%	93.2%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103238	SEP200269	54%	99.1%	93.2%
ECO103238	SHA100773	54%	99.1%	93.2%
ECO103238	SMU100610	53%	96.4%	93.0%
ECO103238	SPN400194	54%	96.4%	93.0%
ECO103238	SPY200042	55%	96.4%	93.0%
ECO103238	TPA100192	41%	95.5%	85.5%
ECO103238	UUR100238	47%	92.7%	33.1%
ECO103238	VCH102554	81%	100%	100%
ECO103238	YPS001865	97%	100%	100%
ECO103239	ABA100084	72%	98.9%	100%
ECO103239	BAN101977	54%	95.7%	96.6%
ECO103239	BAN110916	65%	100%	100%
ECO103239	BFR104321	62%	95.7%	98.9%
ECO103239	BPT104048	70%	98.9%	100%
ECO103239	BBU100481	52%	98.9%	100%
ECO103239	BCE112635	76%	98.9%	100%
ECO103239	BFU104367	76%	98.9%	100%
ECO103239	BMA100281	76%	98.9%	100%
ECO103239	CJU101607	58%	97.8%	96.8%
ECO103239	CPN200102	57%	94.6%	98.9%
ECO103239	CTR200800	58%	94.6%	98.9%
ECO103239	CAC101096	61%	95.7%	94.6%
ECO103239	CBO102193	62%	96.7%	84.5%
ECO103239	CDF103424	59%	100%	98.9%
ECO103239	CDP101567	65%	100%	100%
ECO103239	EBC103663	100%	100%	100%
ECO103239	EFA201997	66%	100%	100%
ECO103239	EFM202484	66%	100%	100%
ECO103239	ECO103239	100%	100%	100%
ECO103239	HIN100761	90%	98.9%	100%
ECO103239	HPY101297	61%	97.8%	96.8%
ECO103239	KPN300699	98%	100%	100%
ECO103239	LMO100277	69%	100%	100%
ECO103239	MCA100252	72%	98.9%	100%
ECO103239	MAV102090	67%	100%	100%
ECO103239	MBV101015	66%	100%	98.9%
ECO103239	MLP101133	67%	100%	100%
ECO103239	MTU200702	66%	100%	98.9%
ECO103239	MGE100158	58%	94.6%	100%
ECO103239	MPN100662	58%	94.6%	100%
ECO103239	NGO102970	73%	100%	100%
ECO103239	NME200119	75%	100%	100%
ECO103239	PMU101411	90%	98.9%	100%
ECO103239	PRT100323	95%	100%	100%
ECO103239	PAE204257	82%	98.9%	100%
ECO103239	PPU111002	81%	98.9%	100%
ECO103239	PSY101086	79%	98.9%	100%
ECO103239	SPA104313	98%	100%	100%
ECO103239	STY101800	98%	100%	100%
ECO103239	SAU802246	65%	100%	100%
ECO103239	SEP200271	66%	100%	100%
ECO103239	SHA100772	66%	100%	100%
ECO103239	SMU102869	65%	41.3%	95%
ECO103239	SPN400192	67%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103239	SPY200041	66%	100%	100%
ECO103239	TPA100191	55%	95.7%	96.8%
ECO103239	UUR100237	60%	95.7%	100%
ECO103239	VCH102555	93%	100%	100%
ECO103239	YPS001864	95%	100%	100%
ECO103240	ABA100083	72%	99.3%	98.9%
ECO103240	BAN100305	61%	58.2%	99.4%
ECO103240	BFR10675	53%	100%	100%
ECO103240	BPT100850	67%	100%	99.6%
ECO103240	BBU100480	55%	100%	100%
ECO103240	BCE100228	71%	100%	99.6%
ECO103240	BFU100271	70%	100%	99.6%
ECO103240	BMA102202	70%	100%	99.6%
ECO103240	CJU101608	55%	99.3%	98.9%
ECO103240	CPN200101	55%	98.5%	98.9%
ECO103240	CTR200801	53%	98.5%	98.9%
ECO103240	CAC101509	56%	99.6%	99.3%
ECO103240	CBO101184	56%	99.3%	98.9%
ECO103240	CDF100747	57%	100%	100%
ECO103240	CDP101565	56%	99.3%	97.1%
ECO103240	EBC103628	99%	100%	100%
ECO103240	EFA201999	58%	100%	100%
ECO103240	EFM200310	59%	82.1%	98.7%
ECO103240	ECO103240	100%	100%	100%
ECO103240	HIN100760	85%	100%	100%
ECO103240	HPY101298	50%	99.3%	98.9%
ECO103240	KPN300698	98%	100%	100%
ECO103240	LMO100597	58%	100%	99.6%
ECO103240	MCA100251	72%	99.3%	98.5%
ECO103240	MAV102089	56%	99.3%	97.1%
ECO103240	MBV101016	56%	99.3%	97.1%
ECO103240	MLP101134	54%	99.3%	97.1%
ECO103240	MTU200701	56%	99.3%	97.1%
ECO103240	MGE100157	48%	99.3%	98.2%
ECO103240	MPN100663	51%	91.2%	88.9%
ECO103240	NGO101613	67%	99.3%	98.2%
ECO103240	NME200120	67%	99.3%	98.2%
ECO103240	PMU101412	86%	100%	100%
ECO103240	PRT100324	92%	100%	99.6%
ECO103240	PAE204258	79%	99.3%	99.6%
ECO103240	PPU104505	76%	99.3%	99.6%
ECO103240	PSY107059	77%	99.3%	99.6%
ECO103240	SPA104315	98%	100%	100%
ECO103240	STY101789	99%	100%	100%
ECO103240	SAU802247	58%	100%	99.6%
ECO103240	SEP200273	58%	100%	99.6%
ECO103240	SHA100771	58%	100%	99.6%
ECO103240	SPN400191	56%	100%	99.6%
ECO103240	SPY200040	56%	100%	99.6%
ECO103240	TPA100190	56%	99.3%	99.6%
ECO103240	UUR100236	53%	100%	100%
ECO103240	VCH102556	83%	100%	100%
ECO103240	YPS001863	95%	100%	99.6%
ECO103241	ABA100082	53%	93%	87.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103241	BFR102748	40%	86%	93.8%
ECO103241	BPT104043	54%	91%	92.9%
ECO103241	BBU100479	40%	85%	88.3%
ECO103241	BCE100645	54%	97%	93.3%
ECO103241	BFU103900	53%	97%	93.3%
ECO103241	BMA108040	54%	97%	93.3%
ECO103241	CJU101609	33%	74%	79.6%
ECO103241	CPN200100	33%	88%	83.8%
ECO103241	CTR200802	37%	76%	71.2%
ECO103241	CAC102428	38%	91%	92.9%
ECO103241	CBO102507	39%	89%	91.8%
ECO103241	CDF101975	48%	89%	92.7%
ECO103241	CDP102947	45%	89%	88.1%
ECO103241	EBC101608	94%	98%	100%
ECO103241	EFA205285	38%	83%	85.4%
ECO103241	ECO103241	100%	100%	100%
ECO103241	HIN100759	73%	97%	98.0%
ECO103241	HPY101299	31%	77%	82.8%
ECO103241	KPN300697	99%	100%	100%
ECO103241	LMO100631	35%	78%	81.9%
ECO103241	MCA100250	52%	95%	88.1%
ECO103241	MAV102088	37%	88%	88%
ECO103241	MBV101017	38%	88%	88%
ECO103241	MLP101135	39%	88%	88%
ECO103241	MTU200700	38%	88%	88%
ECO103241	MGE100156	27%	88%	84.9%
ECO103241	NGO102702	51%	98%	94.2%
ECO103241	NME200121	52%	98%	92.5%
ECO103241	PMU101413	74%	100%	100%
ECO103241	PRT100325	96%	100%	100%
ECO103241	PAE204259	53%	99%	100%
ECO103241	PPU102891	55%	99%	100%
ECO103241	PSY107072	54%	99%	100%
ECO103241	SPA104317	99%	100%	100%
ECO103241	STY101788	99%	100%	100%
ECO103241	SAU802248	38%	81%	87.9%
ECO103241	SEP200275	39%	81%	87.9%
ECO103241	SHA100770	40%	81%	87.9%
ECO103241	SPN400190	39%	81%	82.7%
ECO103241	SPY200039	40%	81%	82.7%
ECO103241	TPA100189	42%	84%	88.3%
ECO103241	VCH102557	81%	100%	100%
ECO103241	YPS005095	92%	100%	100%
ECO103242	ABA100081	70%	93.5%	94%
ECO103242	BFR10676	34%	97.0%	94.7%
ECO103242	BPT100849	58%	98.0%	97.6%
ECO103242	BBU100478	32%	93.0%	90.9%
ECO103242	BCE103118	56%	95.5%	93.7%
ECO103242	BFU100270	54%	100%	100%
ECO103242	BMA104332	55%	64.2%	100%
ECO103242	CJU101610	34%	87.1%	86.3%
ECO103242	CPN200099	32%	86.6%	83.0%
ECO103242	CTR200803	33%	90.5%	87.4%
ECO103242	CAC100377	41%	94.5%	92.2%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103242	CBO103307	43%	94.5%	92.2%
ECO103242	CDF100746	39%	94.5%	88.0%
ECO103242	CDP101562	38%	87.1%	81.6%
ECO103242	EBC101609	98%	100%	100%
ECO103242	EFA202001	42%	94.5%	92.3%
ECO103242	ECO103242	100%	100%	100%
ECO103242	HIN100758	83%	100%	100%
ECO103242	HPY101300	40%	86.1%	84.7%
ECO103242	KPN300696	98%	100%	100%
ECO103242	LMO102640	43%	100%	98.6%
ECO103242	MCA100249	66%	95.5%	96%
ECO103242	MAV102087	37%	92.5%	86.6%
ECO103242	MBV101018	38%	91.0%	83.0%
ECO103242	MLP101136	37%	87.1%	77.0%
ECO103242	MTU200699	38%	91.0%	83.0%
ECO103242	MGE100155	32%	86.1%	84.4%
ECO103242	MPN100665	31%	91.5%	89.2%
ECO103242	NGO101615	55%	98.5%	98.5%
ECO103242	NME200122	54%	98.5%	98.5%
ECO103242	PMU101414	87%	100%	100%
ECO103242	PRT103342	93%	100%	100%
ECO103242	PAE204260	67%	99.5%	99.5%
ECO103242	PPU104504	68%	99.5%	99.5%
ECO103242	PSY108736	68%	99.5%	99.5%
ECO103242	SPA104319	99%	100%	100%
ECO103242	STY101787	100%	100%	100%
ECO103242	SAU802249	40%	94.5%	92.3%
ECO103242	SEP200280	41%	95.0%	92.8%
ECO103242	SHA100769	40%	94.5%	92.3%
ECO103242	SPN400189	42%	94.5%	92.3%
ECO103242	SPY200038	42%	95.5%	93.2%
ECO103242	TPA100188	33%	95.0%	88.9%
ECO103242	UUR100234	35%	80.1%	78.2%
ECO103242	VCH102558	84%	100%	100%
ECO103242	YPS001862	94%	100%	100%
ECO103243	ABA100080	75%	46.9%	100%
ECO103243	BFR10677	52%	97.6%	99.5%
ECO103243	BPT100848	67%	99.5%	92.1%
ECO103243	BBU100477	45%	99.5%	100%
ECO103243	BCE112456	60%	99.0%	96.3%
ECO103243	BFU100269	59%	99.0%	95.4%
ECO103243	BMA106660	60%	99.0%	95.4%
ECO103243	CJU101611	35%	92.3%	93.2%
ECO103243	CPN200098	46%	97.1%	95.9%
ECO103243	CTR200804	43%	97.1%	95.0%
ECO103243	CAC103369	46%	99.0%	98.6%
ECO103243	CBO101061	45%	98.6%	94.9%
ECO103243	CDF100745	51%	99.5%	98.6%
ECO103243	CDP100915	50%	98.6%	94.5%
ECO103243	EBC101610	99%	100%	100%
ECO103243	EFA202003	50%	99.0%	98.1%
ECO103243	ECO103243	100%	100%	100%
ECO103243	HIN100757	85%	100%	100%
ECO103243	HPY101301	35%	92.3%	93.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103243	KPN300695	98%	44.0%	100%
ECO103243	LMO102018	46%	99.0%	98.1%
ECO103243	MCA100248	66%	100%	99.5%
ECO103243	MAV102086	50%	98.6%	96.3%
ECO103243	MBV100990	50%	98.6%	96.3%
ECO103243	MLP101137	50%	98.6%	95.9%
ECO103243	MTU200698	50%	98.6%	96.3%
ECO103243	MGE100154	39%	98.6%	80.9%
ECO103243	MPN100666	39%	98.6%	72.5%
ECO103243	NGO101617	67%	99.0%	97.7%
ECO103243	NME200123	67%	99.0%	97.7%
ECO103243	PMU101415	86%	100%	100%
ECO103243	PRT102977	92%	100%	100%
ECO103243	PAE204261	74%	99.5%	98.1%
ECO103243	PPU111511	74%	99.5%	98.1%
ECO103243	PSY106254	73%	99.5%	93.2%
ECO103243	SPA104320	95%	100%	100%
ECO103243	STY101786	98%	100%	100%
ECO103243	SAU802250	43%	98.6%	96.8%
ECO103243	SEP200281	46%	92.3%	90.9%
ECO103243	SHA100768	45%	61.2%	96.9%
ECO103243	SMU100611	53%	99.0%	97.6%
ECO103243	SPN400188	53%	99.0%	97.6%
ECO103243	SPY200037	51%	99.0%	97.6%
ECO103243	TPA100187	45%	99.5%	98.6%
ECO103243	UUR100233	41%	99.5%	89.3%
ECO103243	VCH102559	83%	100%	100%
ECO103243	YPS001861	93%	100%	100%
ECO103244	ABA100720	80%	64.1%	100%
ECO103244	BAN112470	60%	81.6%	100%
ECO103244	BFR102501	54%	97.1%	99.0%
ECO103244	BPT104019	76%	99.0%	85.7%
ECO103244	BBU100476	53%	93.2%	93.2%
ECO103244	BCE114850	76%	99.0%	82.3%
ECO103244	BFU100268	77%	99.0%	71.3%
ECO103244	BMA104676	76%	99.0%	99.0%
ECO103244	CJU101612	58%	94.2%	94.2%
ECO103244	CPN200200	66%	96.1%	94.3%
ECO103244	CTR200710	67%	96.1%	94.3%
ECO103244	CAC101769	65%	99.0%	100%
ECO103244	CBO101448	66%	99.0%	100%
ECO103244	CDF104153	60%	61.2%	100%
ECO103244	CDP100914	61%	97.1%	99.0%
ECO103244	EBC101611	98%	100%	100%
ECO103244	EFA205288	61%	99.0%	100%
ECO103244	ECO103244	100%	100%	100%
ECO103244	HIN100756	98%	100%	87.3%
ECO103244	HPY101302	57%	95.1%	94.2%
ECO103244	KPN304660	97%	100%	95.4%
ECO103244	LMO100137	63%	99.0%	100%
ECO103244	MCA101858	82%	100%	100%
ECO103244	MAV102085	61%	97.1%	99.0%
ECO103244	MBV100992	61%	97.1%	99.0%
ECO103244	MLP101138	61%	97.1%	99.0%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103244	MTU200697	61%	97.1%	99.0%
ECO103244	MGE100153	37%	93.2%	90.6%
ECO103244	MPN100667	38%	93.2%	88.9%
ECO103244	NGO102546	70%	99.0%	99.0%
ECO103244	NME200127	70%	99.0%	99.0%
ECO103244	PMU101416	98%	100%	100%
ECO103244	PRT100142	98%	100%	100%
ECO103244	PAE204262	90%	100%	100%
ECO103244	PPU104502	88%	91.3%	100%
ECO103244	PSY106273	90%	100%	83.1%
ECO103244	SPA104323	81%	100%	95.5%
ECO103244	STY101785	98%	100%	100%
ECO103244	SAU802251	62%	99.0%	100%
ECO103244	SEP200282	62%	99.0%	100%
ECO103244	SHA102423	60%	99.0%	100%
ECO103244	SMU100612	60%	99.0%	100%
ECO103244	SPN400187	61%	99.0%	100%
ECO103244	SPY200036	59%	99.0%	100%
ECO103244	TPA100186	56%	97.1%	98.0%
ECO103244	UUR100232	52%	97.1%	99.0%
ECO103244	VCH102560	93%	100%	100%
ECO103244	YPS005092	98%	100%	100%
ECO103245	ECO103245	100%	100%	100%
ECO103246	ABA103556	32%	13.1%	48.1%
ECO103246	ECO103246	100%	100%	100%
ECO103246	VCH102409	22%	60.9%	57.1%
ECO103262	ABA100233	85%	33.5%	98.5%
ECO103262	ABA100062	85%	99.5%	99.5%
ECO103262	BAN106076	75%	99.7%	99.7%
ECO103262	BFR12122	72%	99.7%	99.7%
ECO103262	BPT100044	81%	99.7%	99.7%
ECO103262	BPT100847	81%	99.7%	99.7%
ECO103262	BBU100475	64%	99.7%	98.0%
ECO103262	BCE112288	75%	15.5%	98.4%
ECO103262	BCE106056	83%	52.5%	100%
ECO103262	BCE108906	81%	99.7%	99.7%
ECO103262	BFU100267	74%	37.3%	99.3%
ECO103262	BFU100847	80%	99.7%	99.7%
ECO103262	BMA107343	79%	95.9%	100%
ECO103262	BMA106305	80%	99.7%	99.7%
ECO103262	CJU100435	73%	99.7%	99.7%
ECO103262	CPN200689	69%	99.5%	99.5%
ECO103262	CTR200588	68%	99.7%	98.5%
ECO103262	CAC103049	73%	99.7%	99.7%
ECO103262	CBO100671	69%	10.9%	95.6%
ECO103262	CBO101209	75%	59.1%	100%
ECO103262	CBO101304	73%	99.5%	99.5%
ECO103262	CDF100547	74%	99.7%	95.9%
ECO103262	CDP100912	72%	99.7%	99.7%
ECO103262	EBC101615	99%	34.0%	100%
ECO103262	EBC100362	98%	47.7%	100%
ECO103262	EBC102891	98%	100%	100%
ECO103262	EFA202006	77%	99.7%	99.7%
ECO103262	EFM100161	75%	71.3%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103262	ECO103262	100%	100%	100%
ECO103262	HIN100558	92%	99.7%	99.7%
ECO103262	HIN100613	92%	99.7%	99.7%
ECO103262	HPY101188	73%	99.7%	99.7%
ECO103262	KPN300520	98%	23.6%	100%
ECO103262	KPN300653	98%	80.2%	100%
ECO103262	KPN300869	98%	100%	100%
ECO103262	LMO102516	74%	99.5%	99.5%
ECO103262	MCA100162	82%	99.5%	99.5%
ECO103262	MAV102941	75%	99.7%	99.7%
ECO103262	MBV103318	74%	99.7%	99.7%
ECO103262	MLP101139	75%	99.7%	99.7%
ECO103262	MTU200682	74%	99.7%	99.7%
ECO103262	MGE100460	69%	99.7%	99.7%
ECO103262	MPN100177	70%	99.7%	99.7%
ECO103262	NGO101673	83%	99.7%	99.7%
ECO103262	NGO101620	83%	99.7%	99.7%
ECO103262	NME200128	84%	99.7%	99.7%
ECO103262	NME200143	84%	99.7%	99.7%
ECO103262	PMU101746	92%	99.7%	99.7%
ECO103262	PMU101357	92%	99.7%	99.7%
ECO103262	PRT100737	95%	24.6%	100%
ECO103262	PRT100321	94%	100%	100%
ECO103262	PAE204275	84%	99.7%	99.7%
ECO103262	PAE204263	84%	99.7%	99.7%
ECO103262	PPU104463	78%	76.6%	99.7%
ECO103262	PPU104501	77%	99.7%	99.7%
ECO103262	PSY107231	77%	99.7%	99.7%
ECO103262	SPA104331	98%	39.6%	100%
ECO103262	SPA102798	99%	100%	100%
ECO103262	STY101782	99%	100%	100%
ECO103262	STY102689	99%	100%	100%
ECO103262	STM102043	99%	100%	100%
ECO103262	SAU800548	75%	99.7%	99.7%
ECO103262	SEP200072	75%	99.5%	99.5%
ECO103262	SHA101389	75%	99.7%	99.7%
ECO103262	SMU101538	73%	99.5%	99.5%
ECO103262	SPN401342	72%	99.5%	99.5%
ECO103262	SPY200441	72%	99.5%	99.5%
ECO103262	TPA100185	69%	99.7%	79.6%
ECO103262	UUR100528	71%	99.2%	99.2%
ECO103262	VCH100316	87%	99.7%	99.7%
ECO103262	VCH100357	87%	99.7%	99.7%
ECO103262	YPS000510	93%	99.7%	99.7%
ECO103262	YPS001855	95%	99.7%	99.7%
ECO103263	ABA100059	72%	88.1%	99.7%
ECO103263	BAN103750	70%	8.8%	84.9%
ECO103263	BAN113143	56%	76.0%	98.1%
ECO103263	BAN108186	63%	99.4%	98.3%
ECO103263	BFR12249	60%	62.8%	98.0%
ECO103263	BPT100846	74%	100%	100%
ECO103263	BBU100539	48%	97.4%	97.4%
ECO103263	BCE101645	75%	100%	100%
ECO103263	BFU100846	74%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103263	BMA109643	74%	100%	100%
ECO103263	CJU100458	64%	99.7%	99.7%
ECO103263	CPN200199	57%	98.6%	98.8%
ECO103263	CTR200711	58%	98.0%	98.3%
ECO103263	CAC102763	61%	99.3%	99.4%
ECO103263	CBO100608	59%	99.0%	97.4%
ECO103263	CDF100548	64%	99.7%	100%
ECO103263	CDP100910	58%	98.6%	95.6%
ECO103263	EBC102893	97%	100%	100%
ECO103263	EFA202007	60%	99.9%	99.6%
ECO103263	EFM100881	25%	96.0%	96.0%
ECO103263	ECO103263	100%	100%	100%
ECO103263	HIN100559	84%	100%	100%
ECO103263	HPY101178	66%	99.7%	99.7%
ECO103263	KPN300870	97%	98.3%	100%
ECO103263	LMO102926	62%	99.9%	99.1%
ECO103263	MCA100232	72%	99.4%	98.7%
ECO103263	MAV102942	59%	98.7%	98.1%
ECO103263	MBV103317	59%	98.7%	98.1%
ECO103263	MLP101140	59%	98.7%	98.1%
ECO103263	MTU200681	59%	98.7%	98.1%
ECO103263	MGE100091	55%	99.3%	99.4%
ECO103263	MPN100604	55%	99.7%	99.9%
ECO103263	NGO101623	74%	99.7%	99.7%
ECO103263	NME200129	74%	99.7%	99.7%
ECO103263	PMU101356	84%	100%	100%
ECO103263	PRT100253	85%	99.7%	94.1%
ECO103263	PAE204264	68%	99.9%	100%
ECO103263	PPU104500	67%	99.9%	100%
ECO103263	PSY103391	66%	94.3%	100%
ECO103263	SPA102789	92%	100%	100%
ECO103263	STY101781	97%	100%	100%
ECO103263	SAU800547	59%	99.4%	99.3%
ECO103263	SEP200071	58%	99.4%	99.3%
ECO103263	SMU100688	60%	99.4%	99.1%
ECO103263	SPN400250	60%	99.4%	99.1%
ECO103263	SPY200202	60%	99.4%	99.3%
ECO103263	TPA100759	47%	98.6%	97.8%
ECO103263	UUR100529	58%	98.7%	98.8%
ECO103263	VCH100356	73%	99.9%	100%
ECO103263	YPS001853	86%	100%	100%
ECO103264	ABA100054	69%	87.2%	100%
ECO103264	BAN101047	47%	87.2%	100%
ECO103264	BAN102922	56%	87.2%	100%
ECO103264	BFR102620	54%	82.7%	85.8%
ECO103264	BPT100845	66%	87.2%	90.2%
ECO103264	BBU100385	54%	87.2%	100%
ECO103264	BCE114655	66%	87.2%	100%
ECO103264	BFU100845	67%	87.2%	100%
ECO103264	BMA108128	66%	87.2%	100%
ECO103264	CJU100457	58%	86.0%	99.4%
ECO103264	CPN200198	56%	87.2%	100%
ECO103264	CTR200712	57%	85.5%	98.7%
ECO103264	CAC101300	57%	87.2%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103264	CBO100058	56%	87.2%	90.7%
ECO103264	CDF100549	55%	87.2%	100%
ECO103264	CDP100907	54%	86.0%	99.4%
ECO103264	EBC102895	97%	87.2%	100%
ECO103264	EFA202013	53%	87.2%	100%
ECO103264	ECO103264	100%	100%	100%
ECO103264	HIN100560	89%	87.2%	100%
ECO103264	HPY101179	60%	86.0%	99.4%
ECO103264	KPN300871	93%	93.3%	100%
ECO103264	LMO101111	53%	87.2%	100%
ECO103264	MCA100231	68%	87.2%	100%
ECO103264	MAV102943	53%	87.2%	100%
ECO103264	MBV103316	53%	87.2%	100%
ECO103264	MLP101141	53%	87.2%	100%
ECO103264	MTU200680	53%	87.2%	100%
ECO103264	MGE100090	52%	82.7%	95.5%
ECO103264	MPN100605	48%	86.0%	99.4%
ECO103264	NGO101627	66%	87.2%	100%
ECO103264	NME200130	66%	87.2%	100%
ECO103264	PMU101355	89%	87.2%	100%
ECO103264	PRT100252	96%	87.2%	100%
ECO103264	PAE204265	69%	87.2%	100%
ECO103264	PPU112217	71%	87.2%	100%
ECO103264	PSY106485	85%	22.9%	100%
ECO103264	SPA102393	100%	57.5%	91.2%
ECO103264	STY101780	99%	87.2%	100%
ECO103264	SAU800546	60%	87.2%	100%
ECO103264	SEP200070	60%	87.2%	100%
ECO103264	SHA102003	45%	22.3%	100%
ECO103264	SMU100686	55%	87.2%	100%
ECO103264	SPN400249	56%	87.2%	100%
ECO103264	SPY200201	52%	87.2%	100%
ECO103264	TPA100241	57%	87.2%	100%
ECO103264	UUR100530	53%	82.7%	95.5%
ECO103264	VCH100355	87%	87.2%	100%
ECO103264	YPS001851	95%	87.2%	100%
ECO103265	ABA100053	82%	99.2%	100%
ECO103265	BAN100648	67%	100%	97.9%
ECO103265	BFR10866	76%	60.5%	88.2%
ECO103265	BPT100844	81%	99.2%	98.4%
ECO103265	BBU100386	73%	100%	100%
ECO103265	BCE108786	81%	100%	98.4%
ECO103265	BFU100844	82%	100%	98.4%
ECO103265	BMA100034	81%	100%	98.4%
ECO103265	CJU100456	75%	100%	96.9%
ECO103265	CPN200197	71%	99.2%	100%
ECO103265	CTR200713	69%	99.2%	100%
ECO103265	CAC103453	77%	99.2%	98.4%
ECO103265	CBO102727	73%	99.2%	98.4%
ECO103265	CDF102422	66%	99.2%	95.1%
ECO103265	CDP100904	73%	99.2%	90.4%
ECO103265	EBC102897	100%	100%	100%
ECO103265	EFA202015	70%	100%	100%
ECO103265	ECO103265	100%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103265	HIN100561	93%	100%	100%
ECO103265	HPY101180	71%	100%	91.9%
ECO103265	KPN200561	99%	100%	100%
ECO103265	LMO101449	68%	99.2%	99.3%
ECO103265	MCA100230	84%	100%	100%
ECO103265	MAV102944	69%	100%	100%
ECO103265	MBV103315	69%	99.2%	99.2%
ECO103265	MLP101142	68%	100%	100%
ECO103265	MTU200679	69%	99.2%	99.2%
ECO103265	MGE100089	64%	99.2%	97.8%
ECO103265	MPN100606	65%	100%	98.6%
ECO103265	NGO101631	85%	99.2%	100%
ECO103265	NME200131	86%	99.2%	100%
ECO103265	PMU101354	91%	100%	100%
ECO103265	PRT103411	84%	86.3%	100%
ECO103265	PAE204266	88%	99.2%	100%
ECO103265	PPU112031	86%	99.2%	100%
ECO103265	PSY103389	85%	99.2%	100%
ECO103265	SPA102395	100%	100%	100%
ECO103265	STY101779	100%	100%	100%
ECO103265	SAU800545	65%	99.2%	99.3%
ECO103265	SEP201889	65%	99.2%	99.3%
ECO103265	SHA101640	65%	99.2%	99.3%
ECO103265	SMU100684	70%	100%	100%
ECO103265	SPN400248	69%	100%	100%
ECO103265	SPY200200	69%	99.2%	99.3%
ECO103265	TPA100240	70%	100%	100%
ECO103265	UUR100531	63%	99.2%	96.5%
ECO103265	VCH100354	92%	100%	100%
ECO103265	YPS001825	95%	100%	100%
ECO103266	EBC102899	63%	100%	100%
ECO103266	ECO103266	100%	100%	100%
ECO103266	KPN300551	58%	100%	100%
ECO103266	PRT104907	49%	100%	97.9%
ECO103266	PAE202605	36%	98.9%	95.0%
ECO103266	PPU110115	33%	98.9%	95.9%
ECO103266	PSY104174	32%	98.9%	96.0%
ECO103266	SPA102396	68%	100%	100%
ECO103266	STY107465	68%	100%	100%
ECO103266	VCH100353	32%	95.8%	98.9%
ECO103266	YPS003640	50%	100%	100%
ECO103284	BAN111440	23%	42.5%	72.9%
ECO103284	BAN104459	24%	45%	77.1%
ECO103284	EBC103862	65%	77.5%	79.9%
ECO103284	EFM200399	27%	32.5%	83.3%
ECO103284	EFM202078	25%	91%	88.1%
ECO103284	ECO103284	100%	100%	100%
ECO103284	HIN100958	26%	86%	82.7%
ECO103284	HPY101142	27%	77%	79.1%
ECO103284	KPN301330	69%	100%	100%
ECO103284	MBV102382	31%	91%	88.6%
ECO103284	MTU203589	31%	91%	88.6%
ECO103284	NGO101050	43%	80.5%	89.1%
ECO103284	NME200004	29%	62%	59.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103284	PRT103550	24%	53%	43.3%
ECO103284	PAE201365	21%	57.5%	46.1%
ECO103284	SPA103293	86%	100%	100%
ECO103284	STY101440	87%	100%	100%
ECO103284	SMU101037	24%	89.5%	86.6%
ECO103284	SPN400494	24%	51%	41.6%
ECO103287	EBC103866	88%	98.5%	100%
ECO103287	ECO103287	100%	100%	100%
ECO103287	KPN301254	87%	98.7%	98.5%
ECO103287	SPA103290	91%	98.5%	100%
ECO103287	STY101427	91%	100%	100%
ECO103287	STM102826	90%	100%	100%
ECO103287	SPN401452	22%	94.4%	96.3%
ECO103287	YPS001674	74%	99.5%	99.7%
ECO103292	BFR104186	36%	65.5%	56.2%
ECO103292	EBC103865	70%	100%	98.2%
ECO103292	ECO103292	100%	100%	100%
ECO103292	PRT105579	58%	96.4%	96.4%
ECO103292	PPU108816	56%	94.5%	87.3%
ECO103292	SPA104676	74%	49.1%	26.2%
ECO103292	STY101409	81%	98.2%	96.4%
ECO103292	STM102840	81%	98.2%	96.4%
ECO103293	ABA104455	27%	74.0%	67.5%
ECO103293	BAN100527	22%	84.4%	91.5%
ECO103293	BAN102320	27%	93.7%	89.6%
ECO103293	BCE113620	24%	86.8%	96.2%
ECO103293	BFU102503	26%	93.7%	74.4%
ECO103293	BMA105063	24%	87.7%	90.0%
ECO103293	CAC101716	21%	28.6%	92.8%
ECO103293	CAC102152	25%	62.3%	93.7%
ECO103293	CAC102361	27%	73.2%	73.0%
ECO103293	CBO102674	24%	74.0%	78.2%
ECO103293	CBO102827	29%	94.4%	98.4%
ECO103293	CDF100725	24%	93.7%	98.2%
ECO103293	CDF104332	27%	94.4%	98.0%
ECO103293	EFA202143	26%	93.3%	97.5%
ECO103293	EFM202324	53%	96.1%	98.4%
ECO103293	ECO103293	100%	100%	100%
ECO103293	KPN308934	24%	93.3%	94.6%
ECO103293	MBV102542	22%	92.6%	96.4%
ECO103293	MTU201966	23%	95.0%	94.5%
ECO103293	PPU108666	27%	74.0%	65.4%
ECO103293	SAU801437	26%	93.9%	98.4%
ECO103293	SMU101189	23%	89.6%	91.1%
ECO103293	SPN400905	23%	87.9%	89.9%
ECO103293	SPY200012	25%	91.6%	95.2%
ECO103293	UUR100586	24%	52.2%	46.6%
ECO103298	BFR103716	27%	30.6%	24.9%
ECO103298	BFR103746	38%	26.8%	21.5%
ECO103298	BCE107571	27%	80.4%	78.5%
ECO103298	BFU103399	31%	80.4%	87.4%
ECO103298	BMA102306	29%	79.2%	88.0%
ECO103298	CAC102623	30%	85.7%	95.8%
ECO103298	EFM202446	27%	78.9%	85.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103298	ECO103298	100%	100%	100%
ECO103298	PAE202800	25%	85.7%	94.1%
ECO103298	PSY107079	25%	75.8%	80.3%
ECO103298	STY100833	28%	88.3%	97.9%
ECO103298	SEP100200	33%	28.3%	65.8%
ECO103298	VCH101187	28%	84.9%	95.3%
ECO103302	BFU106978	27%	97.9%	95.1%
ECO103302	ECO103302	100%	100%	100%
ECO103302	KPN301663	27%	97.6%	93.6%
ECO103302	LMO100231	32%	99.3%	95.1%
ECO103302	MAV102129	30%	97.9%	93.3%
ECO103302	MBV101106	31%	86.6%	87.3%
ECO103302	MTU200229	31%	97.9%	93.3%
ECO103302	MPN100346	29%	42.5%	96.5%
ECO103302	PRT104876	29%	96.6%	93.9%
ECO103302	SPA103344	28%	91.4%	89.8%
ECO103302	STY101301	27%	96.9%	93.9%
ECO103302	STM103119	27%	96.9%	93.9%
ECO103303	ECO103303	100%	100%	100%
ECO103318	EBC103853	46%	98.9%	100%
ECO103318	ECO103318	100%	100%	100%
ECO103318	KPN303186	42%	92.2%	96.9%
ECO103318	PRT105660	22%	68.3%	65.0%
ECO103318	PPU111548	28%	36.9%	33.6%
ECO103318	SPA102356	64%	98.9%	100%
ECO103318	STY101387	66%	95.9%	99.2%
ECO103318	YPS001609	25%	97.0%	92.7%
ECO103319	ABA100939	40%	89.2%	88.1%
ECO103319	BFR12422	26%	90.8%	92.7%
ECO103319	BPT100929	37%	93.9%	88.9%
ECO103319	BBU100731	26%	91.7%	77.0%
ECO103319	BCE101177	39%	92.0%	89.4%
ECO103319	BFU113279	38%	92.3%	88.7%
ECO103319	BMA101065	38%	93.8%	85.1%
ECO103319	CDF102218	34%	97.6%	83.7%
ECO103319	CDF104052	40%	20.0%	49.7%
ECO103319	EBC106485	62%	12.9%	80%
ECO103319	EBC103851	87%	96.3%	100%
ECO103319	ECO103319	100%	100%	100%
ECO103319	HIN100420	52%	96.5%	95.4%
ECO103319	KPN308134	87%	100%	100%
ECO103319	LPN102619	55%	13.5%	100%
ECO103319	LPN100189	53%	32.9%	94.9%
ECO103319	MCA100561	38%	91.3%	94.7%
ECO103319	MAV100423	29%	82.5%	71.6%
ECO103319	MTU402689	34%	50.8%	86.7%
ECO103319	NGO101656	42%	92.8%	88.6%
ECO103319	NME200606	42%	92.8%	89.3%
ECO103319	PMU101230	52%	97.6%	97.5%
ECO103319	PRT102611	67%	99.1%	100%
ECO103319	PAE205040	41%	97.4%	97.1%
ECO103319	PPU102062	40%	92.5%	97.4%
ECO103319	PSY103737	40%	97.6%	97.1%
ECO103319	SPA100496	90%	47.0%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103319	STY101386	92%	100%	100%
ECO103319	STM102876	92%	100%	100%
ECO103319	SMU101483	28%	71.6%	73.0%
ECO103319	TPA100697	32%	97.2%	87.4%
ECO103319	VCH102598	51%	99.9%	99.6%
ECO103319	YPS001608	77%	99.1%	100%
ECO103331	BAN110202	30%	69.3%	61.2%
ECO103331	CAC102979	35%	68%	65.4%
ECO103331	CBO103674	37%	64%	32.9%
ECO103331	CDF102115	37%	68%	69.9%
ECO103331	EBC103841	89%	98.7%	98.7%
ECO103331	EFA201338	39%	68%	32.5%
ECO103331	EFM201283	31%	68%	32.5%
ECO103331	ECO103331	100%	100%	100%
ECO103331	KPN303175	89%	98.7%	98.7%
ECO103331	LPN100740	52%	66.7%	66.7%
ECO103331	PRT103194	64%	98.7%	94.9%
ECO103331	PAE204357	60%	85.3%	85.3%
ECO103331	SPA103545	96%	100%	100%
ECO103331	STY101363	96%	100%	100%
ECO103331	STM102922	96%	100%	100%
ECO103331	SMU102342	35%	64%	30.4%
ECO103331	VCH102046	40%	72%	71.1%
ECO103331	YPS001553	77%	94.7%	94.7%
ECO103338	ABA105993	44%	100%	98.5%
ECO103338	BCE101546	40%	17.8%	91.9%
ECO103338	BCE111450	45%	100%	98.5%
ECO103338	BFU101199	37%	98.6%	95.2%
ECO103338	BMA102664	44%	100%	98.5%
ECO103338	EBC103745	93%	100%	100%
ECO103338	ECO103338	100%	100%	100%
ECO103338	KPN308603	92%	100%	100%
ECO103338	MAV102128	32%	16.9%	18.4%
ECO103338	PAE202320	45%	99.5%	97.8%
ECO103338	PPU105284	45%	99.5%	97.8%
ECO103338	PSY102864	46%	87.2%	97.2%
ECO103338	SPA103542	94%	99.8%	100%
ECO103338	STY101345	96%	100%	100%
ECO103338	STM102957	96%	100%	100%
ECO103338	TPA100883	28%	17.8%	53.2%
ECO103338	YPS002425	84%	100%	100%
ECO103357	ABA103909	24%	92.4%	91.7%
ECO103357	ABA102959	25%	94.9%	94.1%
ECO103357	BCE106511	45%	97.0%	95.0%
ECO103357	BFU106470	46%	97.0%	96.0%
ECO103357	BMA100278	44%	94.9%	98.4%
ECO103357	CPN200827	30%	95.4%	93.1%
ECO103357	CTR200236	31%	97.0%	93.6%
ECO103357	EBC104285	94%	100%	100%
ECO103357	ECO103357	100%	100%	100%
ECO103357	PAE205481	44%	96.4%	95.9%
ECO103357	SPY201660	34%	52.3%	48.7%
ECO103357	TPA100978	39%	95.9%	67.3%
ECO103357	YPS002413	77%	97.5%	99.0%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103366	ECO103366	100%	100%	100%
ECO103366	KPN205280	26%	87.0%	75.6%
ECO103366	YPS004146	18%	91.3%	75.3%
ECO103366	YPS004144	25%	50.7%	47.4%
ECO103370	ABA106026	32%	90.7%	87.6%
ECO103370	BPT102230	34%	97.1%	98.1%
ECO103370	BCE114044	47%	91.7%	100%
ECO103370	BFU113973	40%	97.9%	95.9%
ECO103370	BFU104436	42%	96.7%	96.0%
ECO103370	BMA104598	43%	97.2%	97.2%
ECO103370	CDF100584	30%	86.4%	89.9%
ECO103370	EBC103795	89%	100%	100%
ECO103370	ECO103370	100%	100%	100%
ECO103370	HPY101101	52%	91.6%	94.5%
ECO103370	KPN308894	87%	100%	100%
ECO103370	LPN103288	40%	90.2%	91.1%
ECO103370	MCA103579	34%	91.0%	95.7%
ECO103370	MAV104222	30%	91.2%	95.4%
ECO103370	MBV101291	32%	93.4%	90.9%
ECO103370	MTU202358	32%	93.4%	89.0%
ECO103370	NGO101177	36%	91.0%	89.1%
ECO103370	NME201155	36%	91.0%	89.3%
ECO103370	PRT102085	51%	89.7%	88.7%
ECO103370	PAE201337	46%	90.2%	93.0%
ECO103370	PPU106319	44%	90.2%	93.3%
ECO103370	PSY102725	51%	92.8%	95.1%
ECO103370	SPA103343	85%	96.7%	96.9%
ECO103370	STY101289	91%	99.8%	100%
ECO103370	SAU800209	34%	86.6%	74.6%
ECO103370	SEP201132	29%	88.1%	87.3%
ECO103370	SHA102213	29%	80.3%	82.7%
ECO103370	VCH100192	35%	96.9%	96.8%
ECO103372	ABA101262	27%	92.3%	95.8%
ECO103372	BAN102127	31%	92.7%	94.6%
ECO103372	BFR106093	28%	80.2%	91.9%
ECO103372	BPT100398	48%	96.8%	96.4%
ECO103372	BCE112820	49%	57.9%	100%
ECO103372	BFU109256	55%	96.8%	91.6%
ECO103372	BMA102573	58%	98.8%	96.8%
ECO103372	CAC101593	26%	92.7%	92.0%
ECO103372	CBO100794	24%	93.1%	91.2%
ECO103372	CBO101257	27%	94.3%	87.2%
ECO103372	CDF103994	27%	93.1%	37.8%
ECO103372	EBC103797	85%	99.6%	99.2%
ECO103372	EFA201725	36%	43.7%	44.4%
ECO103372	EFM200136	29%	92.3%	93.1%
ECO103372	ECO103372	100%	100%	100%
ECO103372	KPN300218	80%	41.3%	95.3%
ECO103372	KPN306040	89%	98.8%	99.2%
ECO103372	LPN101231	43%	87.9%	99.5%
ECO103372	LMO100188	25%	91.9%	93.5%
ECO103372	MAV103895	30%	66.0%	64.7%
ECO103372	MBV102482	37%	32.4%	29.0%
ECO103372	MLP100054	35%	32.8%	29.9%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103372	MTU200316	27%	93.5%	90.6%
ECO103372	MGE100299	26%	87.9%	89.8%
ECO103372	MPN100421	29%	61.9%	63.9%
ECO103372	PRT103897	34%	95.5%	99.6%
ECO103372	PAE202988	30%	91.9%	93.8%
ECO103372	PPU101826	31%	91.9%	94.5%
ECO103372	PSY105774	31%	95.1%	93.7%
ECO103372	SPA103341	87%	98.8%	99.2%
ECO103372	STY101288	87%	98.8%	99.2%
ECO103372	SAU800039	35%	93.1%	96.0%
ECO103372	SEP201213	35%	93.1%	96.0%
ECO103372	SHA100143	27%	80.6%	93.9%
ECO103372	SMU101565	26%	92.3%	92.3%
ECO103372	SPN400897	22%	94.7%	38.2%
ECO103372	VCH101530	28%	91.9%	94.9%
ECO103372	YPS000682	72%	98.4%	98.0%
ECO103376	BAN100778	33%	92.0%	88.4%
ECO103376	BAN112488	35%	91.1%	86.5%
ECO103376	BPT100288	56%	95.4%	95.4%
ECO103376	BCE100818	68%	99.1%	98.9%
ECO103376	BFU102498	68%	99.3%	98.0%
ECO103376	BMA103712	68%	97.3%	94.1%
ECO103376	CAC100193	29%	93.8%	91.9%
ECO103376	CBO100733	23%	93.6%	89.0%
ECO103376	CDF101162	24%	83.6%	81.0%
ECO103376	EBC103794	89%	100%	100%
ECO103376	EFA200222	24%	79.0%	79.8%
ECO103376	EFM201578	24%	95.4%	94.3%
ECO103376	ECO103376	100%	100%	100%
ECO103376	KPN304742	85%	96.6%	100%
ECO103376	LPN100476	36%	93.4%	91.1%
ECO103376	LMO100801	24%	92.2%	90.4%
ECO103376	MBV100369	25%	84.2%	82.6%
ECO103376	MTU202795	26%	84.2%	82.6%
ECO103376	PRT105550	51%	97.5%	98.4%
ECO103376	PAE202336	24%	68.7%	70.9%
ECO103376	PSY106154	30%	95.9%	85.7%
ECO103376	SPA102831	90%	96.6%	100%
ECO103376	STY101284	91%	100%	100%
ECO103376	SPN401710	22%	75.8%	79.0%
ECO103376	SPY100322	24%	44.3%	92.9%
ECO103376	VCH101525	40%	94.7%	94.7%
ECO103376	YPS000694	80%	99.1%	98.9%
ECO103394	BFR102473	26%	66.1%	66.8%
ECO103394	BPT100284	34%	98.2%	97.4%
ECO103394	BBU100050	19%	77.4%	77.7%
ECO103394	CPN200792	25%	87.3%	85.3%
ECO103394	EBC104291	91%	99.5%	99.5%
ECO103394	ECO103394	100%	100%	100%
ECO103394	HIN100842	56%	93.7%	93.2%
ECO103394	KPN304755	87%	100%	100%
ECO103394	LPN100898	48%	87.3%	86.2%
ECO103394	MTU406070	28%	30.8%	30.6%
ECO103394	NGO101678	64%	94.6%	91.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103394	NME202008	66%	94.6%	91.7%
ECO103394	PMU101889	56%	94.1%	93.6%
ECO103394	PRT103889	73%	92.3%	91.1%
ECO103394	PAE200013	61%	91.4%	93.1%
ECO103394	SPA102605	88%	94.6%	100%
ECO103394	STY100921	89%	100%	100%
ECO103394	STM103533	89%	100%	100%
ECO103394	SAU801432	29%	84.2%	80.8%
ECO103394	SEP200384	27%	82.4%	78.6%
ECO103394	SHA102541	28%	67.4%	98.1%
ECO103394	VCH102668	69%	94.6%	93.7%
ECO103394	YPS001314	75%	93.7%	93.2%
ECO103399	BFU100703	27%	96.9%	96.2%
ECO103399	CDP100600	25%	86.3%	77.1%
ECO103399	ECO103399	100%	100%	100%
ECO103399	KPN300173	77%	21.8%	100%
ECO103399	KPN304736	73%	99.8%	100%
ECO103399	MAV103759	24%	66.2%	66.2%
ECO103399	MTU403327	23%	58.4%	93.8%
ECO103399	PRT101741	44%	99.0%	98.7%
ECO103399	PPU106604	50%	93.7%	98.8%
ECO103399	SAU802467	34%	94.3%	93.2%
ECO103399	SEP200050	35%	92.7%	91.7%
ECO103399	SHA102341	24%	97.7%	98.1%
ECO103399	SHA102504	25%	96.0%	96.2%
ECO103399	SPY201537	27%	71.8%	69.0%
ECO103399	VCH103812	25%	88.0%	86.0%
ECO103405	ABA100477	25%	23.8%	97.4%
ECO103405	ABA100225	26%	66.7%	56.5%
ECO103405	BAN104847	19%	21.3%	3.7%
ECO103405	BAN109223	26%	10.2%	65.6%
ECO103405	BAN101440	29%	7.8%	44.3%
ECO103405	BAN110288	24%	22.7%	18.6%
ECO103405	BFR104422	62%	1.9%	27%
ECO103405	BCE104951	26%	27.4%	38.7%
ECO103405	BCE108121	25%	30.0%	70.0%
ECO103405	BFU107935	28%	23.7%	41.6%
ECO103405	BFU100092	47%	6.2%	98.9%
ECO103405	BFU100109	27%	14.2%	55.1%
ECO103405	BFU102581	29%	10.0%	4.6%
ECO103405	BMA107682	25%	49.6%	25.9%
ECO103405	CAC100404	25%	9.6%	44.7%
ECO103405	EBC107494	28%	7.4%	75%
ECO103405	EBC103412	28%	12.3%	35.0%
ECO103405	EBC104888	27%	24.7%	62.3%
ECO103405	ECO100686	92%	24.0%	70.2%
ECO103405	ECO101427	74%	39.5%	82.3%
ECO103405	ECO100488	74%	99.7%	99.6%
ECO103405	ECO100683	96%	88.4%	89.3%
ECO103405	ECO103515	98%	88.6%	90.8%
ECO103405	ECO103405	100%	100%	100%
ECO103405	PRT103688	31%	7.4%	73.6%
ECO103405	PRT103361	34%	8.0%	78.0%
ECO103405	PRT103421	25%	54.9%	65.1%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103405	PAE202682	33%	88.4%	88.7%
ECO103405	PPU107712	31%	7.6%	93.1%
ECO103405	PPU110484	27%	25.4%	83.0%
ECO103405	PPU109654	25%	2.7%	84.4%
ECO103405	PPU107101	39%	3.9%	5.5%
ECO103405	PPU109653	28%	41.5%	95.3%
ECO103405	PPU109652	26%	55.2%	54.6%
ECO103405	PPU110482	26%	11.0%	5.4%
ECO103405	PSY108533	34%	5.0%	83.6%
ECO103405	PSY101322	57%	4.2%	24.3%
ECO103405	PSY105816	45%	7.3%	45.7%
ECO103405	PSY102083	25%	13.5%	11.8%
ECO103405	SPA106438	45%	6.0%	5.5%
ECO103405	SPA100247	28%	49.2%	89.9%
ECO103405	STY104094	26%	50.1%	33.3%
ECO103405	STY104095	30%	24.1%	74.9%
ECO103405	STM103807	31%	15.1%	87.4%
ECO103405	STM103806	26%	50.1%	33.1%
ECO103405	YPS002860	25%	85.4%	75.9%
ECO103408	BAN101523	19%	47.7%	51.7%
ECO103408	BAN101319	22%	96.8%	97.4%
ECO103408	BCE103943	62%	99.5%	99.7%
ECO103408	BFU110636	64%	99.7%	100%
ECO103408	BMA106069	62%	99.7%	100%
ECO103408	CDF103530	22%	90.7%	87.4%
ECO103408	ECO103408	100%	100%	100%
ECO103408	KPN302968	88%	99.7%	100%
ECO103408	MLP101401	24%	42.9%	59.8%
ECO103408	MTU402591	25%	37.6%	30.3%
ECO103408	PMU101981	40%	98.1%	98.1%
ECO103408	PRT102404	74%	100%	100%
ECO103408	PAE205225	69%	99.7%	100%
ECO103408	PPU109044	49%	99.2%	100%
ECO103408	SPA101047	86%	97.1%	100%
ECO103408	SAU802643	23%	46.1%	16.5%
ECO103408	VCH101585	20%	96.3%	91.7%
ECO103414	BFR10501	46%	29.0%	97.3%
ECO103414	CAC102057	24%	46.5%	80.3%
ECO103414	EFM200286	26%	31.3%	34.4%
ECO103414	ECO103414	100%	100%	100%
ECO103414	SAU801442	37%	15.1%	13.0%
ECO103422	ABA100240	38%	99.6%	100%
ECO103422	BPT100396	43%	94.3%	94.4%
ECO103422	BCE102136	47%	92.9%	93.2%
ECO103422	BFU109218	46%	92.9%	75.3%
ECO103422	BMA105078	47%	92.9%	84.8%
ECO103422	EBC103766	91%	100%	100%
ECO103422	ECO103422	100%	100%	100%
ECO103422	HIN100421	66%	100%	100%
ECO103422	KPN300080	91%	40.4%	100%
ECO103422	KPN306391	91%	100%	100%
ECO103422	LPN102191	40%	96.8%	95.7%
ECO103422	MCA100718	29%	99.6%	100%
ECO103422	NGO101163	43%	92.9%	86.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103422	NME201159	43%	92.9%	93.2%
ECO103422	PMU101234	68%	100%	100%
ECO103422	PRT104285	74%	100%	100%
ECO103422	PAE205014	41%	99.6%	100%
ECO103422	PPU104709	43%	99.6%	100%
ECO103422	PSY102791	40%	99.6%	100%
ECO103422	SPA101521	91%	100%	100%
ECO103422	STY100851	92%	100%	100%
ECO103422	STM103579	92%	100%	100%
ECO103422	VCH100185	63%	100%	100%
ECO103422	YPS002520	78%	100%	100%
ECO103423	BPT102974	44%	100%	99.3%
ECO103423	BCE111388	40%	99.1%	98.0%
ECO103423	BMA105613	42%	99.1%	97.6%
ECO103423	EBC103768	92%	100%	100%
ECO103423	EFA200772	59%	99.6%	99.8%
ECO103423	EFM202592	57%	99.1%	99.3%
ECO103423	ECO103423	100%	100%	100%
ECO103423	HIN100154	73%	100%	100%
ECO103423	KPN308114	92%	100%	100%
ECO103423	LPN100559	51%	99.6%	99.3%
ECO103423	LMO100940	69%	100%	100%
ECO103423	MCA101240	67%	100%	100%
ECO103423	MBV100540	30%	97.8%	97.2%
ECO103423	MTU202817	30%	97.8%	97.2%
ECO103423	PMU101235	78%	100%	100%
ECO103423	PRT104768	86%	100%	100%
ECO103423	PAE202023	44%	100%	99.1%
ECO103423	PPU110449	45%	99.1%	98.7%
ECO103423	PSY105457	43%	84.7%	95.0%
ECO103423	SPA101522	91%	49.1%	100%
ECO103423	STY100839	94%	100%	100%
ECO103423	STM103581	94%	100%	100%
ECO103423	SMU100200	63%	100%	100%
ECO103423	SPN400692	61%	99.6%	99.8%
ECO103423	SPY200604	63%	99.1%	99.1%
ECO103423	VCH100184	73%	99.8%	99.1%
ECO103423	YPS002524	85%	100%	100%
ECO103424	ABA101438	51%	67.5%	72.5%
ECO103424	BAN101080	40%	61.5%	71.3%
ECO103424	BPT105662	32%	58.1%	59.8%
ECO103424	BCE103229	41%	57.3%	62.6%
ECO103424	BFU109350	36%	66.7%	62.9%
ECO103424	CJU101467	36%	47.0%	93.2%
ECO103424	CAC103713	43%	55.6%	52.5%
ECO103424	CBO102678	40%	57.3%	61.7%
ECO103424	CDF101466	37%	56.4%	53.7%
ECO103424	CDP100817	40%	55.6%	74.2%
ECO103424	EBC100218	71%	70.9%	74.8%
ECO103424	EBC102830	61%	89.7%	99.1%
ECO103424	EFA200371	43%	59.0%	71.6%
ECO103424	ECO103424	100%	100%	100%
ECO103424	KPN303338	77%	86.3%	92.7%
ECO103424	LMO102929	40%	57.3%	60.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103424	MAV105419	37%	59.0%	50.7%
ECO103424	MBV100521	44%	56.4%	54.0%
ECO103424	MLP100498	36%	59.0%	48.6%
ECO103424	MTU202605	44%	56.4%	54.0%
ECO103424	NGO102340	30%	58.1%	66.0%
ECO103424	PRT104823	62%	86.3%	91.0%
ECO103424	PAE202275	55%	79.5%	80.2%
ECO103424	PPU109423	57%	70.1%	71.3%
ECO103424	SAU801773	44%	57.3%	63.5%
ECO103424	SEP200558	43%	57.3%	63.5%
ECO103424	SHA102314	47%	59.8%	64.8%
ECO103424	SMU101184	25%	59.8%	75%
ECO103424	SPY201653	30%	55.6%	58.0%
ECO103424	VCH101049	46%	86.3%	91.2%
ECO103424	YPS000049	60%	100%	100%
ECO103451	ABA100014	63%	27.8%	95.7%
ECO103451	ABA100763	71%	97.0%	94.9%
ECO103451	BCE107211	63%	94.9%	96.4%
ECO103451	BFU109266	63%	94.9%	96.9%
ECO103451	BMA109143	61%	97.0%	97.0%
ECO103451	CJU101117	45%	96.3%	93.9%
ECO103451	CPN200221	33%	92.8%	96.1%
ECO103451	CTR200671	31%	94.9%	98.5%
ECO103451	CBO102516	25%	91.8%	92.8%
ECO103451	EBC104183	92%	100%	100%
ECO103451	ECO103451	100%	100%	100%
ECO103451	KPN304259	93%	100%	98.2%
ECO103451	LPN100722	48%	94.9%	94.9%
ECO103451	MBV101054	46%	96.0%	83.7%
ECO103451	MTU202407	46%	96.0%	83.7%
ECO103451	PAE201182	77%	95.6%	93.8%
ECO103451	PPU108087	76%	96.3%	93.6%
ECO103451	PSY104546	79%	95.8%	91.1%
ECO103451	SPA101566	93%	100%	100%
ECO103451	STY100803	94%	100%	100%
ECO103451	YPS002604	86%	97.4%	97.2%
ECO103452	EBC104185	77%	99.5%	97.0%
ECO103452	ECO103452	100%	100%	100%
ECO103452	KPN304258	68%	99.5%	97.0%
ECO103452	PRT103877	38%	32.9%	89.8%
ECO103452	SPA101565	76%	74.8%	100%
ECO103452	STY100801	84%	100%	99.1%
ECO103452	YPS002613	48%	99.4%	97.2%
ECO103453	ABA105278	27%	15.3%	79.8%
ECO103453	BAN107265	25%	11.3%	30.5%
ECO103453	BFR11466	24%	14.9%	63.2%
ECO103453	BPT100623	22%	58.0%	19.9%
ECO103453	BBU100194	34%	6.4%	65.2%
ECO103453	BCE105408	28%	0.7%	36.2%
ECO103453	BFU103167	26%	66.4%	35.2%
ECO103453	BMA106265	31%	4.6%	32.7%
ECO103453	CTR200055	23%	14.5%	57.0%
ECO103453	CAC103237	22%	13.5%	46.9%
ECO103453	CDP102065	22%	11.2%	41.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103453	EBC105028	71%	81.5%	100%
ECO103453	ECO103453	100%	100%	100%
ECO103453	KPN304293	67%	99.9%	100%
ECO103453	LMO101740	22%	14.8%	37.6%
ECO103453	PRT101998	42%	74.6%	97.6%
ECO103453	PPU111885	37%	95.0%	98.1%
ECO103453	PSY100822	26%	7.9%	28.3%
ECO103453	SPA100412	70%	39.1%	59.1%
ECO103453	SAU101362	31%	5.2%	27.5%
ECO103453	TPA100066	32%	11.7%	67.7%
ECO103453	VCH101588	25%	10.1%	44.3%
ECO103454	BAN104131	27%	25.5%	21.4%
ECO103454	BAN108214	24%	28.5%	29.9%
ECO103454	BCE102182	49%	93.8%	81.5%
ECO103454	BFU103168	42%	92.4%	91.6%
ECO103454	BMA109533	52%	42.9%	100%
ECO103454	BMA103069	47%	95.1%	88.7%
ECO103454	EBC104189	73%	99.7%	99.7%
ECO103454	ECO103454	100%	100%	100%
ECO103454	KPN300078	72%	31.5%	100%
ECO103454	KPN304291	72%	100%	99.7%
ECO103454	PRT102683	30%	67.4%	71.9%
ECO103454	PPU111883	47%	99.2%	99.2%
ECO103454	PSY100824	41%	98.4%	94.3%
ECO103454	SPA100719	77%	99.7%	99.7%
ECO103454	STY100795	81%	99.7%	99.5%
ECO103454	SMU100322	25%	79.3%	82.1%
ECO103461	BCE109623	35%	95.2%	98.8%
ECO103461	BMA103660	35%	95.2%	98.8%
ECO103461	EBC104191	83%	100%	100%
ECO103461	ECO103461	100%	100%	100%
ECO103461	KPN307938	80%	5.4%	100%
ECO103461	KPN308657	74%	99.1%	99.3%
ECO103461	PRT100405	49%	97.7%	98.2%
ECO103461	PPU111873	45%	98.2%	100%
ECO103461	SPA106506	84%	54.4%	100%
ECO103461	STY105426	84%	100%	100%
ECO103461	STM106756	84%	100%	100%
ECO103461	YPS003633	41%	7.7%	5.3%
ECO103462	BFU109953	25%	25.8%	22.3%
ECO103462	ECO103462	100%	100%	100%
ECO103462	KPN106090	46%	40.4%	90%
ECO103462	SPA101762	85%	100%	100%
ECO103462	STY100775	85%	100%	100%
ECO103462	STM103692	85%	100%	100%
ECO103462	YPS002670	62%	98.8%	97.7%
ECO103466	BCE108241	65%	100%	100%
ECO103466	BFU106008	64%	100%	100%
ECO103466	BMA106393	65%	100%	100%
ECO103466	CJU101489	26%	96.2%	97.1%
ECO103466	CAC100708	33%	99.1%	99.4%
ECO103466	CAC101801	37%	99.1%	99.1%
ECO103466	CAC101940	35%	99.7%	100%
ECO103466	CDP100963	38%	99.4%	99.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103466	EBC101783	96%	91.4%	98.7%
ECO103466	ECO103466	100%	100%	100%
ECO103466	HIN101160	60%	99.4%	100%
ECO103466	HPY100295	48%	99.1%	99.4%
ECO103466	KPN304272	93%	91.2%	98.4%
ECO103466	LPN103397	29%	99.1%	99.4%
ECO103466	MCA100667	28%	69.3%	41.8%
ECO103466	MAV102745	37%	98.5%	98.7%
ECO103466	MBV101684	37%	98.5%	98.7%
ECO103466	MTU203611	37%	98.5%	98.7%
ECO103466	PMU100237	60%	99.4%	99.7%
ECO103466	PRT105623	85%	100%	100%
ECO103466	PAE204501	64%	100%	100%
ECO103466	PPU101447	64%	100%	100%
ECO103466	PSY104822	63%	100%	100%
ECO103466	SPA102841	94%	93.8%	100%
ECO103466	STY100767	97%	100%	100%
ECO103466	SAU504414	32%	99.1%	70.1%
ECO103466	YPS002639	87%	91.2%	98.1%
ECO103467	BCE104912	54%	96.8%	95.6%
ECO103467	BFU115490	52%	95.9%	93.8%
ECO103467	BFU113558	56%	97.2%	96.1%
ECO103467	BMA100120	54%	96.8%	90.2%
ECO103467	CAC102581	48%	9.3%	22.9%
ECO103467	CAC102670	25%	89.2%	83.4%
ECO103467	CAC101493	25%	79.8%	75.2%
ECO103467	CBO100751	26%	83.7%	79.5%
ECO103467	CBO101097	27%	91.2%	86.8%
ECO103467	CBO101308	26%	93.6%	87.5%
ECO103467	CDF101830	19%	53.5%	45.4%
ECO103467	CDF101269	27%	98.3%	97.3%
ECO103467	CDP101702	29%	61.7%	56.5%
ECO103467	EBC100767	91%	100%	100%
ECO103467	EFM101064	24%	53.3%	68.0%
ECO103467	ECO103467	100%	100%	100%
ECO103467	HIN100833	54%	96.6%	94.0%
ECO103467	HPY100294	39%	94.4%	91.1%
ECO103467	KPN300418	89%	29.3%	84.9%
ECO103467	KPN304271	91%	100%	98.0%
ECO103467	LPN103438	24%	57.0%	81.0%
ECO103467	PMU100236	67%	98.3%	99.2%
ECO103467	PRT105891	80%	100%	100%
ECO103467	PAE204498	53%	94.6%	94.9%
ECO103467	PAE204494	52%	97.6%	96.8%
ECO103467	PPU104151	52%	97.8%	98.0%
ECO103467	PSY104769	53%	97.8%	96.9%
ECO103467	SPA102842	92%	96.6%	100%
ECO103467	STY100765	93%	100%	100%
ECO103467	SAU602660	25%	92.5%	90.0%
ECO103467	YPS002641	84%	100%	100%
ECO103468	EBC100465	78%	64.8%	99.7%
ECO103468	ECO103468	100%	100%	100%
ECO103468	KPN303031	82%	96.2%	99.3%
ECO103468	PRT105266	50%	94.9%	98.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103468	SPA102846	86%	98.8%	97.4%
ECO103468	STY100745	84%	97.9%	99.8%
ECO103468	YPS002684	63%	96.7%	98.6%
ECO103478	BAN108883	66%	94.3%	100%
ECO103478	BAN105755	69%	94.3%	97.0%
ECO103478	CAC100946	62%	91.4%	96.9%
ECO103478	CBO101002	64%	91.4%	96.9%
ECO103478	CDF100848	65%	91.4%	95.5%
ECO103478	CDF100586	67%	91.4%	95.5%
ECO103478	CDF103776	67%	91.4%	95.5%
ECO103478	EBC104565	95%	100%	100%
ECO103478	EFA200173	42%	90%	92.5%
ECO103478	EFA202387	69%	90%	93.9%
ECO103478	EFM101712	67%	87.1%	92.3%
ECO103478	EFM101550	67%	87.1%	92.3%
ECO103478	EFM101770	67%	87.1%	90.9%
ECO103478	ECO103478	100%	100%	100%
ECO103478	KPN300213	100%	77.1%	100%
ECO103478	KPN303047	100%	100%	100%
ECO103478	LMO102272	68%	87.1%	90.9%
ECO103478	MAV105135	65%	91.4%	95.5%
ECO103478	PRT104862	74%	100%	100%
ECO103478	PRT100460	77%	100%	100%
ECO103478	PRT101016	78%	100%	100%
ECO103478	PAE203264	59%	95.7%	95.7%
ECO103478	PPU111381	59%	95.7%	95.7%
ECO103478	PSY108061	62%	91.4%	100%
ECO103478	SPA102026	100%	100%	100%
ECO103478	STY100718	100%	100%	100%
ECO103478	STM103774	100%	100%	100%
ECO103478	SAU800816	67%	91.4%	95.5%
ECO103479	BFR103841	20%	85.0%	85.7%
ECO103479	BCE103351	26%	46.2%	93.0%
ECO103479	BCE106925	30%	48.0%	69.0%
ECO103479	BCE114303	28%	62.4%	69.5%
ECO103479	BCE114066	28%	62.4%	75.5%
ECO103479	BCE101996	30%	61.3%	95.7%
ECO103479	BCE114648	30%	61.3%	95.7%
ECO103479	BCE110494	28%	78.0%	93.6%
ECO103479	BCE100189	29%	78.0%	93.6%
ECO103479	BCE106087	29%	78.0%	93.6%
ECO103479	BCE101088	30%	94.2%	91.4%
ECO103479	BFU100233	28%	94.2%	91.4%
ECO103479	BMA108532	32%	94.2%	95.3%
ECO103479	BMA106321	32%	94.2%	89.0%
ECO103479	CBO100985	22%	51.4%	73.5%
ECO103479	CDP102415	23%	89.6%	88.8%
ECO103479	CDP101144	23%	89.6%	88.8%
ECO103479	CDP102452	23%	89.6%	88.8%
ECO103479	CDP101135	23%	89.6%	88.8%
ECO103479	CDP101982	35%	96.0%	90.6%
ECO103479	CDP102843	20%	89.6%	88.8%
ECO103479	EBC101067	59%	96.5%	98.8%
ECO103479	EBC101652	95%	83.2%	92.9%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103479	EBC104471	94%	100%	100%
ECO103479	EFA200870	24%	94.2%	86.5%
ECO103479	EFM202055	30%	91.9%	88.6%
ECO103479	EFM200192	30%	94.2%	85.4%
ECO103479	EFM201962	30%	94.2%	84.0%
ECO103479	EFM201089	30%	94.2%	85.4%
ECO103479	ECO103479	100%	100%	100%
ECO103479	HIN101685	29%	32.4%	60.6%
ECO103479	KPN302648	41%	68.2%	82.3%
ECO103479	KPN301346	37%	96.5%	94.2%
ECO103479	KPN306050	37%	99.4%	97.1%
ECO103479	KPN306422	37%	99.4%	95.5%
ECO103479	MTU405844	36%	27.7%	88.7%
ECO103479	NGO101258	28%	83.8%	81.4%
ECO103479	NGO101211	28%	83.8%	81.4%
ECO103479	PRT103503	96%	66.5%	100%
ECO103479	PSY107047	24%	97.7%	95.9%
ECO103479	PSY109085	24%	97.7%	71.3%
ECO103479	PSY106353	24%	97.7%	85.9%
ECO103479	PSY101205	24%	97.7%	74.5%
ECO103479	PSY106020	24%	97.7%	95.9%
ECO103479	SAU502782	26%	42.2%	41.5%
ECO103479	SAU500044	28%	68.2%	2.1%
ECO103479	SAU502067	28%	68.2%	2.0%
ECO103479	SAU500005	28%	68.2%	2.0%
ECO103479	SAU500516	27%	65.3%	23.1%
ECO103479	SMU101315	20%	51.4%	19.2%
ECO103479	SMU101317	21%	86.7%	83.1%
ECO103479	SMU101999	21%	86.7%	83.1%
ECO103479	SMU101889	21%	86.7%	83.1%
ECO103479	SMU101940	21%	86.7%	74.9%
ECO103479	SMU101868	21%	86.7%	83.1%
ECO103479	SPN102057	20%	54.3%	65.5%
ECO103479	SPN102327	20%	54.3%	65.5%
ECO103479	SPN103482	20%	54.3%	65.5%
ECO103479	SPN102932	20%	54.3%	65.5%
ECO103479	SPY201024	21%	82.7%	78.4%
ECO103479	SPY200151	21%	82.7%	78.4%
ECO103479	YPS002400	30%	39.3%	98.5%
ECO103479	YPS003294	26%	55.5%	86.5%
ECO103479	YPS003683	27%	94.2%	91.2%
ECO103479	YPS003696	27%	94.2%	91.2%
ECO103479	YPS003677	27%	94.2%	91.2%
ECO103479	YPS003267	27%	94.2%	87.6%
ECO103479	YPS004286	27%	94.2%	91.2%
ECO103479	YPS003702	27%	94.2%	91.2%
ECO103479	YPS003739	27%	94.2%	91.2%
ECO103480	BAN100066	27%	42.0%	46.9%
ECO103480	BAN107672	27%	83.7%	96.8%
ECO103480	BAN101189	27%	92.2%	93.6%
ECO103480	BFR11001	48%	96.1%	98.6%
ECO103480	BPT105636	26%	25.8%	35.3%
ECO103480	BPT101318	27%	91.5%	74.5%
ECO103480	BCE103148	53%	15.2%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103480	BCE109512	51%	23.3%	100%
ECO103480	BCE106326	57%	29.3%	95.4%
ECO103480	BCE101065	59%	27.2%	93.9%
ECO103480	BCE104439	57%	29.3%	95.4%
ECO103480	BCE102008	56%	39.2%	98.2%
ECO103480	BCE101347	57%	38.5%	96.5%
ECO103480	BCE112720	55%	42.4%	95.2%
ECO103480	BCE112765	55%	42.4%	96%
ECO103480	BCE113320	53%	68.6%	69.8%
ECO103480	BCE104962	56%	91.9%	98.9%
ECO103480	BCE114240	56%	96.8%	98.6%
ECO103480	BCE104151	57%	96.8%	98.6%
ECO103480	BFU100183	43%	16.3%	86.8%
ECO103480	BFU100232	53%	96.5%	98.9%
ECO103480	BMA107808	50%	47.0%	97.1%
ECO103480	CDP101289	48%	24.0%	91.9%
ECO103480	CDP101898	53%	25.1%	95.9%
ECO103480	CDP102491	48%	43.8%	66.5%
ECO103480	CDP101469	46%	67.5%	94.1%
ECO103480	CDP101278	47%	67.5%	94.1%
ECO103480	CDP101146	47%	67.5%	94.1%
ECO103480	CDP100854	46%	69.3%	96.6%
ECO103480	CDP100589	43%	92.9%	98.1%
ECO103480	CDP101134	45%	92.9%	97.4%
ECO103480	EBC104413	93%	32.5%	100%
ECO103480	EBC104468	94%	100%	100%
ECO103480	EFA200869	41%	89.4%	99.6%
ECO103480	EFM202052	57%	66.1%	99.5%
ECO103480	EFM201053	55%	92.9%	98.1%
ECO103480	EFM201924	55%	92.9%	98.1%
ECO103480	EFM200512	53%	98.2%	100%
ECO103480	ECO103480	100%	100%	100%
ECO103480	HIN101249	53%	27.6%	84.6%
ECO103480	HIN100472	53%	26.9%	64.4%
ECO103480	HIN101686	56%	74.2%	96.8%
ECO103480	KPN306758	68%	41.7%	95.9%
ECO103480	KPN303368	68%	64.7%	92.9%
ECO103480	KPN308870	65%	89.8%	97.3%
ECO103480	KPN306624	62%	97.2%	97.9%
ECO103480	LMO102606	33%	97.2%	96.4%
ECO103480	LMO100732	33%	97.2%	98.9%
ECO103480	MBV104142	27%	92.2%	91.8%
ECO103480	MTU202443	27%	92.2%	78.0%
ECO103480	MTU200790	27%	92.2%	86.5%
ECO103480	MTU201352	27%	92.2%	91.8%
ECO103480	MTU201734	27%	92.2%	91.8%
ECO103480	MTU201742	27%	92.2%	91.8%
ECO103480	MTU202073	27%	92.2%	86.5%
ECO103480	MTU202133	27%	92.2%	78.0%
ECO103480	MTU202245	27%	92.2%	86.5%
ECO103480	MTU203144	27%	92.2%	86.5%
ECO103480	MTU203335	27%	92.2%	91.8%
ECO103480	MTU202612	27%	92.2%	82.3%
ECO103480	MTU202776	27%	92.2%	86.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103480	MTU203142	27%	92.2%	86.5%
ECO103480	MTU203428	27%	92.2%	78.0%
ECO103480	MTU203283	27%	92.2%	86.5%
ECO103480	MTU202320	27%	92.2%	86.5%
ECO103480	NGO101257	54%	91.9%	97.4%
ECO103480	NGO101209	54%	92.9%	96.3%
ECO103480	NME201142	42%	92.9%	96.0%
ECO103480	PRT105818	98%	28.6%	98.8%
ECO103480	PSY102003	58%	96.1%	97.5%
ECO103480	SPA102022	62%	49.5%	100%
ECO103480	SAU801804	29%	64.0%	95.2%
ECO103480	SEP200536	36%	89.8%	98.4%
ECO103480	SMU100679	50%	95.1%	98.2%
ECO103480	SMU102069	51%	95.1%	98.2%
ECO103480	SMU102045	51%	95.1%	98.2%
ECO103480	SMU101759	51%	95.1%	98.2%
ECO103480	SMU101315	51%	95.1%	58.3%
ECO103480	SMU102094	51%	95.1%	98.2%
ECO103480	SPN400754	51%	55.5%	98.8%
ECO103480	SPN401338	50%	55.5%	98.8%
ECO103480	SPN401445	50%	55.5%	98.8%
ECO103480	SPN400496	54%	38.5%	85.3%
ECO103480	SPN400885	51%	27.9%	100%
ECO103480	SPN400352	50%	20.5%	98.4%
ECO103480	SPN400495	44%	12.0%	97.1%
ECO103480	SPY201025	47%	93.3%	99.3%
ECO103480	SPY200150	47%	93.3%	99.3%
ECO103480	UUR100374	28%	66.8%	92.8%
ECO103480	YPS003775	48%	89.8%	97.7%
ECO103480	YPS003983	48%	89.8%	97.7%
ECO103480	YPS003822	48%	89.8%	97.7%
ECO103480	YPS003777	48%	89.8%	97.7%
ECO103480	YPS004197	48%	89.8%	97.7%
ECO103480	YPS003268	48%	89.8%	97.7%
ECO103480	YPS003297	48%	89.8%	97.7%
ECO103480	YPS003731	48%	89.8%	97.7%
ECO103481	ABA103575	48%	100%	99.9%
ECO103481	BCE113806	46%	71.7%	98.0%
ECO103481	BFU101557	43%	99.6%	99.0%
ECO103481	BMA100998	44%	99.3%	100%
ECO103481	CJU101159	31%	99.9%	99.7%
ECO103481	CDF104028	36%	98.7%	98.5%
ECO103481	EBC104561	93%	99.9%	100%
ECO103481	EFA200400	35%	99.4%	69.7%
ECO103481	EFM200195	36%	97.1%	68.8%
ECO103481	ECO103481	100%	100%	100%
ECO103481	HIN100903	69%	100%	100%
ECO103481	HPY100956	29%	99.4%	99.3%
ECO103481	KPN303050	92%	100%	100%
ECO103481	LPN102108	44%	75.9%	97.4%
ECO103481	LMO101909	33%	99.0%	98.8%
ECO103481	MCA101554	47%	99.4%	99.6%
ECO103481	NGO101359	45%	99.9%	99.7%
ECO103481	NME200487	45%	99.9%	99.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103481	PMU101102	69%	100%	100%
ECO103481	PRT101496	79%	100%	100%
ECO103481	PAE200008	51%	99.9%	99.9%
ECO103481	PPU102205	50%	99.9%	99.9%
ECO103481	PSY107524	50%	99.9%	99.9%
ECO103481	SPA102021	89%	72.9%	100%
ECO103481	STY100713	94%	100%	100%
ECO103481	SPN401327	35%	97.5%	97.3%
ECO103481	SPY201298	35%	97.5%	97.3%
ECO103481	VCH100020	68%	99.6%	99.6%
ECO103481	YPS003356	85%	100%	100%
ECO103482	ABA105776	76%	96.0%	88.9%
ECO103482	BPT101206	74%	96.0%	28.7%
ECO103482	BCE104446	71%	96.0%	88.9%
ECO103482	BFU105313	70%	96.0%	87.1%
ECO103482	BMA109515	72%	96.0%	75.8%
ECO103482	CJU100654	66%	92.4%	96.9%
ECO103482	CPN200896	54%	96.0%	28.2%
ECO103482	CTR200173	55%	96.0%	28.4%
ECO103482	CDF102122	63%	95.7%	97.3%
ECO103482	EBC104560	97%	100%	100%
ECO103482	EFA104079	62%	97.7%	96.0%
ECO103482	EFM101836	71%	59.7%	94.8%
ECO103482	ECO103482	100%	100%	100%
ECO103482	HIN100906	90%	98.7%	99.0%
ECO103482	HPY100944	60%	93.7%	93.1%
ECO103482	KPN305504	98%	100%	100%
ECO103482	LMO101725	61%	96.7%	97.0%
ECO103482	MCA102165	74%	99.0%	93.7%
ECO103482	NGO101356	72%	97.0%	99.3%
ECO103482	NME200485	73%	96.0%	97.3%
ECO103482	PMU101098	91%	98.7%	99.7%
ECO103482	PRT101495	94%	99.3%	100%
ECO103482	PAE200009	76%	97.7%	93.3%
ECO103482	PPU103628	76%	97.7%	93.3%
ECO103482	PSY103530	76%	97.7%	82.8%
ECO103482	SPA100735	98%	100%	100%
ECO103482	STY100712	98%	100%	100%
ECO103482	SMU101427	60%	97.0%	29.8%
ECO103482	SPN401328	61%	97.4%	94.8%
ECO103482	SPY201299	62%	97.0%	94.4%
ECO103482	VCH100021	88%	100%	91.8%
ECO103482	YPS003357	93%	100%	99.7%
ECO103483	BAN104874	25%	42.9%	70%
ECO103483	BAN103246	27%	97.0%	97.1%
ECO103483	BFR102685	31%	27.2%	30.9%
ECO103483	BFR101730	20%	85.2%	85.1%
ECO103483	BFR101210	23%	84.9%	85.4%
ECO103483	BPT101994	22%	95.5%	94.6%
ECO103483	BFU100798	25%	35.0%	31.6%
ECO103483	BMA103871	20%	93.4%	90.4%
ECO103483	CBO103448	20%	94.6%	99.7%
ECO103483	EBC106435	81%	100%	100%
ECO103483	ECO103483	100%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103483	KPN301174	65%	43.5%	100%
ECO103483	KPN303040	71%	100%	100%
ECO103483	LMO100418	24%	22.4%	29.2%
ECO103483	MAV100271	30%	17.8%	13.7%
ECO103483	PPU103844	23%	60.7%	68.6%
ECO103483	PSY101101	20%	53.2%	46.7%
ECO103483	SPA100737	81%	100%	100%
ECO103483	STM103799	81%	100%	100%
ECO103483	SEP100270	23%	84.0%	80.3%
ECO103483	SMU101666	25%	95.8%	87.4%
ECO103483	VCH102759	23%	85.2%	83.5%
ECO103483	YPS003266	58%	100%	100%
ECO103487	BFR10693	48%	94.3%	99.5%
ECO103487	BCE111113	66%	99.1%	82.7%
ECO103487	BFU102389	67%	99.1%	99.1%
ECO103487	CDF101665	49%	99.8%	96.5%
ECO103487	EBC104589	91%	100%	95.4%
ECO103487	EFA201077	48%	98.9%	99.5%
ECO103487	EFM101257	46%	98.6%	99.3%
ECO103487	ECO103487	100%	100%	100%
ECO103487	HIN101085	71%	99.5%	99.8%
ECO103487	KPN302422	83%	99.5%	99.8%
ECO103487	KPN301170	90%	100%	100%
ECO103487	PRT101394	81%	99.1%	99.5%
ECO103487	PSY102073	68%	99.1%	99.5%
ECO103487	SPA103028	89%	98.6%	100%
ECO103487	STY100698	92%	100%	100%
ECO103487	YPS002755	85%	99.5%	99.8%
ECO103488	BCE111238	65%	79.7%	79.8%
ECO103488	BFU102365	60%	97.3%	99.1%
ECO103488	EBC104587	90%	100%	100%
ECO103488	EFM202335	36%	99.7%	97.8%
ECO103488	ECO103488	100%	100%	100%
ECO103488	HIN101084	75%	99.4%	99.1%
ECO103488	KPN305781	90%	87.9%	100%
ECO103488	NME300340	23%	29.4%	20.6%
ECO103488	PSY102056	59%	99.4%	94.5%
ECO103488	YPS002753	82%	100%	99.7%
ECO103494	EBC104573	93%	95.0%	99.2%
ECO103494	ECO103494	100%	100%	100%
ECO103494	KPN300323	91%	40.3%	96%
ECO103494	KPN308799	90%	99.5%	99.3%
ECO103494	MCA101391	43%	99.0%	99.5%
ECO103494	NGO101874	46%	99.0%	99.3%
ECO103494	NME200590	47%	99.0%	99.3%
ECO103494	PRT101493	73%	98.8%	99.5%
ECO103494	SPA103032	91%	99.5%	100%
ECO103494	STY100694	92%	99.5%	99.8%
ECO103494	STM103821	92%	99.5%	99.8%
ECO103494	VCH100019	62%	100%	99.8%
ECO103494	YPS003375	79%	99.8%	98.8%
ECO103506	BCE104022	22%	47.2%	35%
ECO103506	EBC104569	56%	100%	100%
ECO103506	ECO103506	100%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103506	PMU100998	21%	91.1%	85.0%
ECO103506	PPU107094	24%	26.4%	12.4%
ECO103506	PSY105244	31%	95.5%	93.4%
ECO103510	ABA100619	66%	92.8%	99.4%
ECO103510	BPT103076	69%	90.6%	92.8%
ECO103510	BCE103462	69%	90.6%	96.7%
ECO103510	BFU107758	70%	90.2%	96.6%
ECO103510	BFU102740	71%	90.6%	97.0%
ECO103510	BMA106098	72%	90.6%	86.6%
ECO103510	CDP101458	64%	92.4%	98.8%
ECO103510	EBC104578	93%	98.5%	100%
ECO103510	EFA201951	48%	90.0%	97.4%
ECO103510	ECO103510	100%	100%	100%
ECO103510	KPN305829	65%	92.4%	99.0%
ECO103510	MCA101417	66%	91.1%	97.6%
ECO103510	MAV101769	67%	92.6%	99.0%
ECO103510	MBV105125	66%	92.6%	99.0%
ECO103510	MTU200456	66%	92.6%	99.0%
ECO103510	PRT105557	48%	93.0%	99.2%
ECO103510	PAE201982	66%	92.4%	99.0%
ECO103510	PAE204019	67%	92.4%	99.0%
ECO103510	PPU108163	67%	92.4%	99.0%
ECO103510	PSY105710	64%	92.4%	99.0%
ECO103510	SPA101536	88%	83.2%	98.9%
ECO103510	STY100416	95%	94.5%	100%
ECO103510	SAU800167	43%	90.0%	97.6%
ECO103510	SEP201069	43%	90.0%	97.4%
ECO103510	SHA101810	43%	90.8%	98.2%
ECO103510	VCH100804	63%	90.0%	90.2%
ECO103510	VCH101789	64%	92.6%	99.2%
ECO103514	ABA100615	35%	44.6%	39.0%
ECO103514	BPT102214	40%	100%	100%
ECO103514	BCE110352	37%	98.5%	98.5%
ECO103514	BFU103486	39%	98.5%	97.6%
ECO103514	BMA102102	35%	98.5%	99.5%
ECO103514	EBC104570	79%	100%	100%
ECO103514	ECO103514	100%	100%	100%
ECO103514	KPN303410	69%	99.5%	99.5%
ECO103514	PMU101100	30%	99.5%	100%
ECO103514	PAE200466	33%	93.6%	93.2%
ECO103514	PPU107390	34%	98.5%	97.6%
ECO103514	PSY102773	29%	99.0%	97.1%
ECO103514	SPA103113	60%	89.1%	99.4%
ECO103514	STY100410	87%	100%	100%
ECO103515	ABA100225	26%	68.3%	56.4%
ECO103515	ABA100477	27%	24.4%	97.4%
ECO103515	BAN104847	19%	21.9%	3.7%
ECO103515	BAN109223	32%	5.6%	34.8%
ECO103515	BAN101440	31%	6.0%	31.7%
ECO103515	BAN110288	24%	23.3%	18.6%
ECO103515	BFR104422	62%	2.0%	27%
ECO103515	BCE108121	25%	30.8%	70.0%
ECO103515	BCE104951	26%	28.1%	38.7%
ECO103515	BFU107935	28%	24.3%	41.6%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103515	BFU100092	47%	6.4%	98.9%
ECO103515	BFU100109	27%	14.5%	55.1%
ECO103515	BFU102581	29%	10.2%	4.6%
ECO103515	BMA107682	25%	50.8%	25.9%
ECO103515	CAC100404	31%	6.3%	31.2%
ECO103515	EBC107494	28%	7.6%	75%
ECO103515	EBC103412	28%	12.6%	35.0%
ECO103515	EBC104888	27%	25.3%	62.3%
ECO103515	ECO100686	96%	23.6%	68.1%
ECO103515	ECO101427	77%	38.0%	77.7%
ECO103515	ECO100488	77%	90.6%	88.2%
ECO103515	ECO100683	96%	91.2%	89.9%
ECO103515	ECO103405	98%	90.8%	88.6%
ECO103515	ECO103515	100%	100%	100%
ECO103515	PRT103688	31%	7.6%	73.6%
ECO103515	PRT103361	34%	8.2%	78.0%
ECO103515	PRT103421	25%	56.2%	65.1%
ECO103515	PAE202682	33%	90.6%	88.7%
ECO103515	PPU107712	33%	7.8%	93.1%
ECO103515	PPU110484	27%	26.0%	83.0%
ECO103515	PPU109654	25%	2.8%	84.4%
ECO103515	PPU107101	42%	4.0%	5.5%
ECO103515	PPU109653	28%	42.6%	95.3%
ECO103515	PPU109652	26%	56.6%	54.6%
ECO103515	PPU110482	26%	11.3%	5.4%
ECO103515	PSY108533	34%	5.1%	83.6%
ECO103515	PSY101322	59%	4.3%	24.3%
ECO103515	PSY105816	47%	7.4%	45.3%
ECO103515	PSY102083	25%	13.9%	11.8%
ECO103515	SPA106438	43%	6.2%	5.5%
ECO103515	SPA100247	28%	54.6%	67.7%
ECO103515	STY104094	26%	51.3%	33.3%
ECO103515	STY104095	30%	24.7%	74.9%
ECO103515	STM103807	43%	8.0%	45.5%
ECO103515	STM103806	26%	51.3%	33.1%
ECO103515	YPS002860	25%	87.5%	75.9%
ECO103523	EBC103810	88%	100%	100%
ECO103523	ECO103523	100%	100%	100%
ECO103523	KPN303392	84%	100%	98.5%
ECO103523	PMU101063	35%	81.5%	94.8%
ECO103523	SPA103110	91%	97.9%	100%
ECO103523	STY100404	92%	97.9%	97.4%
ECO103523	STM104139	92%	97.9%	97.4%
ECO103523	VCH103763	43%	91.3%	96.4%
ECO103523	YPS003321	77%	87.2%	94.0%
ECO103527	ABA104933	86%	96.7%	100%
ECO103527	BAN109344	30%	21.0%	24.4%
ECO103527	BAN107706	33%	21.0%	23.8%
ECO103527	BPT100117	46%	94.9%	97.2%
ECO103527	BBU100683	26%	32.8%	41.4%
ECO103527	BCE101035	37%	94.2%	84.3%
ECO103527	BFU108951	43%	98.5%	90.7%
ECO103527	BMA102489	42%	94.7%	98.7%
ECO103527	CBO101704	51%	31.8%	37.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103527	CDF103639	42%	35.9%	26.2%
ECO103527	EBC103192	94%	95.7%	100%
ECO103527	EFA200385	25%	43.2%	52.2%
ECO103527	EFM200941	31%	86.9%	87.7%
ECO103527	ECO103527	100%	100%	100%
ECO103527	HIN101704	75%	94.9%	98.7%
ECO103527	KPN305761	93%	95.2%	95.7%
ECO103527	LMO101142	32%	24.5%	27.1%
ECO103527	MCA101122	42%	96.7%	96.0%
ECO103527	MAV103878	37%	93.4%	67.6%
ECO103527	MBV102018	37%	93.4%	90.1%
ECO103527	MLP101240	37%	93.4%	88.2%
ECO103527	MTU201839	37%	93.4%	88.2%
ECO103527	NGO101059	43%	92.9%	94.4%
ECO103527	NME201451	43%	92.9%	94.4%
ECO103527	PMU100288	43%	94.9%	96.9%
ECO103527	PRT105377	34%	88.1%	83.4%
ECO103527	PAE204767	86%	96.0%	99.7%
ECO103527	PPU108584	84%	96.0%	99.7%
ECO103527	SPA100379	93%	67.4%	100%
ECO103527	STY100378	93%	100%	100%
ECO103527	STM104153	94%	100%	100%
ECO103527	SAU802346	24%	41.2%	49.3%
ECO103527	SEP200052	23%	41.2%	49.3%
ECO103527	SEP200853	23%	41.2%	49.3%
ECO103527	SHA102078	24%	43.2%	51.6%
ECO103527	SMU100940	20%	53.8%	71.3%
ECO103527	SPN400627	30%	91.7%	88.9%
ECO103527	SPY200298	31%	91.7%	85.1%
ECO103527	TPA100288	33%	30.3%	41.6%
ECO103527	VCH103702	79%	95.2%	99.7%
ECO103527	YPS003024	83%	94.7%	98.4%
ECO103528	ABA105744	53%	95.5%	97.5%
ECO103528	BAN111603	46%	96.2%	94.4%
ECO103528	BAN100700	46%	96.2%	94.4%
ECO103528	BPT100876	51%	98.1%	90.7%
ECO103528	BCE100810	57%	96.8%	98.7%
ECO103528	BFU114284	57%	96.8%	98.7%
ECO103528	BMA108062	56%	96.8%	98.7%
ECO103528	CJU100835	43%	93.6%	95.5%
ECO103528	CPN200085	37%	93.0%	92.9%
ECO103528	CTR200816	40%	93.0%	96.0%
ECO103528	CAC101314	46%	95.5%	93.8%
ECO103528	CBO101580	48%	95.5%	93.8%
ECO103528	CDF102268	49%	95.5%	96.8%
ECO103528	CDP101138	50%	96.8%	97.4%
ECO103528	EBC103195	92%	99.4%	99.4%
ECO103528	EFA200904	47%	97.5%	92.3%
ECO103528	EFM101106	44%	98.7%	94.0%
ECO103528	ECO103528	100%	100%	100%
ECO103528	HIN100746	76%	98.1%	96.2%
ECO103528	KPN303405	91%	99.4%	99.4%
ECO103528	LPN101992	52%	95.5%	98.7%
ECO103528	LMO102766	42%	98.7%	92.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103528	MCA101505	45%	98.1%	89.5%
ECO103528	MAV100739	47%	97.5%	99.4%
ECO103528	MBV100056	49%	98.1%	100%
ECO103528	MLP100266	51%	98.1%	97.5%
ECO103528	MTU203321	49%	98.1%	100%
ECO103528	MGE100355	40%	95.5%	92.8%
ECO103528	MPN100321	38%	94.9%	92.2%
ECO103528	NGO100616	63%	98.1%	100%
ECO103528	NME202053	62%	98.1%	100%
ECO103528	PMU101513	74%	98.1%	97.5%
ECO103528	PRT105528	75%	100%	100%
ECO103528	PAE205122	60%	95.5%	98.0%
ECO103528	PPU102022	59%	97.5%	100%
ECO103528	PSY103965	58%	95.5%	99.3%
ECO103528	SPA102933	78%	95.5%	100%
ECO103528	STY100375	94%	99.4%	99.4%
ECO103528	STM104165	94%	99.4%	99.4%
ECO103528	SAU801855	47%	95.5%	96.8%
ECO103528	SEP200039	44%	94.9%	96.2%
ECO103528	SHA100689	45%	95.5%	96.8%
ECO103528	SMU100459	41%	97.5%	84.6%
ECO103528	SPN400432	41%	97.5%	85.6%
ECO103528	SPY200270	42%	98.1%	85.2%
ECO103528	UUR100270	36%	93.6%	90.7%
ECO103528	VCH102658	61%	97.5%	99.4%
ECO103528	YPS001568	80%	100%	100%
ECO103532	ABA103075	51%	97.6%	96.5%
ECO103532	BAN113633	24%	69.9%	47.5%
ECO103532	BAN111729	26%	78.3%	83.3%
ECO103532	BPT100884	55%	98.8%	96.5%
ECO103532	BCE111871	43%	54.2%	97.9%
ECO103532	BFU102721	53%	100%	96.6%
ECO103532	BMA104651	47%	100%	97.7%
ECO103532	CAC103641	32%	77.1%	84.2%
ECO103532	CBO100935	41%	74.7%	82.7%
ECO103532	EBC103201	91%	98.8%	98.8%
ECO103532	ECO103532	100%	100%	100%
ECO103532	HIN100551	52%	80.7%	27.4%
ECO103532	KPN303391	86%	100%	100%
ECO103532	LPN103574	57%	100%	98.8%
ECO103532	LMO102441	32%	69.9%	65.9%
ECO103532	MCA101632	51%	98.8%	92.3%
ECO103532	MAV105267	32%	66.3%	66.7%
ECO103532	MBV103242	33%	66.3%	66.7%
ECO103532	MTU303412	33%	66.3%	66.7%
ECO103532	NGO101743	46%	98.8%	97.6%
ECO103532	NME200622	46%	98.8%	97.6%
ECO103532	PMU101347	41%	80.7%	27.4%
ECO103532	PAE205124	56%	98.8%	97.6%
ECO103532	PPU111081	50%	98.8%	97.6%
ECO103532	PPU102025	56%	98.8%	97.6%
ECO103532	PSY103987	56%	98.8%	98.8%
ECO103532	SPA102936	89%	100%	100%
ECO103532	STY100347	89%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103532	SEP200786	39%	49.4%	52.6%
ECO103532	SHA102895	32%	90.4%	93.5%
ECO103532	VCH102600	50%	80.7%	26.7%
ECO103532	YPS001530	78%	98.8%	100%
ECO103533	ABA102523	32%	100%	97.8%
ECO103533	BAN106269	27%	85.3%	96.9%
ECO103533	BPT100886	35%	68.5%	67.9%
ECO103533	BCE105965	39%	71.3%	72.1%
ECO103533	BFU102720	39%	71.3%	71.6%
ECO103533	BMA104409	36%	71.3%	74.8%
ECO103533	CDF103903	32%	55.9%	79.8%
ECO103533	EBC103202	83%	100%	100%
ECO103533	EFA200318	34%	85.3%	95.5%
ECO103533	ECO103533	100%	100%	100%
ECO103533	HIN100724	49%	98.6%	98.0%
ECO103533	KPN303388	86%	100%	100%
ECO103533	LPN101562	30%	100%	100%
ECO103533	LMO100345	28%	86.0%	93.7%
ECO103533	MCA103138	31%	97.9%	96.4%
ECO103533	MBV102118	30%	84.6%	52.7%
ECO103533	MTU200323	30%	84.6%	52.7%
ECO103533	PMU101433	49%	94.4%	92.5%
ECO103533	PRT105992	63%	100%	98.6%
ECO103533	PAE205125	34%	98.6%	97.8%
ECO103533	PPU112071	37%	96.5%	97.1%
ECO103533	PSY103984	35%	96.5%	97.1%
ECO103533	SPA102935	90%	100%	100%
ECO103533	STY100345	93%	100%	100%
ECO103533	SAU801534	30%	86.0%	89.1%
ECO103533	SEP200938	30%	57.3%	61.7%
ECO103533	SHA100982	26%	86.0%	92.2%
ECO103533	SMU100073	33%	83.9%	91.5%
ECO103533	SPN400595	28%	83.9%	96.0%
ECO103533	SPY201177	32%	86.7%	94.6%
ECO103533	VCH102617	48%	100%	99.3%
ECO103533	YPS001525	65%	100%	99.3%
ECO103536	BAN110223	31%	60.3%	85.4%
ECO103536	BBU100769	35%	57.8%	54.6%
ECO103536	CJU100594	37%	52.3%	40.3%
ECO103536	EBC103198	80%	96.0%	87.8%
ECO103536	ECO103536	100%	100%	100%
ECO103536	HIN100735	43%	74.0%	87.4%
ECO103536	KPN303397	81%	94.9%	85.1%
ECO103536	PMU101508	39%	80.9%	81.4%
ECO103536	PRT104883	57%	84.1%	71.3%
ECO103536	PAE205130	36%	71.5%	75.9%
ECO103536	PPU102030	40%	65.7%	69.8%
ECO103536	PSY103972	41%	63.9%	66.5%
ECO103536	SPA100812	80%	93.1%	100%
ECO103536	STY100339	81%	99.6%	85.9%
ECO103536	STM104200	81%	99.6%	85.9%
ECO103543	BPT101420	48%	88.7%	88.1%
ECO103543	BCE100302	35%	90.0%	82.7%
ECO103543	BFU110339	40%	92.5%	91.6%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103543	BMA100507	38%	92.5%	85.9%
ECO103543	CJU101059	26%	88.4%	84.5%
ECO103543	EBC101072	78%	99.1%	96.6%
ECO103543	ECO103543	100%	100%	100%
ECO103543	HPY100275	29%	88.4%	85.3%
ECO103543	KPN303383	85%	93.4%	92.3%
ECO103543	MBV100073	28%	23.2%	19.8%
ECO103543	MTU202125	28%	23.2%	19.8%
ECO103543	NGO100727	40%	89.0%	87.9%
ECO103543	NME200227	40%	89.0%	87.9%
ECO103543	PMU101843	53%	100%	98.1%
ECO103543	PRT105756	70%	98.7%	98.7%
ECO103543	PAE205006	55%	92.5%	82.8%
ECO103543	PPU107407	56%	92.5%	83.0%
ECO103543	PSY103596	54%	92.5%	82.8%
ECO103543	SPA104078	80%	99.1%	100%
ECO103543	STY104626	84%	99.1%	99.7%
ECO103543	STM104218	84%	99.1%	99.7%
ECO103543	YPS001475	68%	100%	99.4%
ECO103544	ABA103180	19%	28.9%	24.9%
ECO103544	BAN108790	21%	43.2%	69.8%
ECO103544	BPT104383	24%	49.4%	52.8%
ECO103544	BBU100325	28%	16.0%	7.4%
ECO103544	CDF104322	21%	49.6%	89.5%
ECO103544	EBC103424	28%	91.6%	96.5%
ECO103544	EFM102321	21%	52.7%	66.6%
ECO103544	ECO103544	100%	100%	100%
ECO103544	HIN100855	24%	64.0%	68.2%
ECO103544	HPY101022	22%	91.9%	87.4%
ECO103544	LPN102235	24%	31.5%	30.7%
ECO103544	PMU101863	25%	41.8%	70.0%
ECO103544	SEP201692	23%	44.2%	25.8%
ECO103544	SMU100130	20%	41.3%	27.7%
ECO103544	VCH100235	23%	56.6%	58.9%
ECO103557	ABA100518	45%	99.6%	97.1%
ECO103557	BAN104773	39%	99.6%	98.9%
ECO103557	BPT100625	50%	100%	97.5%
ECO103557	BCE115174	48%	100%	100%
ECO103557	BFU103412	45%	92.9%	99.2%
ECO103557	BMA101577	48%	100%	100%
ECO103557	CDP101174	34%	99.6%	99.0%
ECO103557	EBC103421	92%	100%	100%
ECO103557	EFA200419	42%	100%	97.5%
ECO103557	EFM202622	41%	100%	98.2%
ECO103557	ECO103557	100%	100%	100%
ECO103557	HIN100925	57%	100%	99.3%
ECO103557	KPN301574	91%	100%	100%
ECO103557	LPN103244	62%	13.8%	88.1%
ECO103557	LPN100873	51%	99.6%	98.5%
ECO103557	LMO102025	37%	100%	100%
ECO103557	MCA103356	46%	99.6%	96.0%
ECO103557	MAV106664	33%	99.6%	98.2%
ECO103557	MBV100840	33%	99.6%	98.3%
ECO103557	MLP101011	34%	99.6%	98.2%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103557	MTU202886	33%	99.6%	98.3%
ECO103557	MGE100268	29%	100%	96.1%
ECO103557	MPN100457	29%	99.6%	98.9%
ECO103557	NGO100260	53%	100%	100%
ECO103557	NME201370	53%	100%	100%
ECO103557	PMU101145	57%	100%	99.6%
ECO103557	PRT102120	71%	99.6%	97.8%
ECO103557	PAE200356	54%	100%	100%
ECO103557	PPU102181	57%	100%	100%
ECO103557	PSY102749	56%	100%	100%
ECO103557	SPA100823	92%	100%	100%
ECO103557	STY104574	94%	100%	100%
ECO103557	SAU801689	35%	100%	100%
ECO103557	SEP201682	33%	100%	100%
ECO103557	SHA100371	34%	100%	100%
ECO103557	SMU101121	39%	100%	99.6%
ECO103557	SPN400872	36%	100%	99.3%
ECO103557	SPY200353	37%	100%	98.9%
ECO103557	UUR100417	35%	99.6%	99.6%
ECO103557	VCH100219	61%	99.6%	99.6%
ECO103557	YPS001456	79%	99.6%	99.6%
ECO103558	ABA102882	80%	92.7%	100%
ECO103558	BAN104482	32%	89.1%	100%
ECO103558	BAN113487	34%	89.1%	100%
ECO103558	BFR105168	45%	60%	53.2%
ECO103558	BPT106501	76%	100%	100%
ECO103558	BBU100395	50%	96.4%	89.8%
ECO103558	BCE102651	76%	100%	100%
ECO103558	BFU101229	78%	100%	100%
ECO103558	BMA107218	76%	100%	100%
ECO103558	CJU100436	48%	63.6%	67.3%
ECO103558	CPN200501	52%	96.4%	100%
ECO103558	CTR200421	52%	96.4%	100%
ECO103558	CAC102363	36%	89.1%	100%
ECO103558	CBO103373	34%	89.1%	100%
ECO103558	CDF104289	34%	89.1%	90.7%
ECO103558	CDP102895	57%	89.1%	90.7%
ECO103558	EBC103420	98%	100%	100%
ECO103558	EFA203027	40%	89.1%	100%
ECO103558	EFA202465	42%	89.1%	100%
ECO103558	ECO103558	100%	100%	100%
ECO103558	HIN100930	81%	98.2%	96.4%
ECO103558	HPY101187	57%	63.6%	67.3%
ECO103558	KPN301576	96%	100%	100%
ECO103558	LPN100153	58%	87.3%	88.9%
ECO103558	LMO102322	51%	60%	67.3%
ECO103558	MCA101228	76%	92.7%	100%
ECO103558	MAV102810	53%	89.1%	90.7%
ECO103558	MBV100100	51%	89.1%	90.7%
ECO103558	MLP101160	32%	89.1%	89.1%
ECO103558	MTU202024	51%	89.1%	90.7%
ECO103558	MGE100333	48%	63.6%	66.0%
ECO103558	MPN100370	48%	63.6%	66.0%
ECO103558	NGO101641	76%	92.7%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103558	NME202002	78%	92.7%	100%
ECO103558	PMU101150	81%	98.2%	96.4%
ECO103558	PRT104931	94%	100%	100%
ECO103558	PAE205310	86%	92.7%	100%
ECO103558	PPU101949	78%	92.7%	100%
ECO103558	PSY107951	80%	92.7%	100%
ECO103558	SPA100824	100%	100%	100%
ECO103558	STY104571	100%	100%	100%
ECO103558	SAU801335	45%	60%	67.3%
ECO103558	SEP204223	36%	89.1%	94.2%
ECO103558	SHA100035	45%	60%	67.3%
ECO103558	SMU101280	42%	89.1%	100%
ECO103558	SPN401941	40%	89.1%	100%
ECO103558	SPY201651	40%	89.1%	100%
ECO103558	TPA100231	44%	100%	100%
ECO103558	UUR100539	33%	92.7%	96.2%
ECO103558	VCH100217	83%	100%	100%
ECO103558	YPS001453	96%	100%	100%
ECO103559	ABA103779	74%	98.7%	98.7%
ECO103559	BAN102385	42%	73.1%	88.7%
ECO103559	BFR100362	41%	96.2%	87.2%
ECO103559	BPT102361	75%	97.4%	97.4%
ECO103559	BBU100349	34%	87.2%	88.0%
ECO103559	BCE112085	73%	97.4%	98.7%
ECO103559	BFU101231	72%	97.4%	98.7%
ECO103559	BMA105211	73%	97.4%	98.7%
ECO103559	CJU100415	50%	79.5%	95.3%
ECO103559	CPN200424	36%	94.9%	97.8%
ECO103559	CTR200355	35%	96.2%	98.9%
ECO103559	CAC102140	33%	73.1%	87.3%
ECO103559	CBO103664	45%	42.3%	52.4%
ECO103559	CDF103637	38%	60.3%	75.8%
ECO103559	CDP102158	50%	98.7%	88.5%
ECO103559	EBC103419	96%	84.6%	100%
ECO103559	EFA201573	41%	67.9%	85.5%
ECO103559	EFM101167	43%	67.9%	85.5%
ECO103559	ECO103559	100%	100%	100%
ECO103559	HIN100931	85%	98.7%	98.7%
ECO103559	HPY100486	39%	78.2%	96.8%
ECO103559	KPN301578	100%	100%	100%
ECO103559	LPN101298	70%	98.7%	98.7%
ECO103559	LMO101238	36%	73.1%	88.7%
ECO103559	MCA101216	77%	98.7%	98.7%
ECO103559	MAV102809	48%	98.7%	87.5%
ECO103559	MBV100101	44%	98.7%	98.7%
ECO103559	MTU202025	45%	98.7%	98.7%
ECO103559	MGE100436	32%	79.5%	95.3%
ECO103559	MPN100218	29%	78.2%	92.3%
ECO103559	NGO101643	73%	97.4%	98.7%
ECO103559	NME202003	73%	97.4%	98.7%
ECO103559	PMU101151	87%	98.7%	98.7%
ECO103559	PRT106105	94%	100%	100%
ECO103559	PAE205311	82%	100%	100%
ECO103559	PPU101950	77%	98.7%	98.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103559	PSY101861	78%	97.4%	98.7%
ECO103559	SPA100825	96%	100%	100%
ECO103559	STY104568	96%	100%	100%
ECO103559	SAU801224	45%	73.1%	88.7%
ECO103559	SEP201507	45%	73.1%	88.7%
ECO103559	SHA100085	49%	73.1%	88.7%
ECO103559	SMU103046	42%	60.3%	75.8%
ECO103559	SPN400398	44%	60.3%	75.8%
ECO103559	SPY201454	46%	60.3%	75.8%
ECO103559	TPA100358	30%	98.7%	98.7%
ECO103559	UUR100210	35%	82.1%	96.9%
ECO103559	VCH100216	84%	97.4%	97.4%
ECO103559	YPS001450	92%	100%	100%
ECO103560	ABA100367	36%	97.8%	93.6%
ECO103560	BAN100808	35%	95.1%	95.9%
ECO103560	BAN105506	36%	95.1%	94.7%
ECO103560	BFR102521	30%	100%	97.8%
ECO103560	BPT100226	37%	94.2%	93.8%
ECO103560	RCE105704	40%	93.3%	100%
ECO103560	BFU101233	42%	95.1%	84.2%
ECO103560	BMA109188	41%	95.5%	77.0%
ECO103560	CAC102810	37%	94.2%	92.1%
ECO103560	CBO103355	34%	99.6%	97.8%
ECO103560	CDF101879	35%	98.2%	93.6%
ECO103560	EBC100201	74%	79.0%	97.8%
ECO103560	EFA200193	34%	95.1%	91.8%
ECO103560	EFM200303	37%	94.6%	92.2%
ECO103560	ECO103560	100%	100%	100%
ECO103560	HIN100932	49%	97.8%	93.6%
ECO103560	KPN300918	72%	96.0%	97.3%
ECO103560	LPN101771	35%	73.2%	100%
ECO103560	LMO101629	36%	94.6%	94.6%
ECO103560	MCA100296	35%	17.9%	14.7%
ECO103560	MAV100309	39%	55.8%	66.7%
ECO103560	NGO101171	36%	99.1%	98.7%
ECO103560	NME201319	35%	99.1%	98.7%
ECO103560	PMU101152	47%	98.2%	98.2%
ECO103560	PRT105105	51%	96.9%	97.3%
ECO103560	PAE205314	43%	100%	100%
ECO103560	PPU102092	44%	95.1%	90.6%
ECO103560	PSY101245	44%	94.2%	94.2%
ECO103560	SPA100826	82%	96.0%	100%
ECO103560	STY104565	83%	96.0%	97.3%
ECO103560	SAU801660	34%	79.5%	96.7%
ECO103560	SEP201625	30%	74.6%	90.8%
ECO103560	SHA100476	34%	99.6%	97.8%
ECO103560	SMU100239	35%	97.3%	96.5%
ECO103560	SPN400996	33%	94.6%	91.8%
ECO103560	SPY200848	34%	97.8%	96.9%
ECO103560	VCH100502	46%	54.5%	77.1%
ECO103560	VCH101757	46%	61.2%	93.7%
ECO103560	VCH100215	49%	100%	100%
ECO103560	YPS001448	58%	95.1%	95.9%
ECO103566	BAN100899	30%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103566	BAN111533	30%	100%	100%
ECO103566	BFR101390	29%	98.3%	99.7%
ECO103566	BPT102657	37%	100%	100%
ECO103566	BBU100817	25%	92.0%	92.4%
ECO103566	BCE113092	36%	100%	91.1%
ECO103566	BFU100495	37%	100%	97.5%
ECO103566	BMA101112	35%	100%	100%
ECO103566	CAC102749	31%	100%	100%
ECO103566	CBO102585	31%	100%	99.0%
ECO103566	CDF100438	28%	100%	100%
ECO103566	CDP100884	22%	54.7%	9.7%
ECO103566	EBC103735	93%	100%	100%
ECO103566	EFA201552	31%	99.7%	100%
ECO103566	EFM200008	31%	99.7%	100%
ECO103566	ECO103566	100%	100%	100%
ECO103566	HIN100447	64%	100%	100%
ECO103566	KPN302244	94%	100%	100%
ECO103566	LPN101981	40%	100%	100%
ECO103566	LMO101342	29%	100%	100%
ECO103566	MCA100329	28%	21.6%	14.5%
ECO103566	NGO101791	39%	99.7%	97.6%
ECO103566	NME200847	39%	99.7%	97.6%
ECO103566	PMU101875	62%	100%	100%
ECO103566	PRT105877	78%	100%	100%
ECO103566	PAE205330	47%	100%	100%
ECO103566	PPU102122	48%	100%	100%
ECO103566	PSY101215	46%	100%	100%
ECO103566	SPA102558	96%	100%	100%
ECO103566	STY104537	96%	100%	100%
ECO103566	STM104320	96%	100%	100%
ECO103566	UUR100124	23%	23.3%	16.8%
ECO103566	VCH100207	64%	100%	100%
ECO103566	YPS001406	87%	100%	100%
ECO103572	BAN100143	38%	99.0%	98.8%
ECO103572	BAN104454	39%	99.0%	98.3%
ECO103572	BFR102852	29%	99.4%	97.7%
ECO103572	BFR11417	35%	99.4%	97.9%
ECO103572	BPT102643	47%	98.7%	92.6%
ECO103572	BBU100197	39%	69.9%	73.0%
ECO103572	BCE109011	45%	99.0%	89.8%
ECO103572	BFU100498	45%	99.0%	90.1%
ECO103572	BMA103413	45%	99.1%	89.9%
ECO103572	CJU101197	33%	89.0%	86.3%
ECO103572	CAC103418	42%	96.6%	96.8%
ECO103572	CBO103842	40%	99.6%	99.9%
ECO103572	CDF100493	38%	99.4%	99.2%
ECO103572	CDP100429	38%	99.1%	96.8%
ECO103572	EBC103734	96%	100%	100%
ECO103572	EFA202207	39%	98.4%	97.8%
ECO103572	EFM201858	40%	98.4%	97.8%
ECO103572	ECO103572	100%	100%	100%
ECO103572	HIN101707	57%	96.2%	99.7%
ECO103572	HPY100762	37%	66.7%	61.9%
ECO103572	KPN302246	94%	56.0%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103572	LPN103344	53%	99.9%	99.4%
ECO103572	LMO101019	40%	99.4%	98.8%
ECO103572	MAV102768	40%	87.0%	91%
ECO103572	MBV101549	39%	99.3%	91.2%
ECO103572	MLP100302	38%	99.3%	91.9%
ECO103572	MTU202546	39%	99.3%	91.5%
ECO103572	MGE100284	26%	85.5%	84.9%
ECO103572	MPN100441	27%	87.2%	84.9%
ECO103572	NGO100434	45%	98.0%	96.5%
ECO103572	NME201768	45%	97.6%	95.0%
ECO103572	PMU100920	67%	100%	99.9%
ECO103572	PRT101439	84%	100%	100%
ECO103572	PAE205333	54%	98.6%	98.6%
ECO103572	PPU102134	55%	99.3%	99.3%
ECO103572	PSY101197	53%	99.3%	99.3%
ECO103572	SPA100195	86%	43.7%	94.8%
ECO103572	STY104500	98%	100%	100%
ECO103572	STM104343	98%	100%	100%
ECO103572	SAU801634	39%	98.0%	97.4%
ECO103572	SEP201583	37%	98.0%	97.4%
ECO103572	SHA101077	41%	85.3%	98.3%
ECO103572	SMU100646	40%	97.7%	97.2%
ECO103572	SPN401486	39%	99.0%	98.4%
ECO103572	SPY201522	39%	99.0%	97.8%
ECO103572	UUR100285	28%	95.4%	95.0%
ECO103572	VCH102672	74%	100%	100%
ECO103572	YPS001397	91%	100%	100%
ECO103580	BFU103431	29%	95.4%	86.2%
ECO103580	EBC101476	75%	43.7%	97.2%
ECO103580	ECO102129	71%	99.0%	98.7%
ECO103580	ECO103580	100%	100%	100%
ECO103580	KPN300529	62%	41.4%	100%
ECO103580	KPN301280	67%	99.5%	99.2%
ECO103580	PSY105004	21%	90.6%	93.6%
ECO103580	SPA101502	70%	97.7%	97.9%
ECO103580	STY104305	70%	99.0%	98.7%
ECO103580	STM104054	69%	99.0%	98.7%
ECO103580	SAU800673	27%	95.2%	94.1%
ECO103580	SEP200718	28%	95.2%	94.5%
ECO103581	ABA105827	22%	93.8%	96.0%
ECO103581	ABA101569	22%	92.5%	94.4%
ECO103581	BAN108534	31%	85.7%	94.1%
ECO103581	BAN111690	33%	92.8%	99.3%
ECO103581	BAN109792	33%	95.1%	95.5%
ECO103581	BAN110325	33%	92.8%	91.3%
ECO103581	BFR11827	27%	62.2%	66.6%
ECO103581	BFR103350	25%	88.9%	91.5%
ECO103581	BPT100758	25%	67.4%	66.5%
ECO103581	CJU100799	31%	91.9%	96.9%
ECO103581	CAC100371	37%	93.2%	93.8%
ECO103581	CBO101320	21%	97.7%	77.4%
ECO103581	CDF101274	21%	98.4%	96.8%
ECO103581	EBC104279	84%	97.1%	91.1%
ECO103581	ECO103581	100%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103581	HPY101217	25%	92.8%	94.3%
ECO103581	KPN300433	68%	58.3%	100%
ECO103581	KPN309121	83%	97.1%	99.3%
ECO103581	PMU101475	21%	95.1%	100%
ECO103581	SPA104210	88%	80.1%	100%
ECO103581	STY104430	89%	97.1%	99.3%
ECO103581	STM100075	89%	97.1%	99.3%
ECO103581	SAU802534	32%	95.1%	95.8%
ECO103581	SHA103189	24%	45.3%	89.0%
ECO103581	SMU101118	35%	94.8%	95.1%
ECO103581	SPN401301	37%	94.8%	91.5%
ECO103586	BAN109879	23%	85.2%	86.5%
ECO103586	BAN104603	23%	85.2%	84.9%
ECO103586	BFR102459	34%	85.2%	91.9%
ECO103586	BMA103057	27%	17.2%	23.8%
ECO103586	CAC100931	35%	95.9%	99.1%
ECO103586	CBO103491	32%	96.8%	94.5%
ECO103586	CDF101362	35%	83.5%	99.8%
ECO103586	EFA200688	25%	97.1%	97.5%
ECO103586	EFM200238	35%	93.5%	94.5%
ECO103586	ECO103586	100%	100%	100%
ECO103586	KPN301487	30%	23.0%	77.6%
ECO103586	KPN307303	31%	94.0%	90.9%
ECO103586	LMO100028	38%	97.1%	98.8%
ECO103586	PSY105729	38%	14.1%	23.9%
ECO103594	EBC105902	88%	96.7%	100%
ECO103594	EFA202243	24%	85.4%	86.8%
ECO103594	ECO103594	100%	100%	100%
ECO103594	KPN303658	88%	99.5%	100%
ECO103594	LPN103660	22%	93.7%	92.8%
ECO103594	LPN102872	26%	94.9%	96.9%
ECO103594	LPN102441	26%	93.9%	83.1%
ECO103594	LMO101894	24%	96.5%	97.5%
ECO103594	PRT104202	66%	99.5%	100%
ECO103594	SPA102040	87%	99.5%	100%
ECO103594	STY104078	92%	99.5%	100%
ECO103594	STM100428	92%	99.5%	100%
ECO103594	VCH102948	41%	92.7%	89.4%
ECO103598	ECO103598	100%	100%	100%
ECO103604	BFR105024	30%	13.6%	18.5%
ECO103604	CAC101995	59%	80.9%	69.9%
ECO103604	CDF102102	53%	82.4%	70.6%
ECO103604	EBC104389	78%	94.7%	100%
ECO103604	ECO103604	100%	100%	100%
ECO103604	KPN302271	87%	80.9%	68.1%
ECO103604	MTU301399	21%	50.3%	39.1%
ECO103604	SAU802323	55%	80.7%	68.4%
ECO103604	SEP200433	54%	80.7%	69.0%
ECO103604	SHA100792	53%	80.7%	68.6%
ECO103607	BAN108080	27%	61.1%	62.8%
ECO103607	BCE106766	25%	66.0%	68.1%
ECO103607	EBC104380	83%	99.3%	78.1%
ECO103607	ECO103607	100%	100%	100%
ECO103607	KPN302266	86%	98.6%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103607	PRT105273	37%	71.5%	69.1%
ECO103607	SPA101992	88%	98.6%	100%
ECO103607	STY104052	87%	98.6%	100%
ECO103607	STM102790	31%	84.7%	80%
ECO103607	SAU802387	26%	83.3%	86.4%
ECO103607	YPS003399	59%	98.6%	95.5%
ECO103613	BAN110814	23%	59.8%	100%
ECO103613	BAN113686	26%	61.5%	98.1%
ECO103613	BPT101871	31%	48.4%	76.2%
ECO103613	BCE104783	61%	65.8%	99.7%
ECO103613	BFU103501	64%	65.1%	100%
ECO103613	BMA103147	62%	65.1%	100%
ECO103613	EBC105499	93%	65.1%	100%
ECO103613	EFA100246	50%	65.1%	100%
ECO103613	ECO103613	100%	100%	100%
ECO103613	KPN302276	92%	65.1%	100%
ECO103613	PSY104852	62%	65.1%	100%
ECO103613	SPA101996	83%	53.7%	100%
ECO103613	SPN400287	30%	32.7%	93.3%
ECO103617	ABA106158	25%	33.6%	33.5%
ECO103617	ABA103970	24%	74.0%	79.3%
ECO103617	ECO103617	100%	100%	100%
ECO103617	PRT103243	40%	72.2%	73.5%
ECO103617	SPA101520	46%	71.7%	75.1%
ECO103617	STY100853	46%	71.7%	75.1%
ECO103617	YPS000424	31%	70.9%	70.4%
ECO103624	ABA100986	86%	95.7%	100%
ECO103624	BAN102648	62%	93.5%	97.7%
ECO103624	BAN102568	62%	93.5%	97.7%
ECO103624	BFR106080	75%	97.8%	95.7%
ECO103624	BPT100632	65%	95.7%	100%
ECO103624	BBU100439	73%	97.8%	88.2%
ECO103624	BCE105407	63%	95.7%	100%
ECO103624	BMA109034	63%	95.7%	100%
ECO103624	CJU100891	65%	95.7%	100%
ECO103624	CPN200909	64%	91.3%	93.3%
ECO103624	CTR200163	66%	91.3%	93.3%
ECO103624	CAC101976	58%	93.5%	97.7%
ECO103624	CBO101345	53%	93.5%	74.1%
ECO103624	CDF104319	66%	91.3%	93.3%
ECO103624	CDP101663	59%	91.3%	84%
ECO103624	EBC100048	100%	100%	100%
ECO103624	EFA202663	69%	84.8%	88.6%
ECO103624	ECO103624	100%	100%	100%
ECO103624	HIN100979	88%	93.5%	97.7%
ECO103624	HPY101426	61%	95.7%	100%
ECO103624	KPN204278	100%	100%	100%
ECO103624	LPN103600	72%	93.5%	97.7%
ECO103624	LMO100377	67%	93.5%	97.7%
ECO103624	MCA103596	90%	95.7%	100%
ECO103624	MBV102731	54%	91.3%	91.3%
ECO103624	MLP101605	57%	91.3%	89.4%
ECO103624	MTU203869	54%	91.3%	89.4%
ECO103624	MGE100475	68%	97.8%	93.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103624	MPN100160	68%	97.8%	93.8%
ECO103624	NGO103743	68%	95.7%	100%
ECO103624	NME200511	68%	95.7%	100%
ECO103624	PMU101162	88%	93.5%	97.7%
ECO103624	PRT102996	95%	97.8%	95.7%
ECO103624	PAE205565	88%	95.7%	100%
ECO103624	PPU102199	79%	95.7%	100%
ECO103624	SPA101308	100%	100%	100%
ECO103624	STY104683	100%	100%	100%
ECO103624	STM104752	100%	100%	100%
ECO103624	SAU802714	62%	93.5%	95.6%
ECO103624	SEP201288	62%	93.5%	95.6%
ECO103624	SHA100140	62%	93.5%	95.6%
ECO103624	SMU102293	69%	93.5%	97.7%
ECO103624	SPN401805	74%	84.8%	88.6%
ECO103624	SPY200181	67%	93.5%	97.7%
ECO103624	TPA100941	71%	97.8%	88.2%
ECO103624	UUR100611	75%	97.8%	93.8%
ECO103624	VCH100007	80%	91.3%	93.3%
ECO103624	YPS003462	95%	100%	100%
ECO103625	ABA100989	39%	98.3%	89.5%
ECO103625	BAN113266	32%	84.9%	85.7%
ECO103625	BAN108182	31%	87.4%	91.3%
ECO103625	BFR101294	50%	26.9%	23.2%
ECO103625	BPT105773	33%	73.1%	74.8%
ECO103625	BBU100440	26%	84.9%	87.4%
ECO103625	BCE102411	38%	71.4%	53.8%
ECO103625	BFU113418	34%	92.4%	49.3%
ECO103625	BMA108699	37%	69.7%	52.9%
ECO103625	CJU100890	33%	47.1%	51.9%
ECO103625	CPN200910	36%	75.6%	64.7%
ECO103625	CTR200162	40%	77.3%	77.3%
ECO103625	CAC102336	32%	55.5%	55.5%
ECO103625	CBO103162	27%	87.4%	94.6%
ECO103625	CDF103808	28%	89.1%	93.9%
ECO103625	CDP101660	30%	68.9%	73.9%
ECO103625	EBC100049	91%	76.5%	100%
ECO103625	EFA200678	28%	82.4%	83.9%
ECO103625	ECO103625	100%	100%	100%
ECO103625	HIN100980	69%	100%	100%
ECO103625	KPN302213	96%	100%	100%
ECO103625	LPN100279	42%	89.9%	92.1%
ECO103625	LMO102928	29%	82.4%	83.2%
ECO103625	MCA103188	38%	73.1%	64.2%
ECO103625	MAV100559	28%	80.7%	90.2%
ECO103625	MGE100474	26%	79.0%	73.4%
ECO103625	NGO101432	42%	72.3%	71.9%
ECO103625	NME200510	42%	72.3%	71.9%
ECO103625	PMU101163	63%	100%	91.5%
ECO103625	PRT102997	78%	100%	100%
ECO103625	PAE205564	46%	95.8%	85.2%
ECO103625	PPU102196	46%	95.8%	69.7%
ECO103625	PSY107592	47%	91.6%	66.7%
ECO103625	SPA106865	100%	31.1%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103625	STY104781	98%	100%	100%
ECO103625	STM104793	97%	100%	100%
ECO103625	SAU802713	26%	80.7%	83.5%
ECO103625	SEP201290	29%	80.7%	83.5%
ECO103625	SHA100141	27%	80.7%	83.3%
ECO103625	SMU100665	29%	79.8%	79.0%
ECO103625	SPN401851	31%	74.8%	72.4%
ECO103625	SPY200178	28%	90.8%	89.9%
ECO103625	UUR100610	28%	61.3%	64.6%
ECO103625	VCH100006	54%	99.2%	100%
ECO103625	YPS003466	89%	100%	100%
ECO103626	ABA100996	42%	97.4%	97.6%
ECO103626	BAN106241	26%	32.7%	80.2%
ECO103626	BAN101755	36%	38.1%	84.2%
ECO103626	BFR11357	23%	95.8%	86.7%
ECO103626	BPT100635	36%	98.2%	98.8%
ECO103626	BBU100441	34%	37.6%	41.4%
ECO103626	BCE114096	36%	94.5%	97.8%
ECO103626	BFI101036	37%	97.3%	98.2%
ECO103626	BMA108265	35%	97.6%	98.2%
ECO103626	CJU100888	39%	57.7%	57.4%
ECO103626	CPN200442	33%	42.0%	30.8%
ECO103626	CTR200515	27%	75.4%	59.2%
ECO103626	CAC102265	38%	32.7%	73.2%
ECO103626	CBO101415	36%	37.4%	97.2%
ECO103626	CDF102839	36%	37.2%	91.1%
ECO103626	CDP101656	33%	19.3%	36.3%
ECO103626	EBC104228	92%	100%	100%
ECO103626	EFA200679	35%	34.7%	70.2%
ECO103626	EFM202652	27%	33.0%	63.0%
ECO103626	ECO103626	100%	100%	100%
ECO103626	HIN100982	55%	99.5%	100%
ECO103626	HPY101429	36%	60.6%	58.9%
ECO103626	KPN300252	83%	24.6%	87.1%
ECO103626	KPN302215	86%	98.0%	100%
ECO103626	LPN100622	26%	10.4%	80.3%
ECO103626	LMO102229	36%	36.5%	71.4%
ECO103626	MCA103022	44%	97.4%	98.0%
ECO103626	MAV100557	24%	37.6%	73.1%
ECO103626	MBV106261	23%	37.6%	70.5%
ECO103626	MLP101603	25%	39.1%	70%
ECO103626	MTU203866	23%	37.6%	70.5%
ECO103626	MGE100473	19%	39.8%	66.2%
ECO103626	MPN100162	18%	39.1%	66.2%
ECO103626	NGO101427	33%	98.2%	98.5%
ECO103626	NME200508	33%	98.2%	98.5%
ECO103626	PMU101165	55%	99.5%	100%
ECO103626	PRT103088	68%	98.0%	100%
ECO103626	PAE205563	42%	97.8%	99.0%
ECO103626	PPU103675	45%	97.8%	98.6%
ECO103626	PSY103555	44%	97.3%	98.0%
ECO103626	SPA101311	89%	98.0%	100%
ECO103626	STY103946	95%	100%	100%
ECO103626	STM100542	95%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103626	SAU802090	29%	34.5%	70.7%
ECO103626	SEP201891	30%	34.7%	71.0%
ECO103626	SHA100992	31%	21.7%	78.5%
ECO103626	SMU100666	35%	33.4%	69.0%
ECO103626	SPN401850	29%	37.0%	75%
ECO103626	SPY200179	33%	37.6%	77.5%
ECO103626	TPA100939	38%	36.9%	33.8%
ECO103626	UUR100609	23%	41.4%	69.7%
ECO103626	VCH100004	57%	99.1%	100%
ECO103626	YPS003474	77%	99.8%	100%
ECO103627	ABA100998	56%	100%	100%
ECO103627	BAN111462	35%	66.1%	66.0%
ECO103627	BAN104510	33%	99.1%	99.3%
ECO103627	BFR11527	35%	99.6%	99.8%
ECO103627	BPT102869	55%	98.7%	98.0%
ECO103627	BBU100178	29%	99.3%	98.5%
ECO103627	BCE104176	54%	99.8%	99.4%
ECO103627	BFU101038	54%	99.8%	99.4%
ECO103627	BMA106211	54%	99.8%	99.4%
ECO103627	CJU100886	34%	99.3%	99.8%
ECO103627	CPN201012	37%	100%	100%
ECO103627	CTR200070	36%	100%	100%
ECO103627	CAC100805	35%	100%	100%
ECO103627	CBO101103	34%	100%	100%
ECO103627	CDF100515	41%	68.7%	98.4%
ECO103627	CDF102182	36%	99.3%	98.7%
ECO103627	EBC104229	94%	100%	100%
ECO103627	EFA200716	34%	99.1%	98.3%
ECO103627	EFM200971	33%	99.1%	92.9%
ECO103627	ECO103627	100%	100%	100%
ECO103627	HIN100983	74%	99.1%	97.6%
ECO103627	HPY101431	34%	99.3%	97.4%
ECO103627	KPN302217	93%	100%	100%
ECO103627	LMO101370	34%	99.1%	99.3%
ECO103627	MCA103209	47%	98.9%	98.1%
ECO103627	MGE100008	28%	100%	100%
ECO103627	MPN100146	29%	100%	100%
ECO103627	NGO100139	54%	100%	100%
ECO103627	NME200423	54%	100%	100%
ECO103627	PMU101166	77%	99.1%	96.8%
ECO103627	PRT100712	82%	100%	100%
ECO103627	PAE205562	66%	99.1%	98.9%
ECO103627	PPU102190	65%	94.9%	100%
ECO103627	PSY103429	66%	99.1%	96.0%
ECO103627	SPA101312	85%	100%	100%
ECO103627	STY103943	94%	100%	100%
ECO103627	STM100544	94%	100%	100%
ECO103627	SAU802712	32%	99.6%	99.8%
ECO103627	SEP201292	32%	99.6%	99.8%
ECO103627	SHA101595	32%	99.1%	100%
ECO103627	SMU100160	34%	99.1%	98.7%
ECO103627	SPN400920	33%	99.1%	94.2%
ECO103627	SPY200813	32%	99.1%	98.5%
ECO103627	TPA100544	29%	99.3%	98.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103627	UUR100016	29%	98.9%	99.5%
ECO103627	VCH100003	75%	99.1%	97.0%
ECO103627	YPS003478	88%	100%	100%
ECO103641	CAC101857	27%	14.9%	20.7%
ECO103641	ECO103641	100%	100%	100%
ECO103641	KPN302230	76%	99.6%	99.8%
ECO103641	MCA102901	23%	26.8%	46.5%
ECO103646	ABA105185	58%	96.5%	83%
ECO103646	BAN100509	58%	94.9%	98.0%
ECO103646	BAN112038	58%	98.8%	94.5%
ECO103646	BFR11994	58%	96.5%	98.0%
ECO103646	BPT101009	80%	97.7%	91.6%
ECO103646	BBU100217	57%	96.1%	95%
ECO103646	BCE100052	81%	96.9%	100%
ECO103646	BFU113657	80%	97.7%	89.7%
ECO103646	BMA105767	80%	96.9%	88.3%
ECO103646	CJU100577	49%	94.6%	97.6%
ECO103646	CAC103216	58%	96.1%	98.8%
ECO103646	CRO100411	48%	96.1%	98.8%
ECO103646	CBO102667	59%	96.1%	98.8%
ECO103646	CDF104057	60%	96.5%	97.2%
ECO103646	CDP100486	54%	62.3%	97.0%
ECO103646	EBC104233	95%	100%	100%
ECO103646	EFA200608	50%	97.3%	92.9%
ECO103646	EFM202214	51%	96.1%	98.0%
ECO103646	ECO103646	100%	100%	100%
ECO103646	KPN302234	98%	100%	100%
ECO103646	LMO102534	57%	97.3%	92.3%
ECO103646	MCA100490	70%	96.9%	89.2%
ECO103646	MAV105448	55%	96.5%	98.8%
ECO103646	MBV101896	53%	96.5%	98.8%
ECO103646	MLP101306	52%	96.5%	98.8%
ECO103646	MTU200814	53%	96.5%	98.8%
ECO103646	MGE100422	51%	94.9%	74.5%
ECO103646	MPN100233	49%	94.9%	74.5%
ECO103646	PMU100433	76%	99.2%	98.5%
ECO103646	PRT102833	92%	98.4%	98.1%
ECO103646	PAE205361	65%	96.5%	89.5%
ECO103646	PPU103688	64%	96.1%	87.9%
ECO103646	PSY104951	66%	96.9%	96.1%
ECO103646	SPA100792	98%	85.6%	95.7%
ECO103646	STY103908	98%	100%	100%
ECO103646	SAU801386	56%	94.9%	86.2%
ECO103646	SEP202087	56%	94.9%	83.8%
ECO103646	SHA101138	54%	94.9%	89.4%
ECO103646	SMU100937	49%	96.1%	98.0%
ECO103646	SPN401895	55%	95.3%	98%
ECO103646	SPY200951	51%	96.1%	97.6%
ECO103646	UUR100200	53%	95.7%	75.4%
ECO103646	VCH100713	60%	96.1%	90.5%
ECO103646	YPS003522	90%	100%	100%
ECO103655	ABA102336	75%	99.8%	99.6%
ECO103655	BAN102895	44%	99.0%	98.6%
ECO103655	BAN104850	54%	99.0%	98.6%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103655	BFR12383	55%	95.7%	95.6%
ECO103655	BPT102265	69%	99.0%	99.0%
ECO103655	BCE113271	68%	100%	100%
ECO103655	BFU111824	68%	100%	100%
ECO103655	BMA104609	69%	100%	100%
ECO103655	CJU100094	56%	99.2%	99.4%
ECO103655	CAC101220	56%	99.0%	98.4%
ECO103655	CBO103759	57%	99.0%	98.6%
ECO103655	CDF103688	57%	94.7%	95%
ECO103655	CDP100092	50%	99.4%	91.7%
ECO103655	EBC104234	95%	100%	100%
ECO103655	EFA201608	56%	95.3%	92.3%
ECO103655	EFM200643	53%	99.6%	96.9%
ECO103655	ECO103655	100%	100%	100%
ECO103655	HIN100461	86%	100%	100%
ECO103655	HPY101117	54%	99.6%	99.4%
ECO103655	KPN301117	98%	99.4%	100%
ECO103655	LPN101363	74%	75.4%	99.7%
ECO103655	LMO102357	53%	99.4%	98.6%
ECO103655	MCA100632	76%	99.8%	99.6%
ECO103655	MAV106522	49%	99.0%	91.2%
ECO103655	MBV105525	50%	99.0%	92.0%
ECO103655	MLP100709	49%	99.0%	90.5%
ECO103655	MTU201291	50%	99.0%	92.0%
ECO103655	MGE100413	48%	96.5%	93.2%
ECO103655	MPN100242	48%	96.1%	92.9%
ECO103655	NGO101344	69%	100%	99.6%
ECO103655	NME200481	69%	100%	99.6%
ECO103655	PMU101492	86%	100%	100%
ECO103655	PRT105365	92%	100%	100%
ECO103655	PAE205551	78%	99.8%	99.6%
ECO103655	PPU103565	77%	99.8%	99.6%
ECO103655	PSY106861	78%	90.8%	100%
ECO103655	SPA103402	98%	41.5%	100%
ECO103655	STY103858	98%	100%	100%
ECO103655	SAU802105	54%	96.3%	96.2%
ECO103655	SEP201899	54%	96.3%	96.0%
ECO103655	SHA101055	52%	99.6%	100%
ECO103655	SMU101004	53%	96.5%	96.6%
ECO103655	SPN401361	53%	96.5%	96.6%
ECO103655	SPY200556	52%	99.0%	98.6%
ECO103655	UUR100131	52%	91.8%	57.4%
ECO103655	VCH102727	84%	100%	98.1%
ECO103655	YPS003553	93%	100%	100%
ECO103658	ABA103520	51%	93.7%	91.4%
ECO103658	BAN106091	41%	78.5%	84.9%
ECO103658	BAN113226	45%	88.6%	97.2%
ECO103658	BFR103243	42%	83.5%	77.6%
ECO103658	BPT104646	45%	92.4%	91.2%
ECO103658	BCE104650	45%	88.6%	76.9%
ECO103658	BFU106433	45%	88.6%	76.9%
ECO103658	BMA101499	45%	88.6%	76.9%
ECO103658	CJU100866	35%	84.8%	59.8%
ECO103658	CAC103126	21%	89.9%	86.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103658	CBO102689	30%	82.3%	82.3%
ECO103658	CDP102004	47%	74.7%	74.7%
ECO103658	EBC108003	100%	49.4%	88.6%
ECO103658	EFA203405	40%	96.2%	98.6%
ECO103658	EFM202289	42%	87.3%	97.2%
ECO103658	ECO103658	100%	100%	100%
ECO103658	HIN100464	56%	84.8%	79.8%
ECO103658	HPY101195	34%	65.8%	49.5%
ECO103658	KPN306713	100%	100%	100%
ECO103658	LPN103500	23%	81.0%	70.3%
ECO103658	LMO100841	42%	88.6%	97.2%
ECO103658	MCA100629	52%	84.8%	82.7%
ECO103658	MAV106519	41%	84.8%	79.8%
ECO103658	MBV105519	38%	84.8%	70.5%
ECO103658	MLP100706	38%	84.8%	82.7%
ECO103658	MTU201288	38%	84.8%	82.7%
ECO103658	NGO103623	43%	89.9%	91.0%
ECO103658	NME200478	43%	89.9%	91.0%
ECO103658	PMU101489	55%	84.8%	79.8%
ECO103658	PRT103094	91%	100%	100%
ECO103658	PAE205554	57%	88.6%	82.4%
ECO103658	PPU100894	50%	38.0%	76.9%
ECO103658	PSY103434	57%	88.6%	82.4%
ECO103658	SPA106169	97%	100%	100%
ECO103658	STY107263	100%	100%	100%
ECO103658	SAU802108	46%	73.4%	82.9%
ECO103658	SEP204208	46%	73.4%	82.9%
ECO103658	SHA100057	42%	83.5%	94.3%
ECO103658	SMU102730	37%	54.4%	61.2%
ECO103658	SPN401365	27%	54.4%	65.2%
ECO103658	VCH102730	53%	84.8%	78.8%
ECO103658	YPS003562	100%	100%	100%
ECO103659	ABA102343	57%	100%	100%
ECO103659	BAN111963	37%	47.6%	88.9%
ECO103659	BAN106879	30%	82.3%	89.5%
ECO103659	BFR102190	24%	85.2%	61.4%
ECO103659	BPT104642	44%	99.6%	99.3%
ECO103659	BCE101199	49%	97.4%	96.1%
ECO103659	BFU104286	46%	98.2%	96.8%
ECO103659	BMA101219	49%	97.4%	96.1%
ECO103659	CJU101129	30%	82.7%	89.8%
ECO103659	CAC101894	29%	84.9%	89.6%
ECO103659	CBO100509	31%	80.8%	85.8%
ECO103659	CDF102803	30%	80.4%	87.6%
ECO103659	CDP100087	27%	84.5%	74.0%
ECO103659	EBC104246	93%	100%	100%
ECO103659	EFA203403	32%	70.1%	77.0%
ECO103659	EFM200212	34%	81.2%	88.3%
ECO103659	ECO103659	100%	100%	100%
ECO103659	HIN100465	53%	96.3%	96.2%
ECO103659	HPY100815	30%	85.6%	93.4%
ECO103659	KPN301113	91%	100%	100%
ECO103659	LPN100590	26%	80.1%	82.2%
ECO103659	LMO102867	31%	81.9%	88.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103659	MCA100628	53%	99.6%	99.0%
ECO103659	MAV106517	32%	84.9%	87.7%
ECO103659	MBV105517	34%	84.9%	88.4%
ECO103659	MLP100705	31%	84.9%	88.0%
ECO103659	MTU201287	34%	84.9%	88.4%
ECO103659	MGE100417	25%	82.7%	77.7%
ECO103659	MPN100238	22%	79.0%	73.7%
ECO103659	NGO101341	45%	100%	100%
ECO103659	NME200477	46%	100%	100%
ECO103659	PMU101488	52%	98.2%	97.3%
ECO103659	PRT105765	81%	99.6%	98.9%
ECO103659	PAE205555	53%	100%	99.7%
ECO103659	PPU103681	57%	86.3%	98.8%
ECO103659	PSY103433	53%	97.8%	98.3%
ECO103659	SPA103408	96%	100%	100%
ECO103659	STY103856	96%	100%	100%
ECO103659	SAU802109	34%	80.4%	85.5%
ECO103659	SEP201902	32%	82.7%	89.3%
ECO103659	SHA100056	28%	87.5%	97.1%
ECO103659	SMU101010	29%	85.6%	93.3%
ECO103659	SPN401364	24%	79.3%	85.7%
ECO103659	SPY200553	29%	81.5%	88.2%
ECO103659	UUR100136	25%	81.9%	77.8%
ECO103659	VCH102731	62%	98.9%	97.4%
ECO103659	YPS000004	84%	99.6%	98.9%
ECO103668	ABA104510	51%	96.9%	80.6%
ECO103668	BPT100131	54%	95.4%	77.7%
ECO103668	BCE113335	52%	96.1%	78.5%
ECO103668	BFU102356	54%	96.5%	80.1%
ECO103668	BMA106222	53%	96.9%	80.2%
ECO103668	EBC102338	91%	97.3%	81.2%
ECO103668	EFA200434	36%	84.4%	66.5%
ECO103668	EFM200928	36%	91.5%	72.1%
ECO103668	ECO103668	100%	100%	100%
ECO103668	KPN301443	91%	97.1%	81.2%
ECO103668	LPN102964	42%	96.7%	79.5%
ECO103668	PAE200916	53%	97.1%	79.8%
ECO103668	PPU108700	54%	95.2%	80.7%
ECO103668	PSY105528	54%	95.2%	78.6%
ECO103668	SPA103407	91%	95.2%	80.8%
ECO103668	STY103826	96%	97.3%	81.2%
ECO103668	STM100644	96%	97.3%	81.2%
ECO103668	SPY201083	35%	82.3%	64.3%
ECO103668	VCH103254	51%	96.1%	80.3%
ECO103668	YPS000050	83%	97.3%	81.2%
ECO103669	BAN110638	36%	88.1%	100%
ECO103669	BAN109542	45%	92.1%	100%
ECO103669	EBC102337	90%	98.7%	100%
ECO103669	EFA202098	44%	92.1%	100%
ECO103669	EFM200535	44%	92.1%	100%
ECO103669	ECO103669	100%	100%	100%
ECO103669	HIN100480	58%	92.1%	100%
ECO103669	KPN301442	89%	92.1%	100%
ECO103669	PMU100156	58%	92.1%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103669	PRT105359	60%	92.1%	100%
ECO103669	PPU111206	43%	92.1%	100%
ECO103669	PSY102602	42%	92.1%	100%
ECO103669	SPA105536	85%	37.1%	100%
ECO103669	STY103824	87%	92.1%	100%
ECO103669	STM100985	87%	92.1%	100%
ECO103669	SAU800269	43%	92.1%	100%
ECO103669	SEP201129	42%	92.1%	100%
ECO103669	SHA100905	46%	92.1%	100%
ECO103669	SPY200859	33%	37.1%	24.5%
ECO103669	VCH102863	51%	92.1%	89.1%
ECO103669	YPS000052	68%	92.1%	100%
ECO103671	BAN113187	46%	93.1%	99.3%
ECO103671	BAN101766	55%	95.0%	97.4%
ECO103671	BCE101785	34%	96.0%	92.9%
ECO103671	BCE103924	48%	92.8%	87.8%
ECO103671	BFU101396	41%	96.0%	91.8%
ECO103671	BMA102013	47%	93.1%	87.8%
ECO103671	CDF101478	46%	96.0%	91.9%
ECO103671	CDP101286	28%	93.1%	90.1%
ECO103671	EBC100655	95%	59.8%	100%
ECO103671	EFA200646	24%	77.6%	85.4%
ECO103671	ECO103671	100%	100%	100%
ECO103671	HIN100482	67%	94.4%	93.8%
ECO103671	KPN301440	95%	100%	100%
ECO103671	LPN100459	33%	91.9%	93.6%
ECO103671	MAV106603	31%	27.4%	31.0%
ECO103671	MLP100257	39%	91.9%	47.0%
ECO103671	PMU100154	66%	99.1%	97.8%
ECO103671	PRT101087	84%	99.7%	100%
ECO103671	PAE201946	38%	91.3%	87.0%
ECO103671	PPU111209	37%	91.3%	87.3%
ECO103671	PSY102877	40%	94.7%	92.1%
ECO103671	SPA100608	94%	100%	100%
ECO103671	STY103820	96%	100%	100%
ECO103671	STM100987	96%	100%	100%
ECO103671	SHA102966	57%	80.4%	100%
ECO103671	SPY100941	19%	86.6%	95.6%
ECO103671	VCH102865	73%	99.7%	96.7%
ECO103671	YPS000319	49%	92.8%	89.1%
ECO103672	BAN104641	49%	89.5%	96.4%
ECO103672	BAN105239	57%	90.2%	86.4%
ECO103672	BCE103519	32%	95.9%	91.1%
ECO103672	BFU115574	26%	94.3%	91.8%
ECO103672	BFU107090	29%	94.3%	90.9%
ECO103672	BFU114046	30%	95.9%	93.8%
ECO103672	BMA103821	32%	98.6%	93.7%
ECO103672	CDF101501	30%	90.9%	84.7%
ECO103672	EBC100654	97%	94.9%	100%
ECO103672	ECO103672	100%	100%	100%
ECO103672	HIN100483	73%	98.3%	99.3%
ECO103672	KPN301439	94%	100%	100%
ECO103672	LPN100587	23%	89.2%	91.8%
ECO103672	MLP100258	28%	76.7%	68.1%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103672	PMU100153	75%	99.0%	99.0%
ECO103672	PRT101086	77%	100%	100%
ECO103672	PAE201944	32%	93.9%	93.7%
ECO103672	PPU103878	32%	92.2%	89.7%
ECO103672	PSY101673	34%	98.6%	95.2%
ECO103672	SPA100607	95%	100%	100%
ECO103672	STY103818	97%	100%	100%
ECO103672	STM100988	97%	100%	100%
ECO103672	SHA100365	49%	89.5%	85.6%
ECO103672	SMU100518	24%	90.5%	86.6%
ECO103672	VCH102866	70%	99.7%	100%
ECO103672	YPS003542	31%	97.3%	90.4%
ECO103684	ABA100252	44%	97.1%	97.1%
ECO103684	BAN102540	34%	90.9%	95.2%
ECO103684	BAN100822	38%	90.9%	96.2%
ECO103684	BAN105647	39%	91.3%	92.3%
ECO103684	BAN112796	40%	91.3%	92.6%
ECO103684	BFR10908	28%	95.5%	90.6%
ECO103684	BPT102486	49%	97.1%	97.4%
ECO103684	BCE112712	46%	96.8%	97.7%
ECO103684	BFU103498	44%	96.8%	97.7%
ECO103684	BFU105781	43%	96.8%	95.8%
ECO103684	BMA101998	47%	96.8%	97.7%
ECO103684	CJU100241	45%	94.8%	96.1%
ECO103684	CAC103650	29%	95.5%	90.0%
ECO103684	CBO100231	26%	78.6%	76.3%
ECO103684	CDP100383	29%	95.5%	84.9%
ECO103684	EBC103120	97%	99.7%	99.7%
ECO103684	EFA200551	31%	96.4%	91.2%
ECO103684	EFM100086	30%	70.6%	95.3%
ECO103684	ECO103684	100%	100%	100%
ECO103684	HIN101166	29%	96.4%	91.5%
ECO103684	HPY101447	31%	96.4%	90.6%
ECO103684	KPN302044	94%	100%	100%
ECO103684	LPN100516	26%	90.0%	96.0%
ECO103684	LMO102393	31%	90.0%	93.1%
ECO103684	MCA100073	45%	97.4%	97.1%
ECO103684	MAV101180	29%	96.4%	85.7%
ECO103684	MBV104007	32%	95.5%	85.6%
ECO103684	MLP100526	30%	96.4%	87.5%
ECO103684	MTU202176	32%	95.5%	85.6%
ECO103684	NGO101582	27%	96.4%	91.9%
ECO103684	NME201988	27%	96.4%	91.9%
ECO103684	PMU100566	32%	96.8%	91.2%
ECO103684	PRT101816	88%	99.0%	99.4%
ECO103684	PAE205008	49%	95.5%	95.4%
ECO103684	PPU110137	30%	99.0%	86.1%
ECO103684	PSY104234	32%	97.4%	90.7%
ECO103684	SPA102767	97%	99.4%	100%
ECO103684	STY102144	97%	99.7%	99.7%
ECO103684	STM101003	97%	99.7%	99.7%
ECO103684	SAU800554	33%	96.4%	87.4%
ECO103684	SEP200080	32%	97.7%	88.5%
ECO103684	SHA101064	34%	95.1%	86.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103684	SMU101031	31%	96.8%	91.2%
ECO103684	SPN400758	32%	96.8%	91.5%
ECO103684	SPY200682	31%	96.8%	91.5%
ECO103684	VCH100029	71%	99.4%	96.2%
ECO103684	YPS001659	91%	99.0%	99.4%
ECO103685	ABA101148	72%	98.3%	98.7%
ECO103685	BAN107961	36%	90.2%	90.3%
ECO103685	BAN107556	48%	96.5%	95.0%
ECO103685	BFR12455	65%	96.5%	95.2%
ECO103685	BPT102335	73%	99.2%	96.4%
ECO103685	BCE110053	73%	99.2%	87.3%
ECO103685	BFU102555	73%	99.2%	98.5%
ECO103685	BMA108067	37%	96.4%	94.1%
ECO103685	CJU100013	46%	96.7%	95.7%
ECO103685	CAC101693	44%	97.2%	95.8%
ECO103685	CBO102730	36%	96.0%	93.5%
ECO103685	CDF100406	44%	96.4%	95.8%
ECO103685	CDP100193	66%	98.3%	96.2%
ECO103685	EBC103119	95%	97.5%	100%
ECO103685	ECO103685	100%	100%	100%
ECO103685	HIN100718	76%	99.2%	96.6%
ECO103685	KPN302046	95%	99.5%	96.8%
ECO103685	LMO100576	46%	95.5%	93.3%
ECO103685	MCA101145	71%	99.2%	96.7%
ECO103685	MAV103959	38%	61.7%	98.2%
ECO103685	MBV102695	39%	96.4%	92.7%
ECO103685	MLP101542	38%	96.4%	94.5%
ECO103685	MTU200188	39%	96.4%	92.7%
ECO103685	NGO100339	69%	99.2%	96.4%
ECO103685	NME201248	69%	99.2%	96.4%
ECO103685	PMU101625	79%	99.2%	96.7%
ECO103685	PRT104367	86%	99.5%	96.8%
ECO103685	PAE200352	73%	99.5%	96.7%
ECO103685	PPU102184	72%	99.5%	96.6%
ECO103685	PSY103562	72%	97.2%	99.2%
ECO103685	SPA102766	94%	90.2%	98.9%
ECO103685	STY102141	93%	99.5%	96.8%
ECO103685	STM101004	94%	99.5%	96.8%
ECO103685	SAU802053	46%	95.5%	93.4%
ECO103685	SEP201289	47%	95.5%	93.4%
ECO103685	SHA101345	45%	95.5%	93.4%
ECO103685	SMU101318	37%	96.9%	91.7%
ECO103685	SPN401932	37%	96.9%	93.5%
ECO103685	VCH100028	81%	99.5%	96.7%
ECO103685	YPS001655	86%	99.5%	96.8%
ECO103692	ABA100705	51%	99.0%	99.0%
ECO103692	BPT102270	49%	96.7%	97.0%
ECO103692	BBU100606	37%	94.5%	96.5%
ECO103692	BCE104021	47%	98.8%	87.4%
ECO103692	BFU101736	46%	98.8%	99.0%
ECO103692	BMA101028	46%	98.8%	99.1%
ECO103692	EBC102904	93%	99.3%	99.9%
ECO103692	ECO103692	100%	100%	100%
ECO103692	HIN100630	67%	99.1%	99.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103692	KPN302047	94%	95.4%	100%
ECO103692	LPN100488	50%	99.0%	99.8%
ECO103692	MCA101054	48%	99.6%	97.4%
ECO103692	MGE100248	27%	90.3%	84.4%
ECO103692	NGO100148	48%	94.8%	94.2%
ECO103692	NME201520	48%	94.8%	94.2%
ECO103692	PMU101059	65%	99.6%	100%
ECO103692	PRT102849	78%	99.3%	99.4%
ECO103692	PAE205291	54%	99.0%	99.4%
ECO103692	PPU102306	54%	99.0%	99.4%
ECO103692	PSY103420	53%	97.6%	99.7%
ECO103692	SPA103752	96%	100%	99.9%
ECO103692	STY102114	96%	100%	99.9%
ECO103692	STM101022	96%	100%	99.9%
ECO103692	TPA100101	38%	94.1%	95.0%
ECO103692	VCH100165	72%	99.0%	99.6%
ECO103692	YPS001548	85%	99.3%	99.3%
ECO103696	ECO103696	100%	100%	100%
ECO103697	ABA100304	77%	99.8%	100%
ECO103697	BAN105100	45%	98.8%	96.2%
ECO103697	BAN113042	57%	98.8%	96.5%
ECO103697	BFR103103	62%	87.4%	53.6%
ECO103697	BPT100264	70%	99.8%	100%
ECO103697	BBU100229	57%	99.3%	80.6%
ECO103697	BCE104048	69%	99.8%	99.5%
ECO103697	BFU105309	70%	97.1%	95.5%
ECO103697	BMA101995	69%	99.8%	99.5%
ECO103697	CJU101081	56%	98.8%	95.1%
ECO103697	CPN200135	60%	99.0%	89.0%
ECO103697	CTR200767	61%	99.0%	98.6%
ECO103697	CAC102868	57%	1.7%	14.3%
ECO103697	CBO103912	55%	87.4%	75.7%
ECO103697	CDF100058	60%	79.5%	66.4%
ECO103697	CDP100068	54%	87.6%	54.3%
ECO103697	EBC103271	97%	63.2%	100%
ECO103697	EFA201306	52%	99.0%	95.3%
ECO103697	ECO103697	100%	100%	100%
ECO103697	HIN100281	87%	100%	100%
ECO103697	HPY100543	54%	99.0%	94.1%
ECO103697	KPN301899	99%	95.5%	100%
ECO103697	LMO101598	55%	99.5%	97.9%
ECO103697	MCA100009	69%	46.5%	99.0%
ECO103697	MAV106530	51%	95.9%	65.3%
ECO103697	MBV105502	51%	95.9%	64.6%
ECO103697	MLP100698	51%	95.9%	63.8%
ECO103697	MTU201280	51%	95.9%	64.6%
ECO103697	NGO100759	69%	99.5%	99.5%
ECO103697	NME200762	69%	99.5%	99.5%
ECO103697	PMU101920	88%	100%	100%
ECO103697	PRT102841	95%	100%	100%
ECO103697	PAE205234	81%	99.8%	99.8%
ECO103697	PPU100260	81%	95.9%	99.8%
ECO103697	PSY100590	79%	99.8%	99.8%
ECO103697	SPA103748	99%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103697	STY102102	99%	100%	100%
ECO103697	STM101036	99%	100%	100%
ECO103697	SAU802121	52%	98.6%	93.2%
ECO103697	SEP201911	51%	98.6%	93.2%
ECO103697	SHA100146	51%	98.6%	90.3%
ECO103697	TPA100251	63%	93.8%	75.1%
ECO103697	VCH100303	91%	99.8%	99.8%
ECO103697	YPS001531	95%	100%	100%
ECO103698	ABA100164	24%	82.3%	87.2%
ECO103698	BAN100173	24%	89.6%	94.1%
ECO103698	BAN111934	27%	95.9%	98.0%
ECO103698	BFR11277	27%	74.9%	89.4%
ECO103698	BPT100693	27%	66.5%	66.5%
ECO103698	BCE102990	23%	94.6%	97.6%
ECO103698	BFU101096	25%	84.2%	84.7%
ECO103698	BMA100577	22%	95.9%	100%
ECO103698	CAC103146	23%	78.5%	84.3%
ECO103698	CBO100307	27%	87.5%	94.5%
ECO103698	CDP100086	27%	79.0%	81.2%
ECO103698	EBC103269	86%	100%	100%
ECO103698	EFA201668	25%	88.6%	85.1%
ECO103698	EFM202542	23%	89.9%	88.1%
ECO103698	ECO103698	100%	100%	100%
ECO103698	HIN101681	59%	93.7%	96.9%
ECO103698	HPY101558	23%	77.4%	79.2%
ECO103698	KPN301897	86%	91.0%	100%
ECO103698	LPN100889	25%	82.6%	86.8%
ECO103698	LMO100133	29%	83.9%	85.4%
ECO103698	MAV106513	27%	81.2%	80.3%
ECO103698	MBV105513	27%	79.6%	79.3%
ECO103698	MLP100703	25%	81.2%	82.0%
ECO103698	MTU201285	27%	81.2%	80.9%
ECO103698	PMU100463	59%	95.6%	98.9%
ECO103698	PRT102839	76%	97.3%	98.3%
ECO103698	SPA103747	89%	83.1%	99.7%
ECO103698	STY102099	87%	100%	100%
ECO103698	STM101037	87%	100%	100%
ECO103698	SAU800747	26%	90.5%	90.6%
ECO103698	SEP201371	26%	90.2%	89.1%
ECO103698	SHA102011	25%	90.2%	88.6%
ECO103698	SMU101498	26%	90.7%	88.1%
ECO103698	SPY200209	25%	88.8%	87.1%
ECO103698	YPS001526	80%	97.3%	97.8%
ECO103710	BAN100022	36%	39.0%	67.4%
ECO103710	BAN110606	56%	20.3%	84.7%
ECO103710	BAN100162	51%	30.9%	77.6%
ECO103710	BAN106694	36%	72.4%	88.9%
ECO103710	BAN111095	36%	76.8%	81.9%
ECO103710	BFR104919	31%	76.4%	86.9%
ECO103710	BFU100858	35%	76.0%	76.9%
ECO103710	BFU110458	33%	77.2%	80.8%
ECO103710	CAC102880	25%	85.8%	86.4%
ECO103710	CBO101373	32%	86.2%	93.7%
ECO103710	EBC103267	82%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103710	EFA201299	32%	87.4%	86.3%
ECO103710	EFM201041	23%	75.2%	87.7%
ECO103710	EFM200803	27%	95.1%	86.7%
ECO103710	ECO103710	100%	100%	100%
ECO103710	KPN301891	82%	100%	100%
ECO103710	LMO100605	32%	80.5%	79.5%
ECO103710	PRT100152	69%	99.2%	99.6%
ECO103710	PPU110732	25%	83.7%	79.2%
ECO103710	SPA102856	88%	100%	100%
ECO103710	STY102069	87%	100%	100%
ECO103710	STM101058	88%	100%	100%
ECO103710	SAU800636	32%	81.3%	78.0%
ECO103710	SEP200215	31%	80.5%	74.2%
ECO103710	SHA100117	28%	80.5%	80.3%
ECO103710	VCH100911	38%	77.6%	76.4%
ECO103710	YPS001461	70%	100%	100%
ECO103723	ABA105566	34%	82.6%	83.5%
ECO103723	ABA104216	38%	96.0%	95.1%
ECO103723	BPT100513	45%	96.0%	93.9%
ECO103723	BCE108192	44%	99.3%	99.3%
ECO103723	BFU105837	46%	97.0%	97.4%
ECO103723	BMA109620	45%	96.0%	95.5%
ECO103723	EBC102509	81%	57.4%	100%
ECO103723	ECO103723	100%	100%	100%
ECO103723	HIN100657	59%	98.3%	99.3%
ECO103723	KPN303535	87%	100%	100%
ECO103723	MCA103469	41%	91.9%	86.1%
ECO103723	NGO101576	46%	80.5%	80%
ECO103723	NME200545	46%	80.5%	80%
ECO103723	PMU101701	57%	99.0%	100%
ECO103723	PRT102819	64%	97.7%	95.1%
ECO103723	PAE205275	50%	98.3%	96.7%
ECO103723	PPU109123	49%	97.7%	97.3%
ECO103723	PSY103037	50%	97.0%	96.7%
ECO103723	SPA100310	93%	59.1%	100%
ECO103723	STY102033	90%	99.0%	98.3%
ECO103723	STM101083	90%	100%	100%
ECO103723	SMU100191	26%	72.8%	70.2%
ECO103723	SPN401046	33%	48.7%	41.9%
ECO103723	SPY200913	29%	48.7%	41.9%
ECO103723	UUR100144	25%	94.0%	93.5%
ECO103723	UUR100223	24%	93.3%	95.2%
ECO103723	VCH100127	57%	97.0%	93.2%
ECO103723	YPS001404	72%	99.0%	97.4%
ECO103724	BCE109755	32%	95.8%	94.6%
ECO103724	BFU111719	33%	38.2%	40.9%
ECO103724	EBC101110	79%	100%	100%
ECO103724	ECO103724	100%	100%	100%
ECO103724	KPN303537	76%	100%	100%
ECO103724	MPN100107	37%	22.3%	12.0%
ECO103724	PMU101700	39%	100%	99.6%
ECO103724	PRT102800	51%	100%	100%
ECO103724	PAE205276	33%	97.5%	98.3%
ECO103724	PPU109127	32%	96.2%	97.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103724	PSY103036	33%	96.2%	97.8%
ECO103724	SPA100311	87%	100%	100%
ECO103724	STY102031	86%	100%	100%
ECO103724	STM101084	87%	100%	100%
ECO103724	VCH100128	43%	100%	99.6%
ECO103724	YPS001402	64%	100%	100%
ECO103725	BAN105739	28%	96.4%	96.7%
ECO103725	BAN105118	39%	98.6%	98.0%
ECO103725	BFR10181	39%	87.5%	90.0%
ECO103725	BPT100444	46%	99.3%	96.6%
ECO103725	BCE114095	46%	87.8%	100%
ECO103725	BFU114667	44%	99.3%	99.5%
ECO103725	BMA108211	44%	99.3%	99.5%
ECO103725	CJU101027	34%	97.1%	97.7%
ECO103725	CPN201081	38%	88.8%	99.5%
ECO103725	CTR200887	38%	88.8%	99.8%
ECO103725	CAC100746	36%	98.5%	98.9%
ECO103725	CBO101783	36%	99.3%	99.7%
ECO103725	CDF102800	37%	98.8%	98.3%
ECO103725	CDP100108	37%	97.4%	92.8%
ECO103725	EBC101111	96%	53.6%	99.0%
ECO103725	EFA201050	39%	99.3%	99.2%
ECO103725	EFM200737	23%	86.8%	88.5%
ECO103725	ECO103725	100%	100%	100%
ECO103725	HIN101161	67%	100%	99.7%
ECO103725	HPY101457	32%	95.1%	94.3%
ECO103725	KPN303539	96%	100%	99.7%
ECO103725	LPN100538	58%	73.1%	100%
ECO103725	LMO100030	41%	100%	100%
ECO103725	MAV107704	39%	97.9%	96.6%
ECO103725	MBV101967	39%	97.4%	95.8%
ECO103725	MLP100111	37%	97.9%	96.7%
ECO103725	MTU200940	39%	97.4%	95.8%
ECO103725	MPN100496	30%	87.9%	87.7%
ECO103725	MPN100495	26%	97.5%	97.3%
ECO103725	NGO100682	48%	99.3%	98.8%
ECO103725	NME200026	47%	99.3%	98.8%
ECO103725	PMU100411	67%	100%	99.9%
ECO103725	PRT102802	83%	99.7%	100%
ECO103725	PAE205438	64%	99.9%	99.6%
ECO103725	PPU102313	62%	99.9%	99.5%
ECO103725	PSY103224	60%	94.4%	99.6%
ECO103725	SPA101953	95%	71.1%	100%
ECO103725	STY102029	97%	100%	100%
ECO103725	STM101095	97%	100%	100%
ECO103725	SAU801905	39%	99.0%	99.0%
ECO103725	SEP200564	39%	98.6%	98.5%
ECO103725	SHA100319	39%	98.5%	100%
ECO103725	SMU100987	39%	99.0%	99.3%
ECO103725	SPN400995	37%	99.0%	99.2%
ECO103725	SPY200975	37%	99.0%	99.4%
ECO103725	UUR100506	32%	94.7%	95.0%
ECO103725	VCH100188	71%	100%	99.9%
ECO103725	YPS001400	88%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103734	BAN107067	35%	96.2%	99.0%
ECO103734	BAN107697	38%	95.6%	99.7%
ECO103734	BFR103658	39%	97.0%	83.2%
ECO103734	BFR100902	43%	96.4%	99.7%
ECO103734	BPT102537	45%	95.1%	91.4%
ECO103734	BCE105218	44%	96.7%	99.7%
ECO103734	BFU100843	44%	96.1%	99.0%
ECO103734	BMA100378	44%	96.7%	93.2%
ECO103734	CAC103600	38%	96.2%	81.5%
ECO103734	CBO103824	38%	96.9%	82.5%
ECO103734	CDF101265	39%	96.4%	83.2%
ECO103734	EBC103961	90%	99.7%	100%
ECO103734	EFA200307	41%	96.9%	99.0%
ECO103734	EFM200383	40%	95.7%	98.0%
ECO103734	ECO103734	100%	100%	100%
ECO103734	HIN100708	63%	96.6%	95.8%
ECO103734	KPN303551	90%	99.5%	100%
ECO103734	LPN102588	55%	64.1%	100%
ECO103734	LMO101490	40%	96.2%	98.5%
ECO103734	NGO101892	46%	94.9%	93.0%
ECO103734	NME202048	46%	96.1%	98.7%
ECO103734	PMU101427	62%	97.2%	94.3%
ECO103734	PRT106116	73%	97.0%	99.2%
ECO103734	PAE203342	47%	96.1%	83.4%
ECO103734	PPU100810	48%	97.5%	84.3%
ECO103734	PSY104559	46%	90.8%	83.2%
ECO103734	SPA101175	90%	98.2%	100%
ECO103734	STY102015	94%	99.7%	100%
ECO103734	STM101102	94%	100%	99.3%
ECO103734	SAU800721	37%	96.1%	98.7%
ECO103734	SEP200775	36%	96.4%	99.2%
ECO103734	SHA101682	37%	95.9%	98.6%
ECO103734	TPA100102	32%	59.0%	67.2%
ECO103734	VCH100194	66%	98.2%	96.9%
ECO103734	YPS001354	80%	99.5%	100%
ECO103736	ABA102357	37%	99.3%	76.2%
ECO103736	BPT101441	37%	97.8%	65.6%
ECO103736	BCE108675	40%	97.1%	66.4%
ECO103736	EBC103968	86%	100%	67.0%
ECO103736	ECO103736	100%	100%	100%
ECO103736	KPN305601	88%	100%	67.0%
ECO103736	PAE205244	42%	99.3%	66.0%
ECO103736	PPU105485	39%	98.6%	65.4%
ECO103736	PSY101257	41%	96.4%	64.3%
ECO103736	SPA101173	85%	100%	66.8%
ECO103736	STY102011	88%	100%	67.0%
ECO103736	VCH100135	50%	97.8%	65.9%
ECO103736	YPS001350	75%	98.6%	66.0%
ECO103756	ABA101057	24%	97.4%	67.0%
ECO103756	BPT100580	31%	97.4%	67.5%
ECO103756	BCE107538	31%	97.4%	67.3%
ECO103756	BFU101829	32%	97.4%	67.3%
ECO103756	BFU100980	35%	91.8%	61.4%
ECO103756	BMA108689	31%	97.4%	67.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103756	CPN200966	34%	38.6%	22.0%
ECO103756	CTR200116	32%	38.6%	22.0%
ECO103756	CBO101859	24%	83.3%	65.2%
ECO103756	CBO101032	22%	73.4%	57.6%
ECO103756	CDF100557	28%	47.6%	38.7%
ECO103756	CDP101430	26%	72.5%	45.2%
ECO103756	EBC103300	87%	100%	100%
ECO103756	ECO103756	100%	100%	100%
ECO103756	KPN303516	87%	100%	100%
ECO103756	LPN103089	27%	71.2%	52.8%
ECO103756	MBV104303	27%	87.6%	24.6%
ECO103756	MTU201904	27%	87.6%	24.6%
ECO103756	NGO101111	33%	97.9%	69.0%
ECO103756	NME201430	32%	97.9%	69.0%
ECO103756	PRT105013	67%	100%	100%
ECO103756	PAE205231	30%	98.3%	70.2%
ECO103756	PPU100265	28%	98.3%	87.3%
ECO103756	PSY101307	28%	85.8%	61.5%
ECO103756	SPA101404	90%	100%	100%
ECO103756	STY101987	90%	100%	100%
ECO103756	STM101142	90%	100%	100%
ECO103756	VCH100307	48%	98.7%	99.2%
ECO103756	YPS000586	77%	100%	100%
ECO103766	BAN101805	21%	82.3%	87.6%
ECO103766	BCE107575	42%	96.0%	93.9%
ECO103766	BFU100736	43%	97.6%	91.1%
ECO103766	BMA104037	43%	97.6%	94.5%
ECO103766	EBC101352	80%	100%	100%
ECO103766	ECO103766	100%	100%	100%
ECO103766	KPN300972	80%	100%	100%
ECO103766	LPN100444	22%	73.5%	74.5%
ECO103766	PRT101378	52%	99.4%	99.1%
ECO103766	PAE200485	42%	96.6%	98.5%
ECO103766	PPU105090	44%	96.6%	98.5%
ECO103766	PSY103362	46%	97.6%	99.4%
ECO103766	SPA103893	85%	100%	100%
ECO103766	STY103453	85%	100%	100%
ECO103766	STM101489	85%	100%	100%
ECO103766	VCH100035	55%	100%	96.5%
ECO103766	YPS001282	66%	100%	100%
ECO103775	ABA101332	40%	98.0%	96.7%
ECO103775	BFR10050	31%	33.0%	28.8%
ECO103775	BFR103847	25%	61.0%	49.4%
ECO103775	BFR104769	28%	61.9%	91.3%
ECO103775	BFR102132	26%	65.0%	53.5%
ECO103775	BFR10471	29%	96.0%	71.6%
ECO103775	BPT102677	40%	95.1%	96.3%
ECO103775	BCE114517	37%	80.2%	100%
ECO103775	BFU101390	41%	94.0%	89.2%
ECO103775	BMA104868	42%	96.0%	91.3%
ECO103775	EBC103134	91%	100%	100%
ECO103775	ECO103775	100%	100%	100%
ECO103775	KPN301350	93%	100%	100%
ECO103775	PRT102824	71%	99.7%	98.6%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103775	PAE205119	46%	96.8%	96.6%
ECO103775	PPU106801	46%	96.8%	95.8%
ECO103775	PSY105821	46%	96.8%	95.8%
ECO103775	SPA103890	90%	100%	100%
ECO103775	STY103418	92%	100%	100%
ECO103775	VCH102709	58%	96.3%	96.0%
ECO103775	YPS001316	86%	100%	100%
ECO103777	ABA101290	72%	99.8%	97.5%
ECO103777	BAN108593	52%	99.5%	96.4%
ECO103777	BAN110377	54%	99.5%	96.2%
ECO103777	BFR12436	51%	99.5%	97.7%
ECO103777	BPT100252	63%	100%	95.0%
ECO103777	BCE107416	64%	99.8%	97.2%
ECO103777	BFU101165	65%	100%	84.5%
ECO103777	BMA100582	65%	100%	97.4%
ECO103777	CJU100039	54%	99.8%	97.7%
ECO103777	CAC100624	56%	99.2%	96.7%
ECO103777	CBO103040	56%	99.2%	96.2%
ECO103777	CDF100332	51%	99.3%	96.4%
ECO103777	CDP100988	46%	99.2%	96.2%
ECO103777	EBC103136	96%	100%	97.4%
ECO103777	EFA200305	53%	99.5%	96.4%
ECO103777	EFM200826	52%	87.6%	97.2%
ECO103777	ECO103777	100%	100%	100%
ECO103777	HIN100844	82%	99.7%	95.8%
ECO103777	HPY100476	53%	99.7%	98.0%
ECO103777	KPN301352	96%	100%	97.4%
ECO103777	LPN100213	68%	99.8%	97.0%
ECO103777	LMO100625	53%	99.2%	96.1%
ECO103777	MCA100597	70%	99.8%	97.1%
ECO103777	MAV106479	46%	98.8%	96.5%
ECO103777	MBV101431	46%	98.8%	96.5%
ECO103777	MLP100924	45%	98.8%	96.5%
ECO103777	MTU201150	46%	98.8%	96.5%
ECO103777	NGO100315	64%	99.8%	97.7%
ECO103777	NME201257	63%	99.8%	97.7%
ECO103777	PMU101173	84%	99.7%	95.8%
ECO103777	PRT102826	86%	100%	95.3%
ECO103777	PAE205112	73%	99.8%	97.5%
ECO103777	PPU101976	72%	99.8%	97.4%
ECO103777	PSY103102	73%	99.8%	97.4%
ECO103777	SPA102685	96%	72.3%	96.8%
ECO103777	STY103413	97%	100%	97.4%
ECO103777	STM101499	96%	100%	97.4%
ECO103777	SAU801109	54%	99.5%	95.6%
ECO103777	SEP200827	55%	99.5%	95.6%
ECO103777	SHA100537	55%	99.5%	95.8%
ECO103777	SMU100076	55%	99.5%	96.1%
ECO103777	SPN400598	56%	99.5%	95.2%
ECO103777	SPY201176	56%	99.2%	95.9%
ECO103777	VCH102705	77%	99.7%	96.7%
ECO103777	YPS001324	89%	100%	97.4%
ECO103780	CDF100620	25%	95.0%	93.8%
ECO103780	CDF104341	33%	98.1%	97.1%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103780	ECO103780	100%	100%	100%
ECO103780	MGE100300	21%	89.8%	86.5%
ECO103780	MPN100420	19%	87.6%	84.8%
ECO103780	PRT102426	49%	96.0%	97.1%
ECO103780	YPS000405	48%	96.0%	98.1%
ECO103781	ECO103781	100%	100%	100%
ECO103781	SPA102688	86%	100%	73.5%
ECO103781	STY104820	87%	100%	100%
ECO103785	CAC101851	25%	48.4%	48.5%
ECO103785	CDP101064	30%	87.3%	89.2%
ECO103785	ECO103785	100%	100%	100%
ECO103785	MCA102158	31%	17.2%	91.5%
ECO103785	MAV107238	22%	71.4%	75.3%
ECO103785	SPA103927	54%	94.2%	98.9%
ECO103785	STY103395	53%	84.4%	98.8%
ECO103785	SMU100438	30%	26.9%	28.5%
ECO103797	BCE112972	41%	91.9%	79.9%
ECO103797	BFU111330	38%	95.8%	94.0%
ECO103797	RMA105326	39%	97.7%	93.5%
ECO103797	EBC103442	90%	100%	100%
ECO103797	ECO103797	100%	100%	100%
ECO103797	HIN100008	50%	99.4%	99.3%
ECO103797	KPN302470	91%	100%	100%
ECO103797	PMU100405	52%	98.7%	98.7%
ECO103797	PRT102687	64%	99.4%	100%
ECO103797	PAE204805	40%	92.2%	94.2%
ECO103797	PPU104433	39%	92.6%	91.8%
ECO103797	SPA103932	91%	99.0%	100%
ECO103797	STY103328	93%	100%	100%
ECO103797	YPS003285	68%	99.4%	100%
ECO103798	BPT101903	30%	93.4%	52.7%
ECO103798	BCE109548	55%	92.4%	94.7%
ECO103798	BFU111328	52%	95.7%	93.6%
ECO103798	BMA100819	55%	92.4%	94.7%
ECO103798	EBC103443	92%	100%	100%
ECO103798	ECO103798	100%	100%	100%
ECO103798	KPN302473	94%	100%	100%
ECO103798	LPN100501	33%	25.1%	44.4%
ECO103798	PRT102688	63%	99.5%	96.3%
ECO103798	PPU104432	48%	95.7%	93.6%
ECO103798	PSY102851	23%	28.0%	81.1%
ECO103798	SPA103931	96%	100%	100%
ECO103798	STY103324	96%	100%	100%
ECO103798	YPS003289	79%	99.5%	93.8%
ECO103807	BFR101151	29%	45.2%	47.9%
ECO103807	BFU111580	39%	92.3%	96%
ECO103807	BMA109843	40%	38.5%	35.7%
ECO103807	CJU100453	27%	75%	75.2%
ECO103807	EBC104478	84%	99.0%	99.0%
ECO103807	EFA201217	53%	99.0%	100%
ECO103807	EFM101566	50%	99.0%	100%
ECO103807	ECO103807	100%	100%	100%
ECO103807	KPN302365	86%	99.0%	99.0%
ECO103807	LMO101722	49%	99.0%	99.0%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103807	SPA101051	83%	98.1%	100%
ECO103807	STY103282	91%	99.0%	99.0%
ECO103807	YPS003339	77%	99.0%	99.0%
ECO103809	EBC104517	91%	99.0%	99.0%
ECO103809	EFA201219	57%	99.3%	97.0%
ECO103809	EFM101564	56%	98.8%	99.0%
ECO103809	ECO103809	100%	100%	100%
ECO103809	KPN302368	91%	100%	100%
ECO103809	LMO100814	56%	99.3%	99.0%
ECO103809	PAE202061	29%	21.5%	22.6%
ECO103809	SPA100408	90%	74.0%	100%
ECO103809	STY103273	93%	99.8%	99.8%
ECO103809	YPS003349	85%	99.8%	100%
ECO103820	EBC106068	81%	97.5%	72.6%
ECO103820	ECO103820	100%	100%	100%
ECO103820	KPN302369	81%	97.5%	70.8%
ECO103820	PRT100357	54%	85.2%	56.4%
ECO103820	SPA101676	94%	100%	73.5%
ECO103820	STY103224	93%	100%	73.5%
ECO103820	STM101595	94%	100%	73.5%
ECO103820	VCH102654	30%	77.0%	60.5%
ECO103820	YPS001584	62%	91.8%	69.1%
ECO103831	BAN108705	40%	97.3%	98.1%
ECO103831	BAN102104	49%	97.3%	98.1%
ECO103831	BPT105757	35%	17.6%	17.3%
ECO103831	BFU109396	38%	13.1%	40.4%
ECO103831	CAC101874	45%	96.1%	96.9%
ECO103831	CBO103264	44%	96.4%	97.2%
ECO103831	CDP100933	44%	96.4%	92.3%
ECO103831	EBC104507	90%	100%	100%
ECO103831	ECO103831	100%	100%	100%
ECO103831	HIN100648	69%	96.7%	97.6%
ECO103831	KPN300578	91%	43.2%	93.5%
ECO103831	KPN302251	91%	100%	100%
ECO103831	MAV100810	42%	96.4%	86.9%
ECO103831	MBV104392	43%	96.4%	86.2%
ECO103831	MLP101184	41%	95.2%	93.9%
ECO103831	MTU201084	42%	95.2%	93.9%
ECO103831	PMU101482	71%	97.6%	97.3%
ECO103831	PRT105964	53%	94.9%	97.9%
ECO103831	PAE201167	35%	19.9%	62.3%
ECO103831	SPA100765	90%	86.6%	100%
ECO103831	STY103133	94%	100%	91.8%
ECO103831	VCH102651	80%	100%	100%
ECO103832	ABA103732	71%	98.8%	98.8%
ECO103832	BAN107568	53%	40.4%	91.4%
ECO103832	BAN110463	64%	78.7%	99.7%
ECO103832	BPT102742	54%	99.0%	98.4%
ECO103832	BBU100240	55%	98.2%	98.4%
ECO103832	BCE105610	30%	98.8%	98.4%
ECO103832	BFU103471	60%	99.0%	99.4%
ECO103832	BMA108603	60%	99.0%	95.8%
ECO103832	CAC100927	66%	98.8%	99.8%
ECO103832	CBO103256	64%	99.2%	97.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103832	CDF103106	65%	99.6%	98.8%
ECO103832	CDP100653	49%	99.2%	99.8%
ECO103832	EBC104504	94%	100%	100%
ECO103832	EFA202255	57%	97.8%	97.8%
ECO103832	EFM201617	57%	95.4%	99.8%
ECO103832	ECO103832	100%	100%	100%
ECO103832	HIN100672	76%	100%	99.8%
ECO103832	KPN300967	93%	100%	99.8%
ECO103832	LPN100925	43%	97.8%	99.0%
ECO103832	LMO101597	63%	98.8%	99.8%
ECO103832	MAV103198	53%	98.6%	98.6%
ECO103832	MBV104620	52%	98.0%	99.6%
ECO103832	MLP101379	51%	98.2%	98.2%
ECO103832	MTU203642	52%	98.0%	96.3%
ECO103832	MGE100038	46%	99.4%	99.4%
ECO103832	MPN100104	47%	99.4%	99.4%
ECO103832	PMU101446	77%	100%	100%
ECO103832	PRT101873	83%	99.2%	97.8%
ECO103832	PAE203580	77%	98.8%	98.2%
ECO103832	PPU101510	73%	99.4%	98.8%
ECO103832	PSY105188	74%	99.2%	98.2%
ECO103832	SPA101671	94%	99.8%	100%
ECO103832	STY103131	95%	100%	100%
ECO103832	SAU801301	61%	98.6%	99.4%
ECO103832	SEP201925	60%	99.2%	99.8%
ECO103832	SHA100389	60%	99.2%	99.8%
ECO103832	SPN401988	56%	100%	100%
ECO103832	SPY201295	56%	100%	98.8%
ECO103832	VCH103465	79%	99.0%	98.4%
ECO103832	YPS003517	40%	97.2%	98.0%
ECO103833	BAN104073	33%	90.7%	89.0%
ECO103833	BAN113128	35%	84.7%	82.4%
ECO103833	BBU100239	34%	85.4%	92.9%
ECO103833	BCE106343	34%	86.5%	96.6%
ECO103833	BFU103519	34%	85.4%	95.8%
ECO103833	BMA100563	35%	87.9%	98.3%
ECO103833	CAC100464	29%	88.6%	98.3%
ECO103833	CBO103391	35%	85.4%	96.6%
ECO103833	CDP100666	31%	82.6%	92.3%
ECO103833	EBC104502	90%	100%	100%
ECO103833	EFA202259	33%	87.9%	97.5%
ECO103833	EFM202473	33%	87.5%	97.5%
ECO103833	ECO103833	100%	100%	100%
ECO103833	HIN100671	73%	91.5%	97.3%
ECO103833	KPN300234	87%	31.7%	90.1%
ECO103833	KPN300966	86%	100%	100%
ECO103833	LMO100437	38%	90.7%	88.6%
ECO103833	MCA100082	26%	48.0%	28.5%
ECO103833	MGE100033	25%	83.6%	89.9%
ECO103833	MPN100111	28%	87.5%	95.5%
ECO103833	PMU101445	70%	91.1%	97.7%
ECO103833	PRT103927	70%	95.0%	98.9%
ECO103833	PAE203579	74%	91.5%	92.1%
ECO103833	PPU101511	73%	90.7%	90.1%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103833	PSY105186	70%	94.3%	93.0%
ECO103833	SPA101670	90%	100%	100%
ECO103833	STY103129	93%	100%	100%
ECO103833	SAU801300	36%	85.4%	83.1%
ECO103833	SEP201923	34%	85.4%	82.5%
ECO103833	SHA100072	35%	82.9%	94.8%
ECO103833	SMU100734	27%	90.4%	99.0%
ECO103833	SPN401985	32%	87.2%	98.7%
ECO103833	SPY201293	34%	85.1%	96.6%
ECO103833	YPS001686	82%	99.3%	100%
ECO103844	EBC104495	93%	100%	100%
ECO103844	ECO103844	100%	100%	100%
ECO103844	HIN100280	81%	100%	100%
ECO103844	KPN303238	94%	100%	100%
ECO103844	PMU101290	82%	100%	100%
ECO103844	PRT100952	90%	100%	100%
ECO103844	SPA103063	99%	100%	100%
ECO103844	STY103105	99%	100%	100%
ECO103844	VCH102645	80%	99.0%	99.0%
ECO103844	YPS001438	89%	100%	100%
ECO103848	ABA106113	74%	97.9%	99.2%
ECO103848	BCE103653	62%	98.1%	91.7%
ECO103848	BFU103608	66%	67.9%	69.4%
ECO103848	BFU106833	62%	99.9%	99.9%
ECO103848	BMA101880	63%	97.9%	96.5%
ECO103848	EBC104151	88%	98.3%	100%
ECO103848	ECO103848	100%	100%	100%
ECO103848	KPN300177	74%	16.7%	100%
ECO103848	KPN300043	76%	17.8%	100%
ECO103848	KPN305053	81%	99.9%	100%
ECO103848	LPN100923	60%	72.2%	33.8%
ECO103848	MAV104586	74%	8.0%	96.7%
ECO103848	MAV103801	61%	93.7%	99.4%
ECO103848	MBV102908	59%	72.6%	48.8%
ECO103848	MTU201875	56%	98.3%	97.8%
ECO103848	PPU110377	62%	97.9%	99.2%
ECO103848	PSY104811	60%	97.9%	99.2%
ECO103848	SPA100154	87%	60.3%	100%
ECO103848	STY102770	91%	100%	100%
ECO103848	STM101990	91%	99.9%	99.9%
ECO103848	VCH101536	60%	99.0%	99.7%
ECO103848	YPS003545	55%	96.4%	96.6%
ECO103866	ABA105335	48%	99.3%	98.9%
ECO103866	BAN111700	49%	98.7%	97.4%
ECO103866	BFR11698	36%	79.6%	81.2%
ECO103866	BPT101112	47%	97.2%	88.2%
ECO103866	BCE104584	44%	99.3%	97.4%
ECO103866	BFU101867	44%	99.1%	97.4%
ECO103866	BMA104709	44%	99.3%	97.4%
ECO103866	CJU100861	44%	97.8%	97.0%
ECO103866	CAC102675	48%	94.7%	98.6%
ECO103866	CBO101455	47%	95.6%	97.8%
ECO103866	CDF100712	48%	95.6%	98.6%
ECO103866	CDP101009	39%	97.6%	93.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103866	EBC104143	92%	100%	100%
ECO103866	ECO103866	100%	100%	100%
ECO103866	HIN100791	73%	99.6%	99.6%
ECO103866	KPN305541	94%	99.8%	99.8%
ECO103866	LPN103302	50%	88.0%	97.8%
ECO103866	LMO101296	47%	99.3%	99.3%
ECO103866	MCA102161	46%	99.6%	97.4%
ECO103866	MAV103294	42%	98.0%	94.9%
ECO103866	MBV100214	41%	99.6%	97.4%
ECO103866	MLP100878	41%	99.1%	96.4%
ECO103866	MTU201638	41%	99.6%	97.4%
ECO103866	NGO100829	49%	96.7%	96.3%
ECO103866	NME200783	49%	96.7%	96.3%
ECO103866	PMU101120	76%	99.8%	99.8%
ECO103866	PRT102422	83%	99.8%	99.1%
ECO103866	PAE205258	48%	97.8%	96.1%
ECO103866	PPU100005	48%	99.1%	97.4%
ECO103866	PSY101221	49%	99.1%	97.4%
ECO103866	SPA102618	94%	99.3%	100%
ECO103866	STY102740	94%	99.8%	99.6%
ECO103866	STM102018	94%	99.8%	99.6%
ECO103866	SAU800960	48%	99.1%	98.5%
ECO103866	SEP200167	47%	99.1%	97.6%
ECO103866	SHA101569	47%	99.1%	96.4%
ECO103866	SMU100664	46%	99.3%	98.5%
ECO103866	SPN400103	46%	98.7%	97.2%
ECO103866	VCH102604	74%	99.8%	99.6%
ECO103866	YPS001797	89%	99.8%	99.8%
ECO103873	ABA103721	37%	85.1%	90.5%
ECO103873	BAN108866	23%	75.1%	87.0%
ECO103873	BAN105656	28%	74.7%	79.6%
ECO103873	BAN103658	32%	74.7%	79.6%
ECO103873	BAN100164	33%	75.1%	77.9%
ECO103873	BFR102236	33%	79.9%	84.6%
ECO103873	BBU100100	29%	64.7%	68.6%
ECO103873	BCE107277	37%	71.3%	97.1%
ECO103873	BFU109172	34%	74.4%	82.5%
ECO103873	BMA106607	38%	76.1%	74.8%
ECO103873	CJU101558	32%	79.6%	89.6%
ECO103873	CAC101362	34%	66.4%	74.2%
ECO103873	CBO102188	34%	71.6%	78.5%
ECO103873	CDF101024	32%	74.4%	79.5%
ECO103873	CDP101353	34%	72.0%	77.4%
ECO103873	EBC101695	90%	90.0%	100%
ECO103873	EFA201433	30%	74.7%	77.8%
ECO103873	EFM201002	30%	74.0%	76.5%
ECO103873	ECO103873	100%	100%	100%
ECO103873	HIN101705	49%	91.7%	98.1%
ECO103873	HPY100542	28%	65.4%	73.3%
ECO103873	KPN308897	87%	83.7%	100%
ECO103873	LPN100405	36%	75.1%	76.7%
ECO103873	LMO101688	31%	82.7%	88.3%
ECO103873	MCA100045	34%	79.6%	81.4%
ECO103873	MAV103533	34%	76.1%	80.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103873	MBV101876	33%	79.2%	86.0%
ECO103873	MLP100726	34%	78.5%	84.9%
ECO103873	MTU201321	33%	79.2%	86.0%
ECO103873	NGO101679	33%	75.1%	79.6%
ECO103873	NME201872	34%	75.1%	79.6%
ECO103873	PMU100917	52%	90.3%	96.7%
ECO103873	PRT105607	66%	97.9%	100%
ECO103873	PAE204659	41%	84.8%	92.1%
ECO103873	PPU109719	38%	84.8%	92.1%
ECO103873	PSY106535	42%	74.0%	77.1%
ECO103873	SPA103848	85%	42.9%	100%
ECO103873	STY102718	91%	90.0%	100%
ECO103873	STM102035	91%	97.9%	100%
ECO103873	SAU801151	31%	74.0%	80.1%
ECO103873	SEP200875	30%	74.0%	79.8%
ECO103873	SHA100464	29%	74.0%	80.1%
ECO103873	SMU100491	31%	74.0%	79.9%
ECO103873	SPN401694	30%	74.0%	79.9%
ECO103873	SPY200261	33%	74.0%	79.9%
ECO103873	TPA100402	36%	72.0%	77.6%
ECO103873	VCH100156	49%	91.7%	97.4%
ECO103873	YPS001748	71%	97.9%	100%
ECO103878	ABA100233	85%	33.5%	98.5%
ECO103878	ABA100062	85%	99.5%	99.5%
ECO103878	BAN106076	75%	99.7%	99.7%
ECO103878	BFR12122	72%	99.7%	99.7%
ECO103878	BPT100044	81%	99.7%	99.7%
ECO103878	BPT100847	81%	99.7%	99.7%
ECO103878	BBU100475	64%	99.7%	98.0%
ECO103878	BCE112288	75%	15.5%	98.4%
ECO103878	BCE106056	83%	52.5%	100%
ECO103878	BCE108906	81%	99.7%	99.7%
ECO103878	BFU100267	74%	37.3%	99.3%
ECO103878	BFU100847	80%	99.7%	99.7%
ECO103878	BMA107343	79%	95.9%	100%
ECO103878	BMA106305	80%	99.7%	99.7%
ECO103878	CJU100435	73%	99.7%	99.7%
ECO103878	CPN200689	69%	99.5%	99.5%
ECO103878	CTR200588	68%	100%	98.7%
ECO103878	CAC103049	73%	99.7%	99.7%
ECO103878	CBO100671	69%	10.9%	95.6%
ECO103878	CBO101209	75%	59.1%	100%
ECO103878	CBO101304	73%	99.5%	99.5%
ECO103878	CDF100547	74%	99.7%	95.9%
ECO103878	CDP100912	72%	99.7%	99.7%
ECO103878	EBC101615	99%	33.8%	99.3%
ECO103878	EBC100362	98%	47.7%	100%
ECO103878	EBC102891	98%	99.7%	99.7%
ECO103878	EFA202006	77%	99.7%	99.7%
ECO103878	EFM100161	75%	71.3%	100%
ECO103878	ECO103262	100%	99.7%	99.7%
ECO103878	ECO103878	100%	100%	100%
ECO103878	HIN100558	92%	99.7%	99.7%
ECO103878	HIN100613	92%	99.7%	99.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103878	HPY101188	73%	99.7%	99.7%
ECO103878	KPN300520	98%	23.6%	100%
ECO103878	KPN300653	98%	79.9%	99.7%
ECO103878	KPN300869	98%	99.7%	99.7%
ECO103878	LMO102516	74%	99.5%	99.5%
ECO103878	MCA100162	82%	99.5%	99.5%
ECO103878	MAV102941	75%	99.7%	99.7%
ECO103878	MBV103318	74%	99.7%	99.7%
ECO103878	MLP101139	75%	99.7%	99.7%
ECO103878	MTU200682	74%	99.7%	99.7%
ECO103878	MGE100460	69%	99.7%	99.7%
ECO103878	MPN100177	70%	99.7%	99.7%
ECO103878	NGO101673	83%	100%	100%
ECO103878	NGO101620	83%	100%	100%
ECO103878	NME200128	84%	100%	100%
ECO103878	NME200143	84%	100%	100%
ECO103878	PMU101746	92%	99.7%	99.7%
ECO103878	PMU101357	92%	99.7%	99.7%
ECO103878	PRT100737	95%	24.6%	100%
ECO103878	PRT100321	94%	99.7%	99.7%
ECO103878	PAE204275	84%	99.7%	99.7%
ECO103878	PAE204263	84%	99.7%	99.7%
ECO103878	PPU104463	78%	76.6%	99.7%
ECO103878	PPU104501	77%	99.7%	99.7%
ECO103878	PSY107231	77%	100%	100%
ECO103878	SPA104331	98%	39.3%	99.4%
ECO103878	SPA102798	99%	99.7%	99.7%
ECO103878	STY101782	99%	99.7%	99.7%
ECO103878	STY102689	99%	99.7%	99.7%
ECO103878	STM102043	99%	99.7%	99.7%
ECO103878	SAU800548	75%	99.7%	99.7%
ECO103878	SEP200072	75%	99.5%	99.5%
ECO103878	SHA101389	75%	99.7%	99.7%
ECO103878	SMU101538	73%	99.5%	99.5%
ECO103878	SPN401342	72%	99.5%	99.5%
ECO103878	SPY200441	72%	99.5%	99.5%
ECO103878	TPA100185	69%	99.7%	79.6%
ECO103878	UUR100528	71%	99.2%	99.2%
ECO103878	VCH100316	87%	100%	100%
ECO103878	VCH100357	87%	100%	100%
ECO103878	YPS000510	93%	99.7%	99.7%
ECO103878	YPS001855	95%	100%	100%
ECO103880	ABA101112	59%	96.1%	98.3%
ECO103880	BAN107620	45%	96.7%	98.9%
ECO103880	BFR10520	43%	99.4%	99.4%
ECO103880	BPT100046	60%	96.1%	98.3%
ECO103880	BBU100393	38%	96.1%	98.4%
ECO103880	BCE106900	60%	99.4%	99.5%
ECO103880	BFU104521	61%	99.4%	99.5%
ECO103880	BMA104447	62%	96.1%	94.1%
ECO103880	CJU100438	41%	95.6%	96.6%
ECO103880	CPN200687	39%	95.6%	94.5%
ECO103880	CTR200586	40%	95.6%	94.5%
ECO103880	CAC102306	39%	99.4%	98.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103880	CBO103872	40%	99.4%	98.9%
ECO103880	CDF104265	38%	99.4%	99.4%
ECO103880	CDP100848	37%	95.0%	71.9%
ECO103880	EBC102887	97%	100%	100%
ECO103880	EFA200831	38%	97.8%	97.8%
ECO103880	EFM202000	42%	90.6%	98.8%
ECO103880	ECO103880	100%	100%	100%
ECO103880	HIN100696	75%	96.7%	94.6%
ECO103880	HPY101186	41%	95.0%	97.2%
ECO103880	KPN300526	98%	51.4%	100%
ECO103880	LMO102609	45%	96.7%	98.9%
ECO103880	MCA100998	58%	95.6%	98.3%
ECO103880	MAV102335	42%	95.0%	73.8%
ECO103880	MBV103155	41%	95.0%	79.4%
ECO103880	MLP101155	40%	95.0%	82.9%
ECO103880	MTU200636	41%	95.0%	79.4%
ECO103880	MGE100054	20%	45.3%	26.6%
ECO103880	MPN100087	21%	45.3%	26.2%
ECO103880	NGO101670	61%	96.1%	97.8%
ECO103880	NME200141	61%	96.1%	97.8%
ECO103880	PMU101744	80%	96.7%	95.6%
ECO103880	PRT103295	93%	99.4%	99.4%
ECO103880	PAE204273	72%	96.1%	98.3%
ECO103880	PPU108806	72%	96.1%	98.3%
ECO103880	PSY103335	72%	96.7%	98.9%
ECO103880	SPA102796	98%	100%	100%
ECO103880	STY102686	99%	100%	100%
ECO103880	STM102044	99%	100%	100%
ECO103880	SAU800535	40%	98.3%	97.8%
ECO103880	SEP201880	40%	98.3%	97.8%
ECO103880	SHA101487	40%	98.3%	97.8%
ECO103880	SMU100495	35%	95.0%	95.5%
ECO103880	SPN401818	36%	95.0%	92.9%
ECO103880	SPY200119	35%	98.3%	98.3%
ECO103880	TPA100233	39%	95.6%	97.8%
ECO103880	UUR100588	17%	96.1%	87.2%
ECO103880	VCH100318	86%	99.4%	98.9%
ECO103880	YPS000502	97%	99.4%	99.4%
ECO103881	ABA106058	70%	99.3%	99.3%
ECO103881	BAN106044	64%	79.6%	98.2%
ECO103881	BFR10521	54%	99.3%	95.2%
ECO103881	BPT100048	66%	99.3%	98.6%
ECO103881	BBU100392	49%	97.9%	97.2%
ECO103881	BCE100591	66%	99.3%	98.6%
ECO103881	BFU104508	68%	99.3%	92.8%
ECO103881	BMA106139	68%	99.3%	98.6%
ECO103881	CJU100439	61%	100%	100%
ECO103881	CPN200686	55%	97.9%	97.9%
ECO103881	CTR200585	55%	97.9%	97.9%
ECO103881	CAC101038	66%	100%	100%
ECO103881	CBO102195	65%	100%	100%
ECO103881	CDF104047	64%	100%	100%
ECO103881	CDP100850	60%	97.9%	97.2%
ECO103881	EBC102886	98%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103881	EFA200839	65%	99.3%	100%
ECO103881	ECO103881	100%	100%	100%
ECO103881	HIN100496	87%	100%	100%
ECO103881	HPY101185	56%	100%	100%
ECO103881	KPN300527	99%	100%	100%
ECO103881	LMO100036	65%	100%	100%
ECO103881	MCA100999	68%	99.3%	98.6%
ECO103881	MAV102318	63%	97.9%	97.2%
ECO103881	MBV103157	61%	97.9%	97.2%
ECO103881	MLP101154	61%	97.9%	97.2%
ECO103881	MTU200637	61%	97.9%	97.2%
ECO103881	MGE100083	44%	100%	100%
ECO103881	MPN100612	43%	98.6%	98.5%
ECO103881	NGO101667	68%	99.3%	97.9%
ECO103881	NME200140	68%	99.3%	97.9%
ECO103881	PMU101743	85%	100%	100%
ECO103881	PAB204272	74%	99.3%	98.6%
ECO103881	PPU104469	70%	99.3%	98.6%
ECO103881	PSY106552	70%	99.3%	95.9%
ECO103881	SPA107834	98%	62.7%	90.7%
ECO103881	STY102683	100%	100%	100%
ECO103881	STM102055	100%	100%	100%
ECO103881	SAU800537	67%	99.3%	100%
ECO103881	SEP201881	66%	99.3%	100%
ECO103881	SHA101488	66%	100%	100%
ECO103881	SMU101147	64%	100%	100%
ECO103881	SPN400555	65%	100%	100%
ECO103881	SPY200329	64%	100%	100%
ECO103881	TPA100234	56%	97.9%	95.2%
ECO103881	UUR100547	47%	97.9%	89.3%
ECO103881	VCH100319	86%	99.3%	99.3%
ECO103881	YPS000498	90%	99.3%	99.3%
ECO103882	ABA104945	63%	98.3%	99.6%
ECO103882	BAN101496	53%	40.2%	100%
ECO103882	BAN103921	41%	97.9%	100%
ECO103882	BFR10522	48%	96.2%	97.0%
ECO103882	BPT100050	65%	99.1%	100%
ECO103882	BBU100391	43%	96.2%	98.2%
ECO103882	BCE101116	67%	98.7%	99.6%
ECO103882	BFU100848	67%	98.7%	99.6%
ECO103882	BMA108405	67%	98.7%	99.6%
ECO103882	CJU100440	50%	96.2%	96.6%
ECO103882	CPN200685	46%	99.1%	100%
ECO103882	CTR200584	50%	98.7%	99.6%
ECO103882	CAC102626	52%	90.2%	92.6%
ECO103882	CBO103496	54%	90.2%	92.6%
ECO103882	CDF100546	52%	97.0%	98.3%
ECO103882	CDP100852	49%	96.2%	95.7%
ECO103882	EBC102885	97%	100%	100%
ECO103882	EFA200840	54%	97.0%	99.1%
ECO103882	ECO103882	100%	100%	100%
ECO103882	HIN100495	85%	97.9%	100%
ECO103882	HPY101184	50%	95.3%	95.3%
ECO103882	KPN300590	94%	51.7%	96.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103882	LMO100406	51%	97.9%	100%
ECO103882	MCA101000	65%	96.2%	96.6%
ECO103882	MAV102320	49%	96.2%	95.7%
ECO103882	MBV103159	48%	96.2%	99.1%
ECO103882	MLP101153	49%	96.2%	95.7%
ECO103882	MTU200638	48%	96.2%	95.7%
ECO103882	MGE100084	43%	95.7%	98.2%
ECO103882	MPN100611	44%	95.7%	98.2%
ECO103882	NGO101665	68%	98.3%	99.6%
ECO103882	NME200139	68%	98.3%	99.6%
ECO103882	PMU101742	84%	97.9%	100%
ECO103882	PAE204271	71%	98.7%	100%
ECO103882	PPU104471	70%	98.3%	99.6%
ECO103882	PSY103536	71%	98.7%	100%
ECO103882	SPA102795	97%	100%	100%
ECO103882	STY102680	98%	100%	100%
ECO103882	STM102056	98%	100%	100%
ECO103882	SAU800538	52%	97.0%	98.7%
ECO103882	SEP201882	54%	96.2%	97.4%
ECO103882	SHA101489	53%	96.2%	97.4%
ECO103882	SMU101145	56%	96.2%	98.3%
ECO103882	SPN400556	54%	96.2%	98.3%
ECO103882	SPY200330	57%	97.9%	100%
ECO103882	TPA100235	39%	94.9%	96.9%
ECO103882	UUR100546	41%	95.7%	97.8%
ECO103882	VCH100320	90%	99.6%	100%
ECO103882	YPS000494	91%	100%	100%
ECO103883	ABA104908	46%	99.4%	98.2%
ECO103883	BAN106254	36%	98.8%	97.6%
ECO103883	BAN101384	36%	98.8%	97.6%
ECO103883	BFR101778	26%	84.2%	82.4%
ECO103883	BPT104548	42%	100%	100%
ECO103883	BBU100390	29%	81.2%	78.6%
ECO103883	BCE110567	42%	99.4%	98.2%
ECO103883	BFU104512	40%	97.6%	79.1%
ECO103883	BMA104533	40%	98.2%	87.0%
ECO103883	CJU100441	30%	95.8%	96.9%
ECO103883	CAC103420	36%	97.6%	95.2%
ECO103883	CBO103649	34%	99.4%	98.2%
ECO103883	CDF100545	34%	97.6%	93.2%
ECO103883	CDP100855	33%	85.5%	87.7%
ECO103883	EFA200841	34%	94.5%	93.4%
ECO103883	EFM100720	38%	94.5%	92.8%
ECO103883	ECO103883	100%	100%	100%
ECO103883	HIN100621	78%	100%	99.4%
ECO103883	KPN304658	98%	100%	100%
ECO103883	LMO101102	37%	98.8%	97.6%
ECO103883	MCA101001	81%	99.4%	98.2%
ECO103883	MAV102938	32%	95.8%	85.2%
ECO103883	MBV100919	31%	94.5%	92.7%
ECO103883	MLP101148	31%	94.5%	93.2%
ECO103883	MTU200648	31%	94.5%	92.7%
ECO103883	MGE100371	21%	95.2%	96.9%
ECO103883	MPN100304	23%	95.2%	97.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103883	NGO101663	43%	98.2%	96.4%
ECO103883	NME200138	43%	98.2%	96.4%
ECO103883	PMU101739	80%	100%	99.4%
ECO103883	PRT103043	87%	100%	100%
ECO103883	PAE204270	68%	100%	98.8%
ECO103883	PPU104473	71%	99.4%	83.6%
ECO103883	PSY103338	69%	100%	98.8%
ECO103883	SPA102794	96%	100%	100%
ECO103883	STY102677	98%	100%	100%
ECO103883	STM102057	98%	100%	100%
ECO103883	SAU800539	34%	98.8%	97.6%
ECO103883	SEP201883	34%	98.8%	97.6%
ECO103883	SHA101633	33%	98.8%	97.6%
ECO103883	SMU100974	35%	97.0%	95.2%
ECO103883	SPN401211	36%	95.8%	94.6%
ECO103883	SPY200814	38%	91.5%	90.4%
ECO103883	TPA100236	33%	94.5%	86.1%
ECO103883	VCH100321	76%	100%	100%
ECO103883	YPS000491	90%	100%	100%
ECO103884	ABA105381	65%	69.4%	100%
ECO103884	BAN106592	54%	98.3%	100%
ECO103884	BAN112078	60%	98.3%	100%
ECO103884	BFR106071	59%	92.6%	93.5%
ECO103884	BPT104549	62%	100%	100%
ECO103884	BBU100389	55%	100%	100%
ECO103884	BCE104254	64%	100%	100%
ECO103884	BFU104514	62%	100%	100%
ECO103884	BMA108492	62%	100%	100%
ECO103884	CJU100442	58%	100%	100%
ECO103884	CPN200683	42%	95.9%	93.8%
ECO103884	CTR200582	43%	95.9%	93.8%
ECO103884	CAC103770	57%	98.3%	100%
ECO103884	CBO100998	60%	96.7%	98.4%
ECO103884	CDF100554	57%	100%	99.2%
ECO103884	CDP100862	58%	98.3%	97.6%
ECO103884	EBC100455	97%	100%	100%
ECO103884	EFA200842	59%	100%	100%
ECO103884	EFM100721	58%	100%	100%
ECO103884	ECO103884	100%	100%	100%
ECO103884	HIN100622	81%	100%	100%
ECO103884	HPY101182	54%	100%	100%
ECO103884	KPN205542	97%	100%	100%
ECO103884	LMO102795	57%	100%	100%
ECO103884	MCA101002	66%	100%	100%
ECO103884	MAV102937	48%	98.3%	97.7%
ECO103884	MBV100917	49%	98.3%	97.7%
ECO103884	MLP101147	45%	98.3%	97.7%
ECO103884	MTU200649	49%	98.3%	97.7%
ECO103884	MGE100372	42%	98.3%	97.5%
ECO103884	MPN100303	42%	98.3%	97.5%
ECO103884	NGO101640	62%	100%	100%
ECO103884	NME200137	63%	100%	100%
ECO103884	PMU101738	82%	100%	100%
ECO103884	PRT100056	90%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103884	PAE204269	65%	100%	100%
ECO103884	PPU104475	60%	100%	100%
ECO103884	PSY108092	59%	52.9%	100%
ECO103884	SPA107849	97%	100%	100%
ECO103884	STY102674	97%	100%	100%
ECO103884	STM107215	97%	100%	100%
ECO103884	SAU800540	58%	95.9%	96.7%
ECO103884	SEP201884	57%	96.7%	97.5%
ECO103884	SHA101634	58%	96.7%	97.5%
ECO103884	SMU100975	52%	100%	100%
ECO103884	SPN401210	51%	100%	96.1%
ECO103884	SPY200815	50%	100%	100%
ECO103884	TPA100237	51%	98.3%	97.7%
ECO103884	UUR100009	48%	97.5%	96.7%
ECO103884	VCH100322	76%	100%	100%
ECO103884	YPS005201	79%	99.2%	98.4%
ECO103885	ABA104003	70%	99.9%	99.9%
ECO103885	BAN107104	42%	30.0%	22.8%
ECO103885	BAN105134	45%	99.3%	96.3%
ECO103885	BFR12467	43%	97.5%	100%
ECO103885	BPT100051	64%	99.9%	99.3%
ECO103885	BBU100388	46%	99.4%	98.3%
ECO103885	BCE104307	65%	99.9%	99.9%
ECO103885	BFU100849	65%	84.8%	98.6%
ECO103885	BMA104886	65%	99.9%	99.9%
ECO103885	CJU100443	47%	99.3%	98.8%
ECO103885	CPN200682	45%	98.4%	97.8%
ECO103885	CTR200581	45%	98.8%	99.0%
ECO103885	CAC102610	47%	99.8%	93.2%
ECO103885	CBO100154	46%	99.8%	93.9%
ECO103885	CDF100552	48%	100%	93.8%
ECO103885	CDP100874	56%	9.5%	0.9%
ECO103885	EBC101233	97%	80.3%	99.9%
ECO103885	EFA200805	46%	99.4%	94.1%
ECO103885	EFM202205	48%	99.4%	93.8%
ECO103885	ECO103885	100%	100%	100%
ECO103885	HIN100494	83%	100%	100%
ECO103885	HPY101181	46%	99.3%	47.2%
ECO103885	KPN302483	98%	94.6%	100%
ECO103885	LPN101720	87%	5.2%	100%
ECO103885	LMO101542	47%	99.3%	95.7%
ECO103885	MCA101003	68%	100%	99.9%
ECO103885	MAV102933	58%	9.5%	0.9%
ECO103885	MBV100910	57%	9.5%	0.9%
ECO103885	MLP101145	58%	9.5%	0.8%
ECO103885	MTU200664	57%	9.5%	0.9%
ECO103885	MGE100350	44%	8.0%	0.9%
ECO103885	MPN100326	33%	98.8%	96.0%
ECO103885	NGO101637	64%	99.9%	57.3%
ECO103885	NME200136	64%	99.9%	99.9%
ECO103885	PMU101737	86%	100%	100%
ECO103885	PRT104687	92%	91.4%	54.6%
ECO103885	PAE204268	73%	100%	100%
ECO103885	PPU104497	71%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103885	PSY103339	71%	100%	100%
ECO103885	SPA102792	97%	48.6%	100%
ECO103885	STY102671	98%	100%	100%
ECO103885	STM102058	98%	100%	100%
ECO103885	SAU800542	53%	6.9%	0.8%
ECO103885	SEP201886	53%	6.9%	0.8%
ECO103885	SHA101636	48%	99.1%	100%
ECO103885	SMU100556	44%	99.5%	95.5%
ECO103885	SPN401775	45%	99.5%	93.3%
ECO103885	SPY200071	45%	99.5%	95.5%
ECO103885	TPA100238	45%	98.4%	96.3%
ECO103885	UUR100187	43%	1.0%	5.4%
ECO103885	VCH100323	85%	100%	97.5%
ECO103885	YPS000489	94%	100%	100%
ECO103886	ABA100041	59%	11.7%	91.1%
ECO103886	ABA104621	71%	98.8%	98.9%
ECO103886	BAN107772	27%	95.0%	96.5%
ECO103886	BAN101907	50%	95.7%	97.2%
ECO103886	BFR102987	48%	96.5%	97.8%
ECO103886	BPT101163	66%	99.0%	98.7%
ECO103886	BBU100387	49%	96.2%	98.8%
ECO103886	BCE109927	58%	57.4%	97.7%
ECO103886	BFU100842	69%	71.2%	63.5%
ECO103886	BMA101246	65%	98.7%	98.7%
ECO103886	CJU100444	54%	96.3%	98.6%
ECO103886	CPN200681	49%	96.0%	96.7%
ECO103886	CTR200580	49%	96.5%	97.4%
ECO103886	CAC100576	54%	95.7%	97.0%
ECO103886	CBO100117	52%	95.7%	97.3%
ECO103886	CDF100550	54%	95.7%	98.3%
ECO103886	CDP100877	50%	6.0%	0.4%
ECO103886	EBC103916	97%	100%	100%
ECO103886	EFA200807	49%	97.9%	99.4%
ECO103886	EFM200070	47%	95.7%	99.7%
ECO103886	ECO103886	100%	100%	100%
ECO103886	HIN100493	82%	99.4%	99.7%
ECO103886	KPN300484	90%	12.1%	100%
ECO103886	KPN302484	97%	100%	100%
ECO103886	LPN100508	84%	38.4%	99.4%
ECO103886	LMO101517	49%	95.7%	97.4%
ECO103886	MCA101004	69%	97.5%	96.6%
ECO103886	MAV102932	51%	4.3%	2.0%
ECO103886	MBV100906	50%	4.8%	2.7%
ECO103886	MLP101144	51%	4.6%	1.7%
ECO103886	MTU200665	50%	4.8%	2.7%
ECO103886	MGE100349	39%	84.4%	80.6%
ECO103886	MPN100327	39%	95.6%	97.4%
ECO103886	NME200135	67%	98.4%	99.7%
ECO103886	PMU101736	83%	99.4%	99.6%
ECO103886	PAE204267	75%	99.4%	99.8%
ECO103886	PPU104498	74%	99.4%	99.1%
ECO103886	PSY103340	74%	99.4%	99.8%
ECO103886	SPA101954	97%	68.3%	100%
ECO103886	STY102668	98%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103886	STM102060	98%	100%	100%
ECO103886	SAU800543	52%	96.1%	97.8%
ECO103886	SEP201887	49%	96.1%	97.8%
ECO103886	SHA100756	27%	5.6%	70.9%
ECO103886	SHA101637	50%	97.4%	99.3%
ECO103886	SMU100552	52%	96.1%	97.5%
ECO103886	SPN401774	52%	96.1%	96.2%
ECO103886	SPY200072	47%	96.1%	97.2%
ECO103886	TPA100239	49%	95.7%	96.1%
ECO103886	UUR100188	37%	95.5%	98.0%
ECO103886	VCH100324	82%	99.9%	99.9%
ECO103886	YPS000478	92%	99.8%	99.9%
ECO103911	ECO101689	30%	76.2%	97.7%
ECO103911	ECO103911	100%	100%	100%
ECO103911	LPN100032	24%	19.1%	41.7%
ECO103911	YPS000041	23%	40.0%	74.2%
ECO103911	YPS001066	23%	59.2%	84.1%
ECO103912	ABA105327	29%	54.0%	50.7%
ECO103912	ABA103660	33%	54.4%	58.3%
ECO103912	BCE104678	27%	82.2%	93.6%
ECO103912	BFU100479	26%	80.1%	79.2%
ECO103912	BFU100101	27%	89.9%	95.0%
ECO103912	BFU107845	26%	84.3%	94.5%
ECO103912	BFU107853	29%	90.9%	87.5%
ECO103912	BMA101024	30%	80.1%	86.6%
ECO103912	CDP100258	29%	86.4%	90.5%
ECO103912	EBC103832	91%	95.5%	100%
ECO103912	ECO103912	100%	100%	100%
ECO103912	KPN302605	91%	94.4%	98.6%
ECO103912	PRT102440	67%	93.4%	96.4%
ECO103912	PAE200235	27%	84.7%	95.0%
ECO103912	SPA100853	90%	99.7%	100%
ECO103912	STY101885	91%	95.5%	100%
ECO103914	BAN103675	23%	4.6%	34.3%
ECO103914	BAN109652	24%	97.2%	98.5%
ECO103914	BFR100259	26%	66.5%	68.2%
ECO103914	BPT100260	34%	98.7%	97.5%
ECO103914	BFU109252	57%	98.0%	94.3%
ECO103914	CJU100484	26%	43.1%	64.1%
ECO103914	CBO100644	21%	97.6%	98.9%
ECO103914	CDF100007	27%	53.6%	96.7%
ECO103914	CDF101225	24%	98.0%	99.1%
ECO103914	CDF103463	25%	97.8%	98.7%
ECO103914	EBC103836	90%	98.5%	100%
ECO103914	ECO103914	100%	100%	100%
ECO103914	KPN300005	84%	23.9%	96.3%
ECO103914	KPN300522	84%	29.5%	94.1%
ECO103914	KPN302611	89%	100%	100%
ECO103914	LMO102790	25%	97.4%	97.8%
ECO103914	PRT104772	59%	98.2%	97.8%
ECO103914	PAE205468	67%	99.8%	94.5%
ECO103914	PPU102900	63%	98.5%	97.1%
ECO103914	PSY101200	64%	98.5%	95.9%
ECO103914	SPA101526	92%	98.5%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103914	STY101888	93%	100%	100%
ECO103914	STM102145	93%	100%	100%
ECO103914	SAU800104	22%	95.0%	93.3%
ECO103914	SPN400439	25%	91.0%	91.7%
ECO103914	SPY201303	24%	90.4%	91.2%
ECO103914	TPA100763	26%	56.5%	54.5%
ECO103914	VCH100663	33%	46.0%	35.9%
ECO103919	ABA104828	47%	96.0%	95.1%
ECO103919	BAN113216	23%	66.1%	77.3%
ECO103919	BFR10381	23%	66.7%	78.8%
ECO103919	BPT100657	39%	88.7%	90.8%
ECO103919	BBU100729	34%	92.0%	94.9%
ECO103919	BCE100058	48%	97.6%	95.1%
ECO103919	BFU101343	48%	97.6%	98.0%
ECO103919	BMA107745	50%	96.9%	97.2%
ECO103919	CJU101444	26%	68.3%	85.5%
ECO103919	CPN200812	35%	89.3%	89.5%
ECO103919	CTR200647	34%	92.5%	92.9%
ECO103919	CAC100048	23%	66.1%	77.3%
ECO103919	CBO102016	23%	66.1%	76.5%
ECO103919	CDF103720	23%	68.7%	80.6%
ECO103919	CDP100102	52%	98.9%	99.1%
ECO103919	EBC103837	94%	98.7%	100%
ECO103919	EFA202329	23%	66.7%	78.4%
ECO103919	EFM202538	24%	66.7%	78.3%
ECO103919	ECO103919	100%	100%	100%
ECO103919	HIN101544	77%	99.8%	97.5%
ECO103919	HPY101149	53%	98.2%	98.9%
ECO103919	KPN300161	92%	7.3%	97.6%
ECO103919	KPN302607	95%	99.8%	99.8%
ECO103919	LPN103064	40%	43.2%	97.3%
ECO103919	LMO101990	23%	66.5%	77.8%
ECO103919	MCA101062	45%	95.4%	96.7%
ECO103919	MAV105583	51%	98.9%	97.7%
ECO103919	MBV101975	51%	98.9%	97.8%
ECO103919	MLP100108	50%	98.9%	97.7%
ECO103919	MTU200937	51%	98.9%	97.8%
ECO103919	MGE100113	23%	68.7%	81.8%
ECO103919	MPN100582	23%	68.7%	82.3%
ECO103919	NGO101248	58%	97.3%	94.0%
ECO103919	NME201465	58%	97.3%	97.4%
ECO103919	PMU100416	77%	99.8%	100%
ECO103919	PRT101480	82%	99.8%	100%
ECO103919	PAE204728	48%	98.7%	97.8%
ECO103919	PPU108272	50%	98.2%	97.3%
ECO103919	PPU108446	51%	98.2%	97.3%
ECO103919	PSY100665	48%	98.2%	97.3%
ECO103919	SPA103272	94%	99.5%	100%
ECO103919	STY101906	95%	99.8%	99.8%
ECO103919	STM102761	95%	99.8%	99.8%
ECO103919	SAU800962	28%	38.3%	48.3%
ECO103919	SEP200169	27%	39.2%	49.7%
ECO103919	SHA101567	24%	70.1%	83.1%
ECO103919	SHA102448	28%	39.2%	49.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103919	SMU100622	23%	73.2%	82.6%
ECO103919	SPN401879	25%	67.6%	79.5%
ECO103919	SPY200159	23%	73.2%	82.6%
ECO103919	TPA100471	38%	85.4%	86.4%
ECO103919	VCH100369	77%	99.8%	99.6%
ECO103919	YPS003348	87%	99.8%	100%
ECO103928	BAN103704	29%	98.7%	98.3%
ECO103928	BAN109247	31%	99.0%	98.1%
ECO103928	BCE107035	24%	61.9%	62.6%
ECO103928	BCE101620	28%	42.2%	42.2%
ECO103928	CDF102956	23%	90.9%	88.6%
ECO103928	CDF103650	26%	84.3%	82.8%
ECO103928	CDP101746	25%	90.7%	90.6%
ECO103928	EBC104163	94%	58.6%	80.8%
ECO103928	EFA202424	27%	94.4%	91.6%
ECO103928	EFM202271	29%	94.9%	91.9%
ECO103928	ECO103928	100%	100%	100%
ECO103928	KPN301863	95%	98.5%	100%
ECO103928	LMO101775	30%	90.9%	89.3%
ECO103928	MAV104707	26%	57.6%	58.4%
ECO103928	MBV102941	25%	37.9%	33.9%
ECO103928	MLP100887	22%	63.6%	64.0%
ECO103928	MTU201218	25%	37.9%	33.8%
ECO103928	SPA103511	93%	63.4%	100%
ECO103928	STY101923	93%	100%	100%
ECO103928	SAU800214	30%	93.2%	87.9%
ECO103928	SMU101054	27%	91.2%	89.2%
ECO103928	SPN401915	31%	92.4%	88.4%
ECO103928	SPY201006	27%	96.0%	92.6%
ECO103928	VCH103663	65%	100%	97.3%
ECO103928	YPS003334	84%	98.5%	96.8%
ECO103929	BCE113128	42%	48.8%	94.6%
ECO103929	BCE100669	63%	59.6%	72.6%
ECO103929	BCE107605	53%	99.2%	99.0%
ECO103929	BCE111521	56%	98.4%	98.1%
ECO103929	BFU102346	56%	98.1%	97.8%
ECO103929	BMA105826	54%	98.1%	93.5%
ECO103929	CBO100164	41%	85.7%	86.3%
ECO103929	EBC104175	94%	100%	100%
ECO103929	ECO103929	100%	100%	100%
ECO103929	KPN301865	94%	100%	100%
ECO103929	PAE202339	51%	97.3%	97.6%
ECO103929	PSY100956	53%	99.7%	95.5%
ECO103929	SPA103513	86%	100%	100%
ECO103929	STY101924	94%	100%	100%
ECO103929	STM102778	95%	100%	100%
ECO103929	VCH103664	67%	100%	98.9%
ECO103929	YPS003330	84%	100%	100%
ECO103930	CDF102720	24%	19.5%	26.0%
ECO103930	EBC104174	76%	99.8%	100%
ECO103930	ECO103930	100%	100%	100%
ECO103930	KPN301867	73%	100%	97.5%
ECO103930	PSY100945	23%	84.3%	98.9%
ECO103930	SPA103515	77%	92.8%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103930	STY101925	80%	100%	100%
ECO103930	STM102779	80%	100%	100%
ECO103930	VCH103746	32%	100%	100%
ECO103930	YPS003326	72%	99.8%	100%
ECO103932	BCE102840	23%	34.2%	40.9%
ECO103932	BFU109703	26%	31.2%	43.0%
ECO103932	ECO103932	100%	100%	100%
ECO103932	PAE202459	28%	23.3%	64.8%
ECO103932	SPA103638	20%	86.4%	68.7%
ECO103932	STM103235	20%	84.6%	51.5%
ECO103932	TPA100401	25%	34.4%	73.2%
ECO103943	ABA102462	55%	88.7%	95.3%
ECO103943	BPT101042	51%	90.1%	92.0%
ECO103943	BBU100224	35%	92.2%	96.7%
ECO103943	BCE101833	56%	81.2%	92.4%
ECO103943	BFU102841	60%	88.4%	96.2%
ECO103943	BMA103011	58%	90.1%	82.5%
ECO103943	EBC104218	95%	92.5%	96.4%
ECO103943	ECO103943	100%	100%	100%
ECO103943	HIN100615	69%	94.5%	99.4%
ECO103943	KPN308220	93%	90.7%	100%
ECO103943	LPN100779	46%	85.2%	88.5%
ECO103943	MCA101168	50%	85.5%	91.3%
ECO103943	NGO101471	55%	84.1%	91.8%
ECO103943	NME201976	56%	85.8%	89.0%
ECO103943	PMU101418	72%	92.5%	97.2%
ECO103943	PRT101879	77%	99.7%	100%
ECO103943	PAE202793	59%	95.1%	98.8%
ECO103943	PPU106471	59%	89.6%	99.0%
ECO103943	PSY102953	59%	86.1%	99%
ECO103943	SPA103518	91%	98.3%	100%
ECO103943	STY101946	90%	98.3%	100%
ECO103943	STM102801	90%	98.3%	100%
ECO103943	VCH100374	77%	91.0%	96.0%
ECO103943	YPS002805	74%	97.4%	97.4%
ECO103953	ABA105929	51%	98.3%	99.5%
ECO103953	BAN105418	33%	97.2%	99.4%
ECO103953	BAN102675	35%	97.2%	99.4%
ECO103953	BFR100085	38%	75.3%	84.1%
ECO103953	BFR10599	43%	80.9%	94.7%
ECO103953	BPT100946	53%	88.2%	83.8%
ECO103953	BBU100114	32%	51.7%	60.4%
ECO103953	BCE112892	56%	97.2%	98.4%
ECO103953	BFU103395	54%	97.2%	98.3%
ECO103953	BMA103430	42%	36.0%	50.5%
ECO103953	BMA103994	62%	82.0%	74.5%
ECO103953	CJU100997	34%	96.6%	98.9%
ECO103953	CPN200363	25%	62.4%	65%
ECO103953	CTR200309	26%	67.4%	74.4%
ECO103953	CAC102955	31%	55.1%	87.3%
ECO103953	CAC101327	30%	75.3%	89.6%
ECO103953	CAC103317	37%	55.1%	71.4%
ECO103953	CBO103395	23%	56.2%	85.7%
ECO103953	CBO103707	35%	55.1%	64.2%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103953	CDF104218	31%	56.2%	71.0%
ECO103953	CDF103030	37%	54.5%	66.0%
ECO103953	CDP100636	30%	93.3%	98.8%
ECO103953	CDP100782	34%	94.4%	90.2%
ECO103953	EBC104214	92%	100%	100%
ECO103953	EFA201268	28%	97.2%	99.3%
ECO103953	EFA200661	30%	95.5%	88.8%
ECO103953	EFA200122	40%	52.2%	57.0%
ECO103953	EFA201230	41%	54.5%	68.1%
ECO103953	EFA200024	34%	75.3%	87.3%
ECO103953	EFA200067	28%	97.2%	99.3%
ECO103953	EFM202042	28%	97.2%	99.4%
ECO103953	ECO103953	100%	100%	100%
ECO103953	HIN100237	60%	97.8%	98.8%
ECO103953	HPY101228	46%	50%	49.2%
ECO103953	KPN301041	74%	100%	100%
ECO103953	KPN308310	93%	100%	100%
ECO103953	LPN103463	51%	56.2%	69.3%
ECO103953	LMO101733	32%	97.2%	99.4%
ECO103953	MCA100569	54%	87.6%	72.0%
ECO103953	MAV101548	32%	92.1%	87.5%
ECO103953	MBV106247	31%	92.7%	98.2%
ECO103953	MLP101584	31%	92.7%	98.2%
ECO103953	MTU200054	31%	92.7%	98.2%
ECO103953	MGE100093	25%	56.2%	58.1%
ECO103953	MPN100602	27%	49.4%	48.8%
ECO103953	NGO100403	46%	97.2%	98.9%
ECO103953	NME201532	46%	97.2%	98.9%
ECO103953	PMU101950	57%	97.8%	98.8%
ECO103953	PRT100733	59%	100%	90.9%
ECO103953	PRT101487	80%	100%	100%
ECO103953	PAE204230	59%	98.9%	99.4%
ECO103953	PPU104550	57%	98.9%	99.4%
ECO103953	PSY105770	54%	98.9%	99.5%
ECO103953	STY102277	87%	100%	100%
ECO103953	STM102829	87%	100%	100%
ECO103953	SAU800366	32%	97.2%	99.4%
ECO103953	SAU801983	33%	97.2%	99.4%
ECO103953	SAU800864	35%	83.7%	95.0%
ECO103953	SEP201353	32%	97.2%	99.4%
ECO103953	SHA101079	33%	97.2%	99.4%
ECO103953	SMU101251	32%	97.2%	99.4%
ECO103953	SPN401394	30%	97.2%	99.4%
ECO103953	SPY201407	31%	97.2%	99.4%
ECO103953	TPA100061	38%	66.3%	63.6%
ECO103953	UUR100559	36%	54.5%	54.2%
ECO103953	VCH100392	74%	100%	100%
ECO103953	YPS002815	87%	100%	100%
ECO103959	ABA104561	25%	73.2%	81.2%
ECO103959	BPT105307	27%	83.4%	52.9%
ECO103959	BCE107747	49%	99.1%	98.6%
ECO103959	BFU100526	49%	99.1%	99.1%
ECO103959	BMA104551	29%	89.6%	89.0%
ECO103959	CDF102374	34%	99.5%	99.0%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103959	CDP101057	25%	98.0%	96.6%
ECO103959	EBC104469	94%	99.5%	99.6%
ECO103959	EFA201845	30%	95.3%	74.4%
ECO103959	EFM100464	34%	69.6%	98.4%
ECO103959	ECO103959	100%	100%	100%
ECO103959	KPN304726	91%	99.6%	100%
ECO103959	LMO102860	37%	98.5%	76.7%
ECO103959	MAV102515	27%	93.4%	93.3%
ECO103959	MBV101962	28%	99.1%	96.9%
ECO103959	MTU202253	28%	99.1%	96.9%
ECO103959	PMU100365	28%	63.2%	74.1%
ECO103959	PRT102941	69%	99.8%	99.8%
ECO103959	PAE203658	43%	99.1%	93.8%
ECO103959	PPU107861	45%	99.1%	99.3%
ECO103959	PSY102978	24%	63.9%	77.1%
ECO103959	SPA100660	91%	67.4%	99.7%
ECO103959	STY102320	95%	99.5%	97.0%
ECO103959	STM102875	95%	99.5%	99.6%
ECO103959	SAU800629	35%	76.3%	62.6%
ECO103959	SEP200203	30%	99.1%	76.9%
ECO103959	SHA102124	34%	79.6%	65.3%
ECO103959	SPN400573	27%	97.1%	75.4%
ECO103959	SPY101946	32%	35.7%	92.4%
ECO103959	VCH100384	28%	64.7%	75.7%
ECO103959	YPS003038	75%	99.6%	99.6%
ECO103960	BAN106232	25%	1.4%	66.3%
ECO103960	BAN111224	25%	1.4%	66.3%
ECO103960	BFR10882	21%	68.1%	81.9%
ECO103960	BMA108842	25%	24.0%	48.9%
ECO103960	CAC102031	21%	34.7%	83.3%
ECO103960	CBO103445	23%	45.3%	81.6%
ECO103960	CDF103097	22%	58.8%	75.8%
ECO103960	EFA200376	20%	45.8%	67.3%
ECO103960	EFM201063	23%	10.9%	80%
ECO103960	ECO103960	100%	100%	100%
ECO103960	LPN100851	23%	46.0%	54.5%
ECO103960	LMO100095	20%	42.3%	64.6%
ECO103960	MAV100743	17%	31.6%	73.5%
ECO103960	PMU100591	21%	50.2%	22.1%
ECO103960	PPU105471	29%	25.8%	66.7%
ECO103960	SPA102989	23%	48.6%	48.4%
ECO103960	STY102647	26%	52.8%	17.7%
ECO103960	SAU501627	21%	66.7%	50.9%
ECO103960	SEP201407	26%	43.3%	73.2%
ECO103960	SHA102824	25%	24.2%	73.9%
ECO103960	UUR100310	30%	26.7%	33.9%
ECO103960	YPS000909	19%	26.0%	49.6%
ECO103972	BAN108696	25%	68.6%	73.2%
ECO103972	BAN107676	23%	85.2%	83.6%
ECO103972	EBC104473	63%	99.1%	99.1%
ECO103972	ECO103972	100%	100%	100%
ECO103972	KPN304708	67%	97.4%	98.7%
ECO103972	PRT104736	33%	95.2%	92.7%
ECO103972	SPA101769	88%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO103972	STY102345	88%	100%	100%
ECO103972	SPN203747	30%	28.4%	10%
ECO103973	BAN111819	31%	91.2%	66.0%
ECO103973	BAN104504	34%	79.2%	57.1%
ECO103973	BAN107861	35%	95.8%	68.9%
ECO103973	BAN108797	35%	96.6%	69.6%
ECO103973	BCE100301	37%	98.6%	82.8%
ECO103973	BFU109099	37%	98.6%	71.8%
ECO103973	BMA102600	37%	99.7%	72.5%
ECO103973	CDF102669	59%	77.3%	99.1%
ECO103973	EBC104465	93%	99.9%	100%
ECO103973	EFA202359	42%	96.1%	74.5%
ECO103973	ECO103973	100%	100%	100%
ECO103973	KPN304707	93%	78.0%	99.8%
ECO103973	LMO101763	35%	95.7%	67.9%
ECO103973	MAV102343	27%	95.5%	92.1%
ECO103973	PRT106150	63%	99.2%	98.3%
ECO103973	PPU106426	36%	98.9%	74.7%
ECO103973	SPA101768	96%	95.8%	100%
ECO103973	STY102346	97%	99.9%	99.9%
ECO103973	SAU802309	35%	96.2%	69.4%
ECO103973	SHA101509	34%	91.2%	71.9%
ECO103973	YPS003389	62%	99.9%	99.7%
ECO104010	ABA104217	28%	31.6%	23.5%
ECO104010	ABA101204	34%	32.4%	23.8%
ECO104010	ABA101274	29%	48.2%	31.9%
ECO104010	BFR105341	30%	23.3%	10.3%
ECO104010	BCE113842	27%	34.0%	25.1%
ECO104010	BCE106065	28%	30.4%	70%
ECO104010	BMA107995	22%	30.0%	21.7%
ECO104010	BMA105539	30%	31.6%	39.4%
ECO104010	ECO104010	100%	100%	100%
ECO104010	LPN103151	25%	33.2%	25.1%
ECO104010	MBV100183	31%	40.3%	31.4%
ECO104010	MTU203042	27%	30.0%	22.4%
ECO104010	NME102614	23%	33.2%	27.9%
ECO104010	PRT101349	41%	36.8%	35.4%
ECO104010	PRT104740	27%	61.7%	59.8%
ECO104010	PAB202094	25%	33.6%	24.7%
ECO104010	PAB203213	32%	32.8%	24.6%
ECO104010	SPA103838	35%	52.6%	42.7%
ECO104010	SPA100934	78%	100%	100%
ECO104010	STY102403	32%	60.5%	53.6%
ECO104010	STY102368	79%	100%	100%
ECO104010	STM103734	35%	52.6%	42.7%
ECO104010	SMU100002	27%	32.0%	24.0%
ECO104010	VCH100823	27%	36.0%	33.0%
ECO104016	ABA101468	31%	84.5%	89.0%
ECO104016	BFR11620	76%	99.8%	99.6%
ECO104016	BCE107845	30%	86.3%	91.7%
ECO104016	BFU109166	30%	86.3%	89.4%
ECO104016	BMA106168	30%	86.3%	91.8%
ECO104016	CAC102345	41%	28.3%	81.8%
ECO104016	CBO103442	38%	32.5%	93.0%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO104016	CDF100921	38%	32.3%	95.1%
ECO104016	ECO104016	100%	100%	100%
ECO104016	KPN208187	92%	19.2%	100%
ECO104016	KPN206801	84%	31.6%	100%
ECO104016	KPN208188	88%	67.9%	100%
ECO104016	KPN200435	87%	99.6%	98.9%
ECO104016	MCA100766	30%	58.2%	77.1%
ECO104016	NGO100417	30%	51.1%	93.1%
ECO104016	NME201668	31%	87.4%	87.0%
ECO104016	PPU109005	33%	80.8%	85.6%
ECO104016	PSY105035	32%	80.8%	85.6%
ECO104016	SPA103946	92%	96.9%	99.8%
ECO104016	STY102383	93%	100%	100%
ECO104016	VCH101285	31%	83.8%	89.5%
ECO104019	BAN112898	40%	71.5%	98.5%
ECO104019	BAN112173	36%	96.7%	100%
ECO104019	CBO101185	30%	94.8%	96.1%
ECO104019	EBC102809	58%	98.7%	100%
ECO104019	EFA200707	28%	81.6%	85.3%
ECO104019	EFM102036	32%	25.0%	96.9%
ECO104019	ECO104019	100%	100%	100%
ECO104019	KPN309157	57%	97.6%	97.2%
ECO104019	MLP100485	22%	46.6%	50.6%
ECO104019	SPA103940	78%	99.8%	100%
ECO104019	STY102386	81%	99.8%	99.8%
ECO104019	SPY200840	27%	84.5%	87.3%
ECO104026	ECO104026	100%	100%	100%
ECO104026	KPN302944	93%	100%	100%
ECO104026	SPA102141	89%	95.7%	100%
ECO104026	STY102046	90%	99.1%	99.3%
ECO104026	STM101797	90%	99.1%	99.3%
ECO104026	VCH100277	68%	95.7%	95.5%
ECO104028	ABA104774	23%	88.9%	93.3%
ECO104028	BPT100384	29%	65.8%	59.0%
ECO104028	EBC106218	85%	100%	100%
ECO104028	ECO104028	100%	100%	100%
ECO104028	KPN301450	77%	98.0%	99.5%
ECO104028	MAV102775	22%	76.4%	77.3%
ECO104028	MAV108777	26%	78.4%	75.6%
ECO104028	MBV106082	37%	27.6%	22.1%
ECO104028	MTU200451	37%	27.6%	23.7%
ECO104028	PRT100166	51%	96.0%	100%
ECO104028	PAE203032	24%	92.0%	97.8%
ECO104028	PPU112091	26%	89.4%	92.2%
ECO104028	SPA103939	87%	73.9%	100%
ECO104028	STY103237	87%	96.0%	100%
ECO104028	YPS003382	64%	96.0%	100%
ECO104036	ABA101661	75%	100%	100%
ECO104036	BAN105843	62%	41.1%	99.6%
ECO104036	BAN107569	64%	99.6%	99.8%
ECO104036	BFR12159	59%	99.6%	99.8%
ECO104036	BPT100043	73%	99.3%	99.6%
ECO104036	BBU100648	57%	99.5%	99.8%
ECO104036	BCE110276	75%	98.9%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO104036	BFU115281	75%	99.5%	99.5%
ECO104036	BMA100576	75%	99.5%	99.5%
ECO104036	CJU101146	63%	99.6%	99.8%
ECO104036	CPN200626	61%	98.4%	99.4%
ECO104036	CTR200380	61%	98.4%	99.4%
ECO104036	CAC103249	60%	98.9%	99.6%
ECO104036	CBO103480	58%	98.4%	99.6%
ECO104036	CDF101490	61%	98.4%	99.6%
ECO104036	CDP100703	58%	98.5%	99.6%
ECO104036	EBC104135	95%	100%	100%
ECO104036	EFA201586	60%	99.6%	99.8%
ECO104036	EFM100695	61%	98.9%	99.6%
ECO104036	ECO104036	100%	100%	100%
ECO104036	HIN100522	87%	100%	100%
ECO104036	HPY100009	60%	99.6%	99.8%
ECO104036	KPN301066	94%	60.4%	100%
ECO104036	LMO101766	62%	99.6%	99.8%
ECO104036	MCA101495	73%	99.6%	99.8%
ECO104036	MAV101753	59%	98.4%	99.4%
ECO104036	MBV100502	59%	98.4%	99.4%
ECO104036	MLP100217	59%	98.9%	99.4%
ECO104036	MTU200439	59%	98.4%	99.4%
ECO104036	MGE100404	42%	95.3%	98.0%
ECO104036	MPN100269	44%	95.8%	98.5%
ECO104036	NGO100099	74%	100%	100%
ECO104036	NME200440	75%	100%	100%
ECO104036	PMU101107	89%	100%	100%
ECO104036	PRT101073	92%	60.0%	100%
ECO104036	PAE204383	79%	100%	100%
ECO104036	PPU111089	79%	100%	100%
ECO104036	PSY101748	76%	100%	99.6%
ECO104036	SPA102707	98%	100%	100%
ECO104036	STY103268	98%	100%	100%
ECO104036	STM103468	98%	100%	100%
ECO104036	SAU802029	57%	99.5%	99.6%
ECO104036	SEP200630	56%	99.6%	99.8%
ECO104036	SHA100585	55%	69.9%	100%
ECO104036	SMU100507	61%	98.9%	99.6%
ECO104036	SPN401720	60%	99.6%	99.8%
ECO104036	SPY201582	60%	98.7%	99.6%
ECO104036	TPA100029	58%	98.9%	99.6%
ECO104036	VCH103540	74%	96.7%	100%
ECO104036	VCH102627	85%	100%	100%
ECO104036	YPS003432	91%	100%	100%
ECO104037	BCE103856	38%	93.0%	63.9%
ECO104037	EBC104133	82%	91.4%	100%
ECO104037	ECO104037	100%	100%	100%
ECO104037	KPN301065	83%	91.4%	100%
ECO104037	LPN101974	26%	78.9%	83.9%
ECO104037	PRT104013	58%	89.8%	99.1%
ECO104037	SPA102706	88%	91.4%	100%
ECO104037	STY103271	88%	96.1%	100%
ECO104037	STM103475	89%	96.1%	100%
ECO104037	SAU801531	27%	57.8%	39.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO104037	YPS005860	61%	96.9%	96.9%
ECO104048	ABA100260	46%	95.5%	99.1%
ECO104048	EBC104114	91%	100%	100%
ECO104048	ECO104048	100%	100%	100%
ECO104048	HIN100816	62%	98.8%	98.5%
ECO104048	KPN302137	87%	97.0%	100%
ECO104048	LPN103478	50%	95.5%	98.7%
ECO104048	MCA101775	40%	95.8%	99.1%
ECO104048	PMU100202	65%	97.0%	100%
ECO104048	PRT106167	78%	97.0%	100%
ECO104048	SPA102710	92%	97.0%	100%
ECO104048	STY103321	92%	97.0%	100%
ECO104048	STM103496	92%	97.0%	100%
ECO104048	TPA101030	29%	89.6%	96.9%
ECO104048	VCH102618	60%	95.8%	92.0%
ECO104048	YPS003443	84%	97.0%	100%
ECO104049	CBO100854	54%	94.2%	94.7%
ECO104049	ECO104049	100%	100%	100%
ECO104049	KPN302135	79%	94.4%	98.4%
ECO104049	SPA102711	87%	95.9%	100%
ECO104049	STY103325	87%	97.3%	100%
ECO104049	STM103497	87%	97.3%	100%
ECO104049	SPN203740	21%	45.7%	39.4%
ECO104050	ECO104050	100%	100%	100%
ECO104050	SPA102712	69%	98.1%	95.3%
ECO104050	STY103329	69%	98.1%	80.8%
ECO104081	ECO104081	100%	100%	100%
ECO104081	KPN302203	86%	100%	100%
ECO104081	PMU100762	53%	99.2%	99.2%
ECO104081	SPA103252	95%	100%	100%
ECO104081	STY103787	96%	100%	100%
ECO104081	VCH102980	58%	100%	100%
ECO104090	ABA101593	60%	95.4%	100%
ECO104090	BAN105775	31%	69.5%	96.8%
ECO104090	BAN110631	32%	69.5%	95.8%
ECO104090	BFR100626	33%	84.7%	99.1%
ECO104090	BPT101390	58%	97.7%	100%
ECO104090	BCE111148	59%	93.1%	97.6%
ECO104090	BFU105918	59%	93.1%	89.0%
ECO104090	BMA108586	58%	94.7%	100%
ECO104090	CJU100996	31%	69.5%	73.6%
ECO104090	CPN200891	28%	53.4%	62.5%
ECO104090	CTR200179	28%	53.4%	62.5%
ECO104090	CAC102614	31%	68.7%	95.8%
ECO104090	CBO100194	37%	68.7%	93.8%
ECO104090	CDF103506	34%	68.7%	97.8%
ECO104090	CDP100784	31%	69.5%	96.8%
ECO104090	EBC103612	94%	100%	100%
ECO104090	EFA200662	26%	68.7%	93%
ECO104090	EFM100453	25%	67.2%	91.9%
ECO104090	ECO104090	100%	100%	100%
ECO104090	HIN100526	76%	95.4%	99.2%
ECO104090	HPY101229	30%	96.2%	95.8%
ECO104090	KPN302207	93%	96.9%	98.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO104090	LPN101590	58%	84.0%	98.2%
ECO104090	LMO102694	28%	68.7%	94.8%
ECO104090	MCA101349	49%	98.5%	97.0%
ECO104090	MAV101547	34%	71.8%	100%
ECO104090	MBV100941	35%	71.8%	100%
ECO104090	MLP101585	35%	71.8%	100%
ECO104090	MTU200053	35%	71.8%	100%
ECO104090	MGE100092	23%	67.2%	41.8%
ECO104090	MPN100603	28%	66.4%	40%
ECO104090	NGO100178	75%	81.7%	90.2%
ECO104090	NME201396	74%	81.7%	90.2%
ECO104090	PMU101180	78%	95.4%	99.2%
ECO104090	PRT104507	84%	100%	100%
ECO104090	PAE204930	63%	100%	95.7%
ECO104090	PPU106677	61%	100%	93.6%
ECO104090	PSY101040	59%	100%	95.0%
ECO104090	SPA102213	90%	100%	100%
ECO104090	STY103809	99%	100%	100%
ECO104090	STM103613	99%	100%	100%
ECO104090	SAU800365	30%	69.5%	94.9%
ECO104090	SEP201352	30%	69.5%	94.9%
ECO104090	SHA101078	24%	64.9%	94.6%
ECO104090	SMU101253	26%	69.5%	96.9%
ECO104090	SPN401395	24%	69.5%	96.9%
ECO104090	SPY201408	25%	69.5%	96.9%
ECO104090	TPA100062	27%	69.5%	96.8%
ECO104090	UUR100560	26%	95.4%	78.1%
ECO104090	VCH100361	81%	85.5%	91.8%
ECO104090	YPS002210	88%	100%	100%
ECO104091	BPT106954	27%	94.2%	88.8%
ECO104091	BCE114526	29%	92.3%	93.9%
ECO104091	BFU105920	27%	92.3%	93.9%
ECO104091	BMA100821	26%	92.3%	93.9%
ECO104091	EBC103611	91%	100%	100%
ECO104091	ECO104091	100%	100%	100%
ECO104091	HIN100525	61%	89.4%	98.9%
ECO104091	KPN300650	93%	72.1%	100%
ECO104091	NGO100181	30%	86.5%	87%
ECO104091	NME201395	29%	71.2%	71%
ECO104091	PMU101179	64%	95.2%	91.7%
ECO104091	PRT105182	72%	52.9%	100%
ECO104091	SPA102212	99%	100%	100%
ECO104091	STY103811	99%	100%	100%
ECO104091	STM103616	99%	100%	100%
ECO104091	VCH100362	49%	96.2%	100%
ECO104091	YPS002207	77%	99.0%	97.2%
ECO104092	ABA105585	80%	100%	100%
ECO104092	BAN110583	60%	86.7%	84.4%
ECO104092	BAN103323	60%	86.7%	84.4%
ECO104092	BFR100885	53%	86.7%	72.2%
ECO104092	BPT101387	70%	94.7%	78.9%
ECO104092	BBU100113	56%	92%	70.8%
ECO104092	BCE105745	69%	94.7%	78.0%
ECO104092	BFU105922	66%	94.7%	78.0%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO104092	BMA104982	69%	94.7%	78.0%
ECO104092	CJU100998	52%	84%	73.3%
ECO104092	CPN200890	52%	86.7%	82.9%
ECO104092	CTR200180	52%	86.7%	84.0%
ECO104092	CAC102549	56%	86.7%	72.2%
ECO104092	CBO100272	58%	86.7%	81.2%
ECO104092	CDF103531	54%	88%	88%
ECO104092	CDP100127	45%	90.7%	82.9%
ECO104092	EBC103610	100%	100%	100%
ECO104092	EFA200660	51%	93.3%	88.6%
ECO104092	EFM100455	53%	86.7%	83.3%
ECO104092	ECO104092	100%	100%	100%
ECO104092	HIN100524	93%	100%	100%
ECO104092	HPY101227	41%	93.3%	82.4%
ECO104092	KPN300649	100%	100%	100%
ECO104092	LPN101987	70%	100%	100%
ECO104092	LMO102748	56%	86.7%	82.3%
ECO104092	MCA101348	74%	100%	100%
ECO104092	MAV101549	50%	81.3%	72.6%
ECO104092	MBV106246	50%	81.3%	72.6%
ECO104092	MLP101583	49%	81.3%	72.6%
ECO104092	MTU200055	50%	81.3%	72.6%
ECO104092	MGE100094	45%	86.7%	62.9%
ECO104092	MPN100601	46%	86.7%	63.5%
ECO104092	NGO100183	68%	100%	100%
ECO104092	NME201394	68%	100%	100%
ECO104092	PMU101178	93%	100%	100%
ECO104092	PRT102061	100%	100%	100%
ECO104092	PAE204929	83%	98.7%	97.4%
ECO104092	PPU106680	78%	98.7%	97.4%
ECO104092	PSY101038	78%	98.7%	97.4%
ECO104092	SPA102211	98%	100%	100%
ECO104092	STY103813	100%	100%	100%
ECO104092	STM103619	98%	100%	100%
ECO104092	SAU800367	58%	93.3%	87.5%
ECO104092	SEP201354	60%	93.3%	87.5%
ECO104092	SHA101080	63%	86.7%	81.2%
ECO104092	SMU101249	44%	89.3%	84.8%
ECO104092	SPN401393	44%	89.3%	84.8%
ECO104092	SPY201406	47%	90.7%	87.3%
ECO104092	TPA100060	52%	90.7%	67.7%
ECO104092	UUR100558	46%	85.3%	81.0%
ECO104092	VCH100363	92%	100%	100%
ECO104092	YPS002204	97%	100%	100%
ECO104093	ABA101589	64%	100%	100%
ECO104093	BAN106894	34%	85.2%	94.0%
ECO104093	BAN102021	34%	98.0%	98.0%
ECO104093	BFR100594	33%	100%	100%
ECO104093	BPT101383	52%	100%	98.7%
ECO104093	BBU100112	33%	100%	85.5%
ECO104093	BCE105322	51%	100%	98.7%
ECO104093	BFU105903	53%	100%	98.7%
ECO104093	BMA104683	53%	100%	98.7%
ECO104093	CJU100620	30%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO104093	CPN200889	24%	99.3%	87.0%
ECO104093	CTR200181	30%	99.3%	88.0%
ECO104093	CAC102107	32%	96.6%	96.6%
ECO104093	CBO101031	35%	100%	100%
ECO104093	CDF103514	32%	98.0%	97.3%
ECO104093	CDP100781	38%	99.3%	99.3%
ECO104093	EBC103609	93%	100%	100%
ECO104093	EFA200658	37%	100%	100%
ECO104093	EFM100758	34%	100%	100%
ECO104093	ECO104093	100%	100%	100%
ECO104093	HIN100523	72%	100%	100%
ECO104093	HPY100509	31%	100%	99.3%
ECO104093	KPN300648	93%	100%	100%
ECO104093	LPN100854	51%	98.7%	98.0%
ECO104093	LMO101215	36%	100%	100%
ECO104093	MCA101347	58%	100%	93.1%
ECO104093	MAV101550	39%	100%	99.3%
ECO104093	MBV104721	38%	100%	99.3%
ECO104093	MLP101582	39%	99.3%	98.7%
ECO104093	MTU200056	38%	100%	99.3%
ECO104093	MGE100095	30%	100%	96.7%
ECO104093	MPN100600	30%	100%	97.3%
ECO104093	NGO100185	58%	99.3%	98%
ECO104093	NME201393	57%	99.3%	98%
ECO104093	PMU101177	77%	100%	100%
ECO104093	PRT102059	85%	100%	100%
ECO104093	PAE204927	62%	100%	100%
ECO104093	PPU106686	62%	99.3%	99.3%
ECO104093	PSY101034	64%	99.3%	99.3%
ECO104093	SPA102210	95%	100%	100%
ECO104093	STY103815	95%	100%	100%
ECO104093	STM103622	95%	100%	100%
ECO104093	SAU800015	32%	100%	100%
ECO104093	SEP201248	32%	100%	100%
ECO104093	SHA102269	33%	98.7%	98.6%
ECO104093	SMU101352	32%	92.6%	92.7%
ECO104093	SPN402006	27%	98.0%	98%
ECO104093	SPY201668	33%	95.3%	95.3%
ECO104093	TPA100059	34%	98.0%	92.9%
ECO104093	UUR100557	32%	100%	100%
ECO104093	VCH100364	76%	100%	100%
ECO104093	YPS002201	89%	100%	99.3%
ECO104105	ECO104105	100%	100%	100%
ECO104108	ABA104354	57%	97.1%	98.6%
ECO104108	BAN109563	26%	25.7%	98.3%
ECO104108	BAN109192	19%	66.4%	81.2%
ECO104108	BAN109684	21%	93.5%	99.5%
ECO104108	BAN111154	21%	91.5%	99.1%
ECO104108	BAN100457	23%	74.3%	93.1%
ECO104108	BAN110077	23%	95.1%	97.1%
ECO104108	BFR102710	29%	93.7%	98.1%
ECO104108	BCE107496	22%	92.6%	95.5%
ECO104108	BMA105472	22%	91.1%	93.5%
ECO104108	CJU100171	23%	94.9%	93.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO104108	CPN300392	21%	93.5%	97.3%
ECO104108	CTR200520	21%	91.9%	95.9%
ECO104108	CAC100920	25%	94.9%	99.3%
ECO104108	CBO101778	25%	93.1%	97.1%
ECO104108	CDF103911	25%	94.2%	97.8%
ECO104108	CDP101089	27%	74.3%	96%
ECO104108	EBC103219	93%	98.9%	99.3%
ECO104108	EFA201100	25%	97.3%	94.1%
ECO104108	EFM201455	23%	95.7%	99.5%
ECO104108	ECO104108	100%	100%	100%
ECO104108	HIN100432	52%	95.1%	98.1%
ECO104108	HPY101469	24%	94.4%	94.9%
ECO104108	KPN300265	93%	23.7%	100%
ECO104108	KPN303792	91%	99.6%	100%
ECO104108	LPN101474	19%	94.4%	98.6%
ECO104108	LMO100643	20%	94.0%	94.6%
ECO104108	MCA100528	56%	95.3%	97.0%
ECO104108	MBV102031	24%	75.2%	97.7%
ECO104108	MTU201808	24%	75.2%	97.7%
ECO104108	PMU101677	51%	94.6%	94.2%
ECO104108	PRT102472	72%	100%	97.6%
ECO104108	PAE205357	23%	94.4%	96.0%
ECO104108	PPU102210	22%	94.4%	96.0%
ECO104108	PSY103237	22%	94.4%	96.0%
ECO104108	SPA101428	91%	100%	100%
ECO104108	STY103853	91%	100%	100%
ECO104108	SAU800702	25%	92.6%	92.7%
ECO104108	SEP200743	24%	92.6%	92.7%
ECO104108	SHA102372	25%	85.7%	84.3%
ECO104108	SMU100422	23%	99.3%	97.5%
ECO104108	SPN200328	22%	88.1%	88.4%
ECO104108	VCH103557	59%	94.6%	96.8%
ECO104108	YPS002180	82%	97.8%	98.6%
ECO104111	ABA100443	24%	8.2%	13.6%
ECO104111	BPT101450	25%	14.1%	12.5%
ECO104111	BCE101350	27%	18.8%	90.0%
ECO104111	BFU101638	23%	58.9%	53.2%
ECO104111	BMA101700	23%	58.9%	56.0%
ECO104111	EBC100027	68%	9.2%	76.7%
ECO104111	EBC103222	85%	100%	100%
ECO104111	ECO104111	100%	100%	100%
ECO104111	HIN100677	33%	99.7%	98.1%
ECO104111	KPN303797	81%	100%	100%
ECO104111	LPN102776	25%	59.3%	34.3%
ECO104111	MCA101238	21%	15.8%	6.3%
ECO104111	NGO100807	25%	35.3%	32.3%
ECO104111	NME200276	24%	37.0%	32.7%
ECO104111	PMU101808	33%	99.9%	98.1%
ECO104111	PRT102475	51%	100%	99.9%
ECO104111	PAE202540	25%	100%	100%
ECO104111	PPU110598	26%	98.6%	99.1%
ECO104111	PSY102554	25%	99.4%	100%
ECO104111	SPA100314	82%	56.6%	98.9%
ECO104111	STY103859	86%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO104111	STM103693	86%	100%	100%
ECO104111	VCH102510	33%	99.8%	99.4%
ECO104111	YPS002176	57%	99.7%	99.7%
ECO104131	CDF100692	25%	95.9%	93.6%
ECO104131	EBC103305	86%	100%	100%
ECO104131	ECO104131	100%	100%	100%
ECO104131	KPN303807	83%	100%	100%
ECO104131	PRT101423	44%	98.1%	96.3%
ECO104131	SPA100383	89%	63.2%	100%
ECO104131	STY103932	87%	100%	100%
ECO104131	SAU802042	25%	97.8%	99.1%
ECO104131	SEP201102	26%	98.1%	99.1%
ECO104131	SHA101974	25%	97.8%	98.1%
ECO104131	VCH100893	49%	95.6%	95.3%
ECO104131	YPS003282	62%	99.7%	99.7%
ECO104132	ABA100801	61%	96.3%	95.9%
ECO104132	BAN106611	26%	88.8%	94.1%
ECO104132	BAN106191	28%	89.3%	93.2%
ECO104132	BFR101432	52%	94.8%	97.1%
ECO104132	BCE112176	54%	46.3%	99.3%
ECO104132	BFU102571	52%	94.7%	94.7%
ECO104132	BMA105621	50%	92.8%	94.1%
ECO104132	CAC102180	26%	92.3%	97.9%
ECO104132	CBO103123	53%	94.8%	97.0%
ECO104132	CDF100087	45%	19.6%	88.5%
ECO104132	CDF101158	48%	94.8%	96.4%
ECO104132	EBC103306	87%	100%	100%
ECO104132	EFA202419	50%	94.4%	95.9%
ECO104132	EFM201349	47%	59.0%	90.3%
ECO104132	ECO104132	100%	100%	100%
ECO104132	KPN303809	86%	99.8%	99.3%
ECO104132	LPN100436	43%	92.1%	96.0%
ECO104132	LMO101489	49%	95.0%	98.0%
ECO104132	MAV101838	28%	72.7%	42.6%
ECO104132	MBV102540	30%	74.9%	79.9%
ECO104132	MLP101576	28%	73.3%	42.5%
ECO104132	MTU201964	30%	76.6%	80.1%
ECO104132	MGE100073	30%	74.9%	79.2%
ECO104132	MPN100622	28%	92.0%	98.4%
ECO104132	PAE204820	54%	93.0%	94.9%
ECO104132	PPU111815	52%	93.4%	93.8%
ECO104132	SPA100073	97%	8.7%	100%
ECO104132	SPA102080	86%	56.5%	100%
ECO104132	STY103935	90%	99.8%	99.3%
ECO104132	STM104099	90%	99.8%	99.3%
ECO104132	SMU101048	30%	79.5%	82.4%
ECO104132	SPN401409	28%	94.3%	97.8%
ECO104132	SPY200449	30%	76.7%	79.1%
ECO104132	UUR100266	29%	75.1%	71.1%
ECO104132	YPS000377	51%	94.3%	96.6%
ECO104144	ABA105759	37%	98.2%	97.4%
ECO104144	BAN113013	34%	99.1%	97.4%
ECO104144	BAN113324	37%	97.0%	93.7%
ECO104144	BFR12921	25%	90.4%	84.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO104144	BPT100142	37%	96.4%	93.6%
ECO104144	BFU115965	57%	98.2%	98.2%
ECO104144	BFU101445	59%	99.7%	99.7%
ECO104144	BMA106998	58%	98.2%	97.6%
ECO104144	CBO101831	59%	99.4%	99.1%
ECO104144	EFA202435	50%	99.1%	97.1%
ECO104144	EFM200632	52%	99.1%	96.8%
ECO104144	ECO104144	100%	100%	100%
ECO104144	HIN100575	62%	98.2%	98.2%
ECO104144	KPN303779	89%	100%	100%
ECO104144	MCA103610	36%	96.4%	95.1%
ECO104144	MAV103297	36%	98.2%	98.4%
ECO104144	MBV100238	37%	98.2%	99.0%
ECO104144	MLP100875	34%	98.2%	95%
ECO104144	MTU201635	37%	98.2%	99.0%
ECO104144	MPN100530	46%	77.2%	98.2%
ECO104144	PMU100808	68%	98.5%	98.2%
ECO104144	PRT101184	73%	99.7%	94.0%
ECO104144	PAE205167	58%	98.5%	97.9%
ECO104144	SPA102327	89%	100%	100%
ECO104144	STY103975	89%	100%	100%
ECO104144	SAU801169	58%	100%	99.7%
ECO104144	SEP202228	57%	100%	99.7%
ECO104144	SHA100088	59%	94.6%	100%
ECO104144	SPN401954	53%	99.1%	96.7%
ECO104144	SPY201192	54%	98.5%	96.4%
ECO104144	VCH102472	67%	98.5%	98.2%
ECO104144	YPS000950	79%	100%	99.7%
ECO104147	ABA100831	25%	33.8%	73.5%
ECO104147	BFR105965	26%	17.8%	19.2%
ECO104147	ECO104147	100%	100%	100%
ECO104147	SPA102322	39%	51.4%	82.0%
ECO104147	STY103989	42%	98.5%	97.2%
ECO104147	STM104138	42%	98.5%	97.2%
ECO104147	SPN401200	19%	91.1%	79.0%
ECO104147	YPS000029	31%	90.3%	89.7%
ECO104148	ABA101795	58%	99.7%	98.7%
ECO104148	BAN107436	33%	99.1%	98.3%
ECO104148	BAN109623	42%	99.1%	98.3%
ECO104148	BFR103128	38%	99.6%	99.0%
ECO104148	BPT100020	49%	99.4%	97.9%
ECO104148	BBU100737	37%	98.5%	97.9%
ECO104148	BCE114033	50%	99.3%	98.8%
ECO104148	BFU109684	50%	99.3%	98.2%
ECO104148	BMA104351	51%	99.9%	99.5%
ECO104148	CJU100714	37%	97.3%	97.6%
ECO104148	CPN200668	37%	97.3%	97.0%
ECO104148	CTR200568	36%	98.7%	99.3%
ECO104148	CAC100067	43%	99.7%	99.2%
ECO104148	CBO100672	43%	99.2%	98.6%
ECO104148	CDF100033	35%	22.9%	92.6%
ECO104148	CDF102611	43%	98.4%	97.5%
ECO104148	CDP101232	39%	98.9%	98.3%
ECO104148	EBC104048	93%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO104148	EFA200179	43%	99.6%	98.9%
ECO104148	EFM201966	43%	98.8%	98.0%
ECO104148	ECO104148	100%	100%	100%
ECO104148	HIN101359	70%	100%	99.4%
ECO104148	HPY101136	40%	98.9%	98.3%
ECO104148	KPN303513	95%	97.5%	99.6%
ECO104148	LPN102949	53%	94.8%	100%
ECO104148	LMO102840	41%	99.3%	98.2%
ECO104148	MCA101259	55%	100%	99.2%
ECO104148	MAV104126	43%	94.5%	99.9%
ECO104148	MBV101058	43%	97.8%	97.7%
ECO104148	MLP100909	41%	99.5%	98.4%
ECO104148	MTU202412	43%	97.8%	97.7%
ECO104148	MGE100341	31%	99.9%	98.7%
ECO104148	MPN100361	30%	99.6%	98.3%
ECO104148	NGO100851	52%	99.1%	99.5%
ECO104148	NME200089	51%	99.6%	99.4%
ECO104148	PMU100818	70%	100%	99.4%
ECO104148	PRT105161	80%	100%	98.9%
ECO104148	PAE203831	62%	100%	100%
ECO104148	PPU109466	62%	99.5%	100%
ECO104148	PSY104286	64%	100%	100%
ECO104148	SPA100729	91%	70.3%	99.9%
ECO104148	STY104006	95%	100%	100%
ECO104148	SAU801663	40%	98.4%	98.2%
ECO104148	SEP201629	40%	98.4%	98.2%
ECO104148	SHA100785	41%	98.4%	98.2%
ECO104148	SMU100583	43%	97.8%	96.9%
ECO104148	SPN400492	43%	98.2%	97.4%
ECO104148	SPY201210	44%	97.8%	97.1%
ECO104148	TPA101025	39%	98.3%	96.2%
ECO104148	UUR100269	31%	99.2%	98.4%
ECO104148	VCH102467	75%	100%	100%
ECO104148	YPS000947	87%	100%	98.5%
ECO104149	BPT103974	26%	80.3%	82.8%
ECO104149	BFU115196	23%	79.6%	83.3%
ECO104149	BMA104809	23%	79.6%	83.3%
ECO104149	EBC104045	91%	100%	100%
ECO104149	ECO104149	100%	100%	100%
ECO104149	HIN101365	50%	96.6%	95.8%
ECO104149	KPN303511	90%	100%	100%
ECO104149	LPN102121	36%	81.6%	96.0%
ECO104149	NGO101318	29%	94.6%	92.5%
ECO104149	NME201616	29%	94.6%	92.5%
ECO104149	PMU100822	51%	96.6%	95.8%
ECO104149	PRT100708	62%	98.6%	97.3%
ECO104149	PAE203829	34%	83.7%	84.5%
ECO104149	PPU104071	33%	95.9%	94.4%
ECO104149	PSY104282	28%	94.6%	93.0%
ECO104149	SPA100450	93%	100%	100%
ECO104149	STY104009	95%	100%	91.9%
ECO104149	VCH102466	41%	97.3%	96.0%
ECO104149	YPS000946	71%	98.6%	97.3%
ECO104157	ABA100184	24%	90.1%	89.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO104157	BCE102585	42%	97.7%	97.7%
ECO104157	ECO104157	100%	100%	100%
ECO104157	SPA101511	83%	100%	100%
ECO104160	BCE113197	34%	94.7%	91%
ECO104160	BCE108719	42%	94.7%	89.9%
ECO104160	EBC102943	71%	99.7%	100%
ECO104160	ECO104160	100%	100%	100%
ECO104160	KPN303490	75%	99.7%	100%
ECO104160	PPU102659	75%	8.3%	35.9%
ECO104160	SPA102170	64%	63.1%	99.2%
ECO104160	STY104029	58%	99.0%	93.6%
ECO104160	YPS001277	63%	15.2%	98.4%
ECO104160	YPS000925	78%	98.7%	93.6%
ECO104164	EBC102171	42%	96.6%	27.5%
ECO104164	ECO100791	42%	96.6%	27.5%
ECO104164	ECO104164	100%	100%	100%
ECO104164	HIN101041	36%	98.0%	30.7%
ECO104164	HIN100985	40%	98.6%	28.3%
ECO104164	KPN301162	40%	96.6%	27.9%
ECO104164	NME101282	40%	98.6%	26.5%
ECO104164	PRT100704	36%	95.9%	28.3%
ECO104164	SPA102068	41%	96.6%	37.0%
ECO104164	STY102390	43%	96.6%	27.6%
ECO104165	ECO104165	100%	100%	100%
ECO104165	YPS003651	40%	26.8%	32.5%
ECO104167	EFM201272	23%	43.7%	50.9%
ECO104167	ECO101210	38%	27.1%	61.7%
ECO104167	ECO104167	100%	100%	100%
ECO104168	ABA103574	23%	86.4%	87.0%
ECO104168	ABA104393	26%	92.7%	96.9%
ECO104168	ABA100187	26%	91.3%	93.6%
ECO104168	BAN101891	26%	84.2%	90.0%
ECO104168	BAN111995	27%	89.2%	95.7%
ECO104168	BCE111986	26%	92.5%	93.1%
ECO104168	BFU102922	28%	92%	84.2%
ECO104168	CDF103974	21%	86.1%	87.3%
ECO104168	EFM202262	31%	84.5%	95.8%
ECO104168	ECO104168	100%	100%	100%
ECO104168	HIN101078	27%	91.8%	98.5%
ECO104168	KPN202674	27%	88.9%	92.0%
ECO104168	PMU100835	29%	89.6%	94.6%
ECO104168	PRT102108	26%	89.2%	93.6%
ECO104168	PAE202112	28%	92%	94.1%
ECO104168	SPA103461	56%	92.7%	100%
ECO104168	STY103701	57%	92.7%	95.3%
ECO104168	STM102259	56%	92.7%	95.3%
ECO104168	SPY201028	25%	86.6%	91.4%
ECO104168	VCH103392	24%	83.1%	86.1%
ECO104176	ABA104707	40%	93.7%	93.0%
ECO104176	BPT102450	40%	100%	100%
ECO104176	CPN200407	33%	92.2%	89.2%
ECO104176	CTR200334	30%	92.5%	89.6%
ECO104176	CBO101131	42%	98.8%	96.9%
ECO104176	CBO101508	44%	98.8%	91.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO104176	EBC103339	79%	100%	100%
ECO104176	ECO104176	100%	100%	100%
ECO104176	HIN100341	36%	89.8%	74.5%
ECO104176	MCA100484	35%	92.2%	77.5%
ECO104176	NGO100089	44%	92.2%	92.9%
ECO104176	NME200417	43%	92.2%	92.9%
ECO104176	PMU100128	53%	100%	99.2%
ECO104176	PSY102150	52%	98.8%	95.8%
ECO104176	SEP101306	37%	98.4%	95.8%
ECO104176	UUR100440	26%	93.3%	73.1%
ECO104176	UUR100067	41%	88.6%	78.0%
ECO104177	BAN102006	29%	84.0%	85.6%
ECO104177	BAN106411	32%	99.1%	98.5%
ECO104177	BAN101873	33%	99.7%	97.3%
ECO104177	BAN106549	37%	94.7%	92.6%
ECO104177	CAC101855	31%	99.4%	97.3%
ECO104177	CBO103619	29%	98.7%	96.1%
ECO104177	CBO103030	37%	98.4%	95.1%
ECO104177	CDF102385	35%	98.4%	94.1%
ECO104177	EBC103337	91%	100%	100%
ECO104177	EFA202024	35%	94.7%	91.4%
ECO104177	EFM202344	29%	94.3%	94.3%
ECO104177	ECO104177	100%	100%	100%
ECO104177	HPY100875	37%	85.8%	83.1%
ECO104177	KPN103323	34%	99.4%	97.9%
ECO104177	LMO100925	41%	85.8%	81.5%
ECO104177	PMU100129	52%	99.1%	94.5%
ECO104177	PSY102148	47%	98.7%	97.2%
ECO104177	SAU802175	42%	86.2%	85.7%
ECO104177	SEP201999	44%	85.8%	85.7%
ECO104177	SHA101593	34%	99.4%	96.2%
ECO104177	UUR100360	19%	84.6%	77.1%
ECO104177	UUR100522	20%	83.3%	81.5%
ECO104177	UUR100068	24%	83.6%	80.9%
ECO104180	BFR10661	22%	72.0%	93.6%
ECO104180	EBC103344	98%	100%	100%
ECO104180	ECO104180	100%	100%	100%
ECO104180	HPY101380	23%	49.9%	55.8%
ECO104180	HPY100677	22%	81.7%	92.4%
ECO104180	HPY100794	24%	79.1%	89.1%
ECO104180	NGO100096	25%	19.3%	22.0%
ECO104180	NME101919	23%	19.3%	21.8%
ECO104180	PAE203898	62%	99.1%	99.5%
ECO104180	PPU108419	61%	99.0%	99.6%
ECO104180	PSY101287	63%	92.6%	99.7%
ECO104180	VCH103300	19%	79.8%	89.3%
ECO104180	VCH102800	22%	80.1%	90.2%
ECO104181	BFR104817	23%	56.8%	53.9%
ECO104181	BFR104751	21%	61.2%	61.7%
ECO104181	BFR102219	22%	75.7%	74.4%
ECO104181	BFR103060	24%	49.5%	48.1%
ECO104181	BFR104874	20%	84.5%	87.2%
ECO104181	BFR103005	24%	47.6%	41.0%
ECO104181	BFR101497	23%	59.6%	50%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO104181	BFR103599	29%	44.8%	45.0%
ECO104181	BFR102926	24%	59.0%	59.5%
ECO104181	BFR100732	23%	57.1%	64.5%
ECO104181	BFR103796	25%	47.3%	51.4%
ECO104181	BFR104849	22%	89.6%	86.6%
ECO104181	BFR104724	25%	57.4%	57.2%
ECO104181	BFR104421	24%	75.7%	83.5%
ECO104181	BFR104845	25%	54.9%	57.3%
ECO104181	BFR104846	26%	48.9%	42.1%
ECO104181	BFR100316	22%	76.0%	75.6%
ECO104181	BFR104616	23%	76.3%	73.6%
ECO104181	BFR105670	23%	75.4%	60.1%
ECO104181	BPT102473	31%	99.7%	96.0%
ECO104181	BCE113436	37%	95.6%	94.8%
ECO104181	BFU111075	31%	97.2%	97.8%
ECO104181	BMA107603	35%	40.7%	96.3%
ECO104181	EBC103342	96%	100%	100%
ECO104181	ECO104181	100%	100%	100%
ECO104181	KPN101346	72%	19.6%	100%
ECO104181	PRT104465	25%	93.7%	88.4%
ECO104181	PAE203897	36%	96.5%	95.9%
ECO104181	PPU104167	37%	94.3%	94.9%
ECO104181	PSY101289	35%	95.0%	93.2%
ECO104183	CAC101282	31%	79.1%	52.1%
ECO104183	ECO104183	100%	100%	100%
ECO104183	YPS001038	41%	95.6%	98.9%
ECO104183	YPS001009	43%	98.9%	98.9%
ECO104183	YPS001004	43%	98.9%	98.9%
ECO104187	BAN113191	24%	82.1%	89.3%
ECO104187	BAN102445	27%	83.7%	88.6%
ECO104187	CDF101615	33%	91.2%	98.0%
ECO104187	CDP101690	28%	77.1%	79.1%
ECO104187	EBC100789	58%	89.7%	97.9%
ECO104187	ECO100260	58%	90.9%	93.9%
ECO104187	ECO104187	100%	100%	100%
ECO104187	MAV103039	25%	91.8%	98.6%
ECO104187	STM103039	42%	92.8%	98.3%
ECO104206	BPT101287	33%	95.3%	93.8%
ECO104206	ECO104206	100%	100%	100%
ECO104206	KPN303324	79%	86.8%	100%
ECO104206	PRT101726	52%	96.5%	96.8%
ECO104206	PAE200993	35%	96.1%	96.9%
ECO104206	PPU101846	35%	82.2%	94.9%
ECO104206	PSY105014	33%	94.3%	97.1%
ECO104206	SAU402924	19%	25.5%	25.9%
ECO104206	YPS001103	36%	94.4%	96.7%
ECO104212	ECO104212	100%	100%	100%
ECO104212	MAV105559	38%	98.4%	96.4%
ECO104212	PAE202340	43%	96.9%	95.5%
ECO104212	PSY101120	40%	93.8%	92.1%
ECO104212	SPA103867	77%	99.4%	100%
ECO104212	STY100399	79%	99.4%	98.8%
ECO104212	STM100679	79%	99.4%	98.8%
ECO104212	SHA101546	27%	19.1%	38.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO104213	BCE114465	33%	87.9%	86.0%
ECO104213	BFU107523	30%	84.8%	87.4%
ECO104213	ECO104213	100%	100%	100%
ECO104213	HIN100053	49%	94.9%	89.8%
ECO104213	KPN301618	46%	95.3%	94.2%
ECO104213	MBV102351	32%	63.0%	67.6%
ECO104213	MTU200492	32%	63.0%	64.7%
ECO104213	PMU101764	20%	84.0%	91.1%
ECO104213	PPU100354	32%	87.2%	94.0%
ECO104213	SPA102961	88%	100%	100%
ECO104213	STY104415	89%	100%	100%
ECO104213	STM104238	89%	100%	100%
ECO104213	YPS000365	51%	94.6%	90.6%
ECO104214	ECO104094	41%	81.5%	84.5%
ECO104214	ECO104214	100%	100%	100%
ECO104218	BAN109731	25%	83.0%	61.4%
ECO104218	BAN101242	25%	83.0%	61.7%
ECO104218	BFR104541	32%	47.7%	18.5%
ECO104218	BPT106864	29%	59.5%	28.8%
ECO104218	CAC103483	25%	68.0%	57.8%
ECO104218	CBO103698	31%	69.9%	59.9%
ECO104218	CDF103367	47%	95.4%	86.9%
ECO104218	ECO104218	100%	100%	100%
ECO104218	LPN103427	32%	53.6%	21.5%
ECO104218	PAE205473	25%	75.8%	31.8%
ECO104218	PPU102004	25%	77.8%	32.5%
ECO104218	PSY101204	26%	75.8%	31.5%
ECO104218	SPA100039	97%	26.1%	72.7%
ECO104218	STY104427	96%	100%	100%
ECO104218	SAU800319	22%	100%	29.1%
ECO104218	VCH103730	53%	94.8%	93.5%
ECO104227	ECO104227	100%	100%	100%
ECO104233	BFR103759	34%	35.5%	7.3%
ECO104233	ECO104233	100%	100%	100%
ECO104233	PSY108408	47%	21.4%	19.6%
ECO104233	SPA103792	64%	61.7%	34.0%
ECO104233	STY104385	64%	0.7%	58.5%
ECO104237	CBO102806	21%	80.4%	90.8%
ECO104237	CDP102071	23%	31.9%	36.0%
ECO104237	EBC104003	22%	90.3%	45.7%
ECO104237	EFM100817	25%	12.1%	81.8%
ECO104237	ECO104237	100%	100%	100%
ECO104237	HPY101363	32%	14.7%	51.2%
ECO104237	KPN204112	22%	44.4%	95.6%
ECO104237	NGO101210	22%	28.4%	32%
ECO104237	NME101733	23%	40.5%	46.3%
ECO104237	PAE202732	23%	20.7%	22.3%
ECO104237	PPU100120	23%	55.4%	6.6%
ECO104237	PSY109124	21%	45.5%	45.1%
ECO104237	SPA100829	42%	99.4%	100%
ECO104237	STY104453	42%	100%	100%
ECO104237	SAU801807	21%	89.0%	47.9%
ECO104237	SPN400445	26%	25%	28.2%
ECO104237	SPN400448	19%	84.1%	83.9%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO104237	SPY201468	26%	19.8%	21.8%
ECO104237	UUR100451	21%	62.9%	52.3%
ECO104241	BAN105415	34%	97.2%	87.9%
ECO104241	BAN100610	36%	98.2%	88.3%
ECO104241	BPT100527	34%	96.1%	76.8%
ECO104241	BCE105851	33%	96.8%	79.6%
ECO104241	BFU104903	34%	96.8%	88.7%
ECO104241	BMA105285	34%	96.8%	85.4%
ECO104241	CDP100497	25%	81.0%	75.7%
ECO104241	EBC103564	89%	100%	100%
ECO104241	EFA201443	26%	100%	88.0%
ECO104241	ECO104241	100%	100%	100%
ECO104241	HPY100308	31%	52.5%	47.7%
ECO104241	KPN303969	88%	100%	89.3%
ECO104241	PRT105871	69%	99.3%	87.1%
ECO104241	PAE204602	50%	98.2%	85.3%
ECO104241	PPU108515	50%	99.3%	88.3%
ECO104241	PSY105304	49%	99.3%	88%
ECO104241	SPA100149	84%	70.1%	76.0%
ECO104241	STY104465	90%	100%	89.3%
ECO104241	SAU800450	25%	96.8%	83.2%
ECO104241	SHA102676	26%	80.3%	69.3%
ECO104242	ABA102199	40%	82.1%	55%
ECO104242	BAN106862	42%	73.1%	81.7%
ECO104242	BAN100124	40%	92.5%	78.4%
ECO104242	BCE111053	56%	100%	100%
ECO104242	CJU100846	35%	95.5%	98.5%
ECO104242	CDP102875	32%	73.1%	69.7%
ECO104242	EBC103562	89%	100%	100%
ECO104242	ECO104242	100%	100%	100%
ECO104242	KPN303965	91%	100%	100%
ECO104242	NGO100488	31%	86.6%	85.9%
ECO104242	NME201558	31%	86.6%	85.9%
ECO104242	PRT102284	85%	100%	100%
ECO104242	PAE204603	67%	100%	100%
ECO104242	PPU108517	68%	100%	100%
ECO104242	PSY105303	65%	100%	100%
ECO104242	SPA100318	73%	100%	100%
ECO104242	STY104469	94%	100%	100%
ECO104242	STM101111	73%	100%	100%
ECO104242	YPS000934	42%	73.1%	48.5%
ECO104243	EBC103560	93%	97.1%	100%
ECO104243	ECO104243	100%	100%	100%
ECO104243	HIN101100	29%	47.6%	88.7%
ECO104243	KPN303963	94%	78.8%	97.6%
ECO104243	PRT105711	89%	99.3%	100%
ECO104243	PAE204604	69%	97.9%	99.6%
ECO104243	PPU108519	69%	97.9%	99.6%
ECO104243	PSY105302	68%	89.3%	99.2%
ECO104243	SPA100405	96%	63.9%	100%
ECO104243	STY104486	96%	99.3%	100%
ECO104248	BPT100647	22%	48.7%	53.8%
ECO104248	CJU100983	21%	24.3%	28.8%
ECO104248	CBO100209	22%	29.3%	36.2%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO104248	EBC102765	83%	99.7%	97.8%
ECO104248	EFA200629	21%	39.9%	45.3%
ECO104248	ECO104248	100%	100%	100%
ECO104248	HIN101218	22%	36.8%	40.6%
ECO104248	HPY100571	22%	31.1%	35.5%
ECO104248	KPN300147	83%	18.4%	100%
ECO104248	KPN303987	86%	100%	98.3%
ECO104248	PMU101683	22%	45.2%	50.1%
ECO104248	PAE201688	24%	33.7%	35.4%
ECO104248	PPU105635	27%	28.1%	27.3%
ECO104248	PSY104669	23%	35.5%	37.4%
ECO104248	SPA101818	92%	70.7%	88.2%
ECO104248	STY104492	91%	99.9%	98.2%
ECO104248	SMU100078	19%	46.8%	53.0%
ECO104248	VCH103522	23%	31.1%	33.5%
ECO104257	ABA105495	32%	95.9%	98.8%
ECO104257	BAN109779	30%	30.3%	53.5%
ECO104257	BAN106573	32%	46.9%	81.4%
ECO104257	CJU100460	33%	22.2%	33.0%
ECO104257	CDP100325	31%	42.9%	30.9%
ECO104257	EBC100359	84%	64.7%	100%
ECO104257	ECO104257	100%	100%	100%
ECO104257	HIN100011	46%	94.8%	97.3%
ECO104257	KPN302168	89%	93.9%	100%
ECO104257	LMO100106	30%	47.2%	81.6%
ECO104257	MBV104557	35%	27.1%	39.4%
ECO104257	MTU200557	35%	27.1%	39.4%
ECO104257	PMU100958	48%	94.8%	97.3%
ECO104257	PRT100948	54%	97.4%	99.1%
ECO104257	PAE204625	40%	95.9%	98.5%
ECO104257	PPU103990	37%	95.9%	98.5%
ECO104257	PSY102430	37%	95.9%	98.5%
ECO104257	STY104541	90%	99.7%	100%
ECO104257	SAU800541	31%	47.2%	82.7%
ECO104257	SHA101635	28%	50.4%	88.1%
ECO104257	SMU100923	32%	47.2%	80.8%
ECO104257	SPN400743	31%	49.3%	85.2%
ECO104257	SPY200944	32%	49.0%	84.3%
ECO104257	VCH100611	42%	97.4%	99.4%
ECO104257	YPS000089	69%	98.5%	97.4%
ECO104266	CBO103949	43%	94.8%	97.6%
ECO104266	EBC103570	86%	87.8%	100%
ECO104266	ECO104266	100%	100%	100%
ECO104266	HIN100500	40%	87.8%	88.7%
ECO104266	PRT104710	71%	99.0%	99.6%
ECO104266	PSY100831	28%	23.1%	21.5%
ECO104266	SPA102180	75%	81.2%	100%
ECO104266	STY104578	89%	100%	100%
ECO104277	ABA100489	71%	99.8%	99.8%
ECO104277	BFR12450	57%	46.7%	99.1%
ECO104277	BPT101569	70%	99.6%	100%
ECO104277	BCE110991	72%	94.6%	99.8%
ECO104277	BFU107313	72%	100%	100%
ECO104277	BMA109904	71%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO104277	CDF101289	40%	97.5%	38.7%
ECO104277	CDP101266	53%	100%	100%
ECO104277	EBC103175	95%	100%	100%
ECO104277	EFM100646	36%	96.4%	43.4%
ECO104277	ECO104277	100%	100%	100%
ECO104277	HIN101224	86%	99.8%	99.6%
ECO104277	KPN302187	96%	99.6%	100%
ECO104277	LMO101330	37%	95.9%	39.4%
ECO104277	MCA100198	68%	99.6%	99.6%
ECO104277	MAV100344	57%	100%	99.8%
ECO104277	MBV101523	56%	100%	99.8%
ECO104277	MLP100773	56%	100%	99.8%
ECO104277	MTU202441	56%	100%	99.8%
ECO104277	NGO100693	68%	99.6%	99.5%
ECO104277	NME201942	69%	99.6%	99.5%
ECO104277	PMU100425	87%	99.8%	99.6%
ECO104277	PRT101954	89%	100%	100%
ECO104277	PAE204593	74%	99.8%	100%
ECO104277	PPU109750	72%	98.7%	100%
ECO104277	PSY100129	71%	31.0%	97.6%
ECO104277	SPA101244	94%	97.3%	56.5%
ECO104277	STY104621	97%	100%	100%
ECO104277	VCH100685	79%	100%	100%
ECO104286	BCE106333	34%	91.3%	91.8%
ECO104286	ECO104286	100%	100%	100%
ECO104286	KPN302096	63%	100%	99.8%
ECO104286	PMU100722	30%	19.1%	27.5%
ECO104286	PAE200464	38%	93.8%	96.0%
ECO104286	SPA103705	72%	100%	100%
ECO104286	STY100644	73%	100%	100%
ECO104286	STM100405	73%	100%	100%
ECO104286	SHA102806	29%	16.2%	80.6%
ECO104286	SMU101645	36%	12.7%	25.3%
ECO104286	VCH101112	31%	15.1%	15.8%
ECO104286	YPS000166	46%	94.9%	87.0%
ECO201063	EBC107300	65%	75.3%	98.2%
ECO201063	ECO101962	97%	100%	100%
ECO201249	ECO201249	100%	100%	100%
ECO201472	BFU102395	44%	89.2%	65.3%
ECO201472	EBC103227	79%	63.9%	100%
ECO201472	ECO102590	76%	88.6%	87.5%
ECO201472	ECO100239	80%	100%	100%
ECO201472	ECO101961	97%	93.7%	100%
ECO201472	LPN103162	46%	66.5%	95.5%
ECO201472	SEP200678	41%	38.0%	57.1%
ECO201937	ECO201937	100%	100%	100%
ECO201962	BFR100408	21%	19.5%	25.7%
ECO201962	BPT101287	30%	92.0%	89.6%
ECO201962	ECO101476	98%	43.3%	100%
ECO201962	ECO104206	57%	97.6%	97.0%
ECO201962	KPN305983	36%	94.8%	95.1%
ECO201962	KPN303324	61%	85.1%	98.2%
ECO201962	PRT101028	43%	95.2%	96.0%
ECO201962	PRT101726	45%	96.0%	96.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO201962	PAE200993	33%	97.6%	97.9%
ECO201962	PPU101846	33%	84.7%	98.1%
ECO201962	PSY104278	33%	70.4%	97.5%
ECO201962	PSY105014	32%	91.7%	91.6%
ECO201962	SPA104864	44%	95.5%	100%
ECO201962	STM100755	44%	96.9%	97.5%
ECO201962	YPS001103	34%	97.1%	98.8%
ECO201962	YPS000524	35%	92.0%	91.4%
ECO202164	ABA104543	28%	41.3%	19.8%
ECO202164	BCE101745	31%	47.0%	20.9%
ECO202164	CDP101707	37%	90.9%	43.5%
ECO202164	ECO202164	100%	100%	100%
ECO202164	KPN100079	91%	30%	100%
ECO202164	SAU802473	39%	96.5%	43.2%
ECO202164	SHA101725	39%	96.5%	43.0%
ECO202228	EBC104921	68%	95%	100%
ECO202228	ECO202228	100%	100%	100%
ECO202228	KPN305748	66%	95%	69.4%
ECO202228	SPA104369	66%	95%	100%
ECO202238	EBC106405	50%	74.6%	78.6%
ECO202238	ECO202238	100%	100%	100%
ECO202238	SPA106377	26%	94.9%	100%
ECO202902	ECO202902	100%	100%	100%
ECO202902	SPA105152	78%	39.6%	14.6%
ECO204438	EBC105029	68%	96.4%	100%
ECO204438	ECO204438	100%	100%	100%
ECO204438	KPN205390	58%	94.0%	100%
ECO204438	PRT104175	36%	73.5%	69.9%
ECO204438	SPA100720	75%	74.7%	73.4%
ECO204448	ECO204448	100%	100%	100%
ECO204448	SPA101764	69%	98.8%	100%
ECO204448	STY105423	78%	47.5%	88.4%
ECO204845	ECO204845	100%	100%	100%
ECO204845	PAE107444	24%	33.0%	45.5%
ECO204900	ABA100225	27%	35.8%	38.1%
ECO204900	ABA100477	27%	34.3%	61.1%
ECO204900	BAN104847	33%	20.2%	18.2%
ECO204900	BAN109223	32%	7.8%	34.8%
ECO204900	BAN101440	31%	8.3%	31.7%
ECO204900	BAN110288	23%	31.9%	18.9%
ECO204900	BCE108121	27%	67.7%	57.0%
ECO204900	BFU107935	31%	7.1%	31.6%
ECO204900	BFU100092	46%	8.9%	98.9%
ECO204900	BFU100109	27%	23.2%	47.7%
ECO204900	BFU102581	29%	56.8%	5.1%
ECO204900	CAC100404	30%	8.8%	33.2%
ECO204900	EBC107494	28%	13.9%	85%
ECO204900	EBC103412	27%	12.8%	59.2%
ECO204900	ECO100490	77%	9.4%	39.4%
ECO204900	ECO103517	90%	15.6%	66.1%
ECO204900	ECO100686	95%	33.0%	68.1%
ECO204900	ECO101427	76%	53.0%	77.6%
ECO204900	ECO100488	67%	98.8%	69.6%
ECO204900	ECO100683	92%	73.4%	31.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO204900	ECO103515	86%	78.7%	33.7%
ECO204900	ECO103405	85%	78.7%	32.9%
ECO204900	PRT103688	31%	10.6%	73.6%
ECO204900	PRT103361	33%	11.5%	78.0%
ECO204900	PRT103421	25%	67.7%	57.2%
ECO204900	PAE202682	32%	31.4%	37.7%
ECO204900	PPU107712	31%	10.9%	93.1%
ECO204900	PPU110484	27%	9.2%	58.3%
ECO204900	PPU109654	25%	38.7%	86.8%
ECO204900	PPU107101	40%	5.6%	5.5%
ECO204900	PPU109653	27%	58.8%	69.8%
ECO204900	PPU110482	25%	63.8%	22.1%
ECO204900	PPU109652	25%	60.3%	22.3%
ECO204900	PSY108533	29%	4.2%	80.6%
ECO204900	PSY101322	55%	6.0%	24.3%
ECO204900	PSY105816	42%	11.6%	51.6%
ECO204900	PSY102083	26%	55.5%	21.6%
ECO204900	SPA106438	42%	8.6%	5.5%
ECO204900	SPA100247	28%	65.1%	49.1%
ECO204900	STY104095	29%	60.1%	45.3%
ECO204900	STM103807	42%	11.0%	44.7%
ECO204900	STM103806	26%	46.7%	19.0%
ECO204900	YPS002988	30%	55.6%	24.5%
ECO204900	YPS002860	25%	63.7%	38.3%
ECO204942	ABA100233	85%	33.5%	98.5%
ECO204942	ABA100062	84%	99.5%	99.5%
ECO204942	BAN106076	74%	99.7%	99.7%
ECO204942	BFR12122	71%	99.7%	99.7%
ECO204942	BPT100044	80%	99.7%	99.7%
ECO204942	BPT100847	80%	99.7%	99.7%
ECO204942	BBU100475	64%	99.7%	98.0%
ECO204942	BCE112288	75%	15.5%	98.4%
ECO204942	BCE106056	81%	52.5%	100%
ECO204942	BCE108906	80%	99.7%	99.7%
ECO204942	BFU100267	74%	37.3%	99.3%
ECO204942	BFU100847	79%	99.7%	99.7%
ECO204942	BMA107343	78%	95.9%	100%
ECO204942	BMA106305	79%	99.7%	99.7%
ECO204942	CJU100435	72%	99.7%	99.7%
ECO204942	CPN200689	68%	99.5%	99.5%
ECO204942	CTR200588	67%	100%	98.7%
ECO204942	CAC103049	72%	99.7%	99.7%
ECO204942	CBO100671	69%	10.9%	95.6%
ECO204942	CBO101209	74%	59.1%	100%
ECO204942	CBO101304	72%	99.5%	99.5%
ECO204942	CDF100547	73%	99.7%	95.9%
ECO204942	CDP100912	71%	99.7%	99.7%
ECO204942	EBC101615	99%	33.8%	99.3%
ECO204942	EBC100362	97%	47.7%	100%
ECO204942	EBC102891	97%	99.7%	99.7%
ECO204942	EFA202006	76%	99.7%	99.7%
ECO204942	EFM100161	74%	71.3%	100%
ECO204942	ECO103262	99%	99.7%	99.7%
ECO204942	ECO103878	99%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO204942	HIN100558	92%	99.7%	99.7%
ECO204942	HIN100613	92%	99.7%	99.7%
ECO204942	HPY101188	72%	99.7%	99.7%
ECO204942	KPN300520	98%	23.6%	100%
ECO204942	KPN300653	97%	79.9%	99.7%
ECO204942	KPN300869	97%	99.7%	99.7%
ECO204942	LMO102516	74%	99.5%	99.5%
ECO204942	MCA100162	81%	99.5%	99.5%
ECO204942	MAV102941	74%	99.7%	99.7%
ECO204942	MBV103318	73%	99.7%	99.7%
ECO204942	MLP101139	74%	99.7%	99.7%
ECO204942	MTU200682	73%	99.7%	99.7%
ECO204942	MGE100460	69%	99.7%	99.7%
ECO204942	MPN100177	69%	99.7%	99.7%
ECO204942	NGO101673	82%	100%	100%
ECO204942	NGO101620	82%	100%	100%
ECO204942	NME200128	83%	100%	100%
ECO204942	NME200143	83%	100%	100%
ECO204942	PMU101746	91%	99.7%	99.7%
ECO204942	PMU101357	92%	99.7%	99.7%
ECO204942	PRT100737	95%	24.6%	100%
ECO204942	PRT100321	94%	99.7%	99.7%
ECO204942	PAB204275	83%	99.7%	99.7%
ECO204942	PAB204263	83%	99.7%	99.7%
ECO204942	PPU104463	77%	76.6%	99.7%
ECO204942	PPU104501	76%	99.7%	99.7%
ECO204942	PSY107231	76%	100%	100%
ECO204942	SPA104331	98%	39.3%	99.4%
ECO204942	SPA102798	98%	99.7%	99.7%
ECO204942	STY102689	98%	99.7%	99.7%
ECO204942	STY101782	98%	99.7%	99.7%
ECO204942	STM102043	98%	99.7%	99.7%
ECO204942	SAU800548	74%	99.7%	99.7%
ECO204942	SEP200072	74%	99.5%	99.5%
ECO204942	SHA101389	74%	99.7%	99.7%
ECO204942	SMU101538	72%	99.5%	99.5%
ECO204942	SPN401342	72%	99.5%	99.5%
ECO204942	SPY200441	72%	99.5%	99.5%
ECO204942	TPA100185	68%	99.7%	79.6%
ECO204942	UUR100528	71%	99.2%	99.2%
ECO204942	VCH100316	86%	100%	100%
ECO204942	VCH100357	86%	100%	100%
ECO204942	YPS000510	92%	99.7%	99.7%
ECO204942	YPS001855	94%	100%	100%
ECO205169	BAN110650	28%	67.7%	98.2%
ECO205169	BAN102654	29%	94.0%	98.9%
ECO205169	CDF104202	39%	19.9%	84.5%
ECO205169	CDF102535	35%	26.1%	85.8%
ECO205169	CDF103887	34%	52.5%	97.1%
ECO205169	CDF100871	33%	76.6%	95.2%
ECO205169	CDF103297	32%	92.0%	96.2%
ECO205169	CDF101218	32%	92.0%	96.2%
ECO205169	CDF103939	32%	92.0%	96.2%
ECO205169	CDF100573	32%	92.0%	96.2%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
ECO205169	CDF101412	33%	92.0%	96.2%
ECO205169	CDF100312	33%	92.0%	96.2%
ECO205169	CDF103189	33%	92.0%	96.2%
ECO205169	EFA200364	25%	80.8%	89.6%
ECO205169	EFM201897	23%	80.1%	91.4%
ECO205169	EFM201232	31%	93.0%	96.9%
ECO205169	ECO101403	96%	100%	100%
ECO205169	HPY100981	30%	91.3%	83.4%
ECO205169	HPY100434	30%	91.3%	83.4%
ECO205169	HPY100973	30%	91.3%	83.4%
ECO205169	HPY101512	30%	91.3%	83.4%
ECO205169	HPY101078	30%	91.3%	83.4%
ECO205169	KPN204073	83%	99.5%	100%
ECO205169	MCA103372	29%	54.7%	96.1%
ECO205169	MBV101240	25%	97.3%	91.7%
ECO205169	MTU203772	25%	79.6%	85.3%
ECO205169	MTU202753	25%	97.3%	91.7%
ECO205169	NME102130	55%	56.0%	100%
ECO205169	PRT106097	80%	11.4%	100%
ECO205169	PRT104808	90%	31.6%	96.9%
ECO205169	PRT103046	80%	53.7%	99.5%
ECO205169	PRT105185	83%	90.8%	100%
ECO205169	PRT102105	81%	94.8%	99.7%
ECO205169	PRT102853	82%	99.8%	97.8%
ECO205169	PRT105904	82%	99.3%	99.3%
ECO205169	PRT105312	82%	99.8%	97.8%
ECO205169	PRT101071	83%	99.8%	99.8%
ECO205169	SPA101059	64%	97.0%	100%
ECO205169	STY101241	64%	96.0%	97.3%
ECO205169	STM101920	35%	95.5%	88.5%
ECO205205	ECO205205	100%	100%	100%
ECO205289	BAN102833	31%	28.5%	66.7%
ECO205289	BMA106255	28%	44.6%	71.2%
ECO205289	CDF103560	27%	39.2%	65.2%
ECO205289	ECO205289	100%	100%	100%
ECO301060	ECO302213	90%	39.6%	46.5%
ECO301060	ECO301060	100%	100%	100%
ECO302213	ECO301060	90%	46.5%	39.6%
ECO302213	ECO302213	100%	100%	100%
ECO302775	BPT101815	28%	18.0%	18.6%
ECO302775	CAC103385	20%	13.3%	41.9%
ECO302775	CAC102155	28%	14.8%	18.3%
ECO302775	EFM200948	23%	33.8%	46.9%
ECO302775	ECO100289	53%	18.4%	82.0%
ECO302775	ECO101940	85%	99.2%	94.0%
ECO302775	PRT101411	28%	86.0%	82.5%
ECO302775	SPA102738	40%	24.8%	93.9%
ECO302775	SPN103543	23%	33.2%	93.8%
ECO302775	SPY100972	22%	15.1%	98.6%
ECO302775	YPS002407	32%	96.9%	91.6%
ECO304472	ECO304472	100%	100%	100%
ECO305338	ECO305338	100%	100%	100%
EFA104836	BAN108189	52%	95.5%	36.8%
EFA104836	BAN100435	52%	95.5%	36.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA104836	CBO101665	34%	97.7%	38.9%
EFA104836	CDF103326	41%	88.6%	37.1%
EFA104836	EFA202216	97%	90.9%	35.1%
EFA104836	EFM200511	75%	90.9%	35.1%
EFA104836	LMO102819	43%	68.2%	28.6%
EFA104836	SAU801646	41%	70.5%	27.7%
EFA104836	SEP201611	41%	70.5%	29.2%
EFA104836	SHA100023	43%	72.7%	30.2%
EFA104836	SMU100756	55%	90.9%	35.1%
EFA104836	SPN401013	55%	90.9%	35.1%
EFA104836	SPY200611	50%	90.9%	37.0%
EFA104836	TPA100736	51%	65.9%	26.9%
EFA200179	ABA101795	41%	99.5%	99.3%
EFA200179	BAN107436	55%	99.3%	99.3%
EFA200179	BAN109623	72%	99.3%	99.3%
EFA200179	BFR103128	43%	99.3%	99.8%
EFA200179	BPT100020	40%	99.7%	98.9%
EFA200179	BBU100737	44%	99.0%	99.2%
EFA200179	BCE114033	41%	99.0%	99.6%
EFA200179	BFU109684	42%	99.0%	98.6%
EFA200179	BMA104351	41%	99.3%	99.6%
EFA200179	CJU100714	40%	99.1%	98.9%
EFA200179	CPN200668	35%	99.5%	98.8%
EFA200179	CTR200568	37%	99.3%	99.8%
EFA200179	CAC100067	51%	99.8%	100%
EFA200179	CBO100672	51%	99.8%	100%
EFA200179	CDF100033	38%	25.9%	98.7%
EFA200179	CDF102611	52%	99.7%	99.5%
EFA200179	CDP101232	44%	99.1%	99.2%
EFA200179	EBC104048	42%	97.7%	99.2%
EFA200179	EFA200179	100%	100%	100%
EFA200179	EFM201966	89%	100%	99.9%
EFA200179	ECO104148	43%	98.9%	99.6%
EFA200179	HIN101359	43%	100%	100%
EFA200179	HPY101136	41%	98.9%	99.0%
EFA200179	KPN303513	43%	96.1%	99.1%
EFA200179	LPN102949	45%	93.3%	99.1%
EFA200179	LMO102840	69%	99.7%	99.3%
EFA200179	MCA101259	40%	99.4%	99.6%
EFA200179	MAV104126	44%	93.5%	100%
EFA200179	MBV101058	44%	99.1%	99.9%
EFA200179	MLP100909	43%	99.1%	98.8%
EFA200179	MTU202412	44%	99.1%	99.9%
EFA200179	MGE100341	35%	99.7%	99.5%
EFA200179	MPN100361	35%	99.7%	99.5%
EFA200179	NGO100851	41%	98.6%	99.8%
EFA200179	NME200089	41%	98.8%	99.6%
EFA200179	PMU100818	44%	100%	100%
EFA200179	PRT105161	43%	99.8%	99.0%
EFA200179	PAE203831	44%	98.5%	99.6%
EFA200179	PPU109466	44%	96.5%	97.9%
EFA200179	PSY104286	43%	98.9%	99.6%
EFA200179	SPA100729	39%	66.9%	98.4%
EFA200179	STY104006	43%	98.9%	99.6%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200179	SAU801663	65%	98.9%	99.4%
EFA200179	SEP201629	65%	98.9%	99.4%
EFA200179	SHA100785	64%	99.3%	99.9%
EFA200179	SMU100583	71%	99.3%	99.3%
EFA200179	SPN400492	71%	99.5%	99.5%
EFA200179	SPY201210	72%	99.3%	99.4%
EFA200179	TPA101025	42%	96.9%	96.0%
EFA200179	UUR100269	41%	97.3%	97.3%
EFA200179	VCH102467	42%	98.5%	99.6%
EFA200179	YPS000947	41%	99.7%	98.9%
EFA200192	ABA100922	34%	98.4%	96.7%
EFA200192	BAN110804	52%	98.4%	98.6%
EFA200192	BAN108869	65%	98.4%	99.2%
EFA200192	BFR102616	34%	94.5%	99.0%
EFA200192	BPT102905	40%	97.4%	92.7%
EFA200192	BBU100371	36%	97.1%	97.1%
EFA200192	BCE100150	43%	58.0%	97.8%
EFA200192	BFU100071	38%	96.5%	99.1%
EFA200192	BMA103736	38%	98.2%	98.9%
EFA200192	CJU101212	38%	98.2%	98.7%
EFA200192	CPN200187	39%	97.6%	92.5%
EFA200192	CTR200720	38%	99.2%	94.5%
EFA200192	CAC101596	38%	97.8%	97.5%
EFA200192	CBO103047	37%	97.6%	96.1%
EFA200192	CDF100252	44%	97.4%	98.0%
EFA200192	CDP100231	37%	98.0%	96.6%
EFA200192	EBC100212	39%	98.4%	99.1%
EFA200192	EFA200192	100%	100%	100%
EFA200192	EFM202131	85%	98.8%	99.8%
EFA200192	ECO102355	38%	98.4%	97.7%
EFA200192	HIN100261	36%	98.4%	95.6%
EFA200192	HPY100472	37%	98.8%	99.6%
EFA200192	KPN305021	44%	42.2%	99.5%
EFA200192	LPN103492	38%	98.2%	97.4%
EFA200192	LMO101411	65%	97.8%	97.8%
EFA200192	MCA102322	35%	97.4%	94.7%
EFA200192	MAV101415	34%	93.7%	97.0%
EFA200192	MBV101327	36%	97.4%	99.4%
EFA200192	MLP101032	35%	97.8%	95.6%
EFA200192	MTU202954	36%	97.4%	96.7%
EFA200192	MGE100471	41%	98.8%	98.8%
EFA200192	MPN100164	40%	98.8%	98.8%
EFA200192	NGO100018	36%	97.4%	99.1%
EFA200192	NME200234	36%	97.4%	99.1%
EFA200192	PMU101115	36%	98.4%	95.6%
EFA200192	PRT100735	36%	98.8%	97.9%
EFA200192	PAE203132	35%	98.8%	95.3%
EFA200192	PPU101878	34%	98.8%	95.5%
EFA200192	PSY105734	35%	98.8%	95.5%
EFA200192	SPA103535	34%	98.4%	97.7%
EFA200192	STY101161	38%	92.9%	91.4%
EFA200192	STM101572	29%	25.5%	21.1%
EFA200192	SAU800528	64%	98.0%	99.0%
EFA200192	SEP201872	64%	98.4%	99.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200192	SHA101478	62%	94.7%	99.6%
EFA200192	SMU100660	63%	98.4%	98.6%
EFA200192	SPN401878	62%	98.2%	98.1%
EFA200192	SPY200174	61%	98.2%	99.2%
EFA200192	TPA100665	33%	98.4%	97.2%
EFA200192	UUR100606	41%	98.4%	99.0%
EFA200192	VCH102180	38%	99.0%	92.5%
EFA200192	YPS000590	38%	98.4%	97.7%
EFA200195	BAN110506	69%	98.0%	100%
EFA200195	BAN101466	70%	98.0%	99.1%
EFA200195	CJU101614	39%	98.0%	83.1%
EFA200195	CAC102576	46%	96.8%	98.0%
EFA200195	CBO101502	45%	96.8%	98.2%
EFA200195	CBO103283	47%	96.8%	95.6%
EFA200195	CDF101226	47%	93.9%	99.1%
EFA200195	CDP100435	38%	98.0%	80.1%
EFA200195	EFA200195	100%	100%	100%
EFA200195	EFM202397	92%	70.8%	100%
EFA200195	ECO103977	24%	30.7%	28.4%
EFA200195	HPY101409	38%	97.9%	80.1%
EFA200195	LPN100348	25%	19.8%	23.7%
EFA200195	LPN101706	28%	19.3%	30.7%
EFA200195	LMO101604	72%	98.0%	99.1%
EFA200195	MAV101957	36%	96.8%	94.2%
EFA200195	MBV104272	37%	96.8%	96.6%
EFA200195	MLP100931	36%	96.8%	96.6%
EFA200195	MTU202715	37%	96.8%	96.6%
EFA200195	MGE100141	37%	97.1%	97.0%
EFA200195	MPN100555	39%	96.3%	96.1%
EFA200195	STY103504	58%	4.3%	9.1%
EFA200195	SAU801089	63%	97.5%	97.0%
EFA200195	SEP200794	62%	98.0%	98.4%
EFA200195	SHA100488	63%	97.5%	98.6%
EFA200195	SMU100700	73%	98.6%	98.8%
EFA200195	SPN400125	74%	98.9%	91.0%
EFA200195	SPY201445	74%	98.6%	98.8%
EFA200195	UUR100577	36%	99.5%	94.1%
EFA200198	ABA101300	46%	98.1%	96.2%
EFA200198	BAN108420	56%	100%	99.4%
EFA200198	BAN110909	56%	100%	100%
EFA200198	BFR11201	51%	99.4%	98.1%
EFA200198	BPT100080	55%	98.7%	40.4%
EFA200198	BCE101526	58%	98.7%	38.3%
EFA200198	BFU110885	55%	97.5%	91.1%
EFA200198	BMA106181	58%	97.5%	35.2%
EFA200198	CJU101513	48%	93.6%	39.6%
EFA200198	CPN200202	26%	95.5%	86.4%
EFA200198	CTR200708	26%	95.5%	85.4%
EFA200198	CAC103092	55%	98.1%	99.4%
EFA200198	CBO102643	58%	98.7%	100%
EFA200198	CDF102172	54%	94.3%	38.6%
EFA200198	CDP100612	33%	98.7%	95%
EFA200198	EBC104342	52%	99.4%	98.7%
EFA200198	EFA200198	100%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200198	ECO102686	53%	99.4%	98.1%
EFA200198	HIN100652	55%	98.7%	98.1%
EFA200198	HPY101003	48%	91.7%	35.5%
EFA200198	KPN306639	63%	19.1%	83.3%
EFA200198	KPN306058	53%	99.4%	98.1%
EFA200198	LMO100427	61%	100%	100%
EFA200198	MCA101636	47%	100%	97.5%
EFA200198	MAV100054	39%	97.5%	94.3%
EFA200198	MBV100383	47%	45.2%	93.4%
EFA200198	MLP100221	40%	97.5%	94.9%
EFA200198	MTU203529	37%	97.5%	94.3%
EFA200198	MGE100468	26%	70.7%	71.0%
EFA200198	MPN100169	25%	98.7%	95.9%
EFA200198	NGO100248	52%	98.1%	96.2%
EFA200198	NME201571	51%	98.1%	96.2%
EFA200198	PMU101609	53%	100%	99.4%
EFA200198	PRT101944	53%	99.4%	97.5%
EFA200198	PAE203625	51%	98.1%	98.1%
EFA200198	PPU101189	50%	98.1%	98.1%
EFA200198	PSY104319	50%	98.1%	98.1%
EFA200198	SPA100750	52%	97.5%	98.1%
EFA200198	STY103432	53%	99.4%	98.1%
EFA200198	TPA100508	44%	99.4%	39.1%
EFA200198	VCH100519	51%	100%	99.4%
EFA200198	YPS000097	53%	98.1%	96.3%
EFA200239	ABA105771	24%	96.0%	90.2%
EFA200239	BAN101572	39%	96.0%	98.3%
EFA200239	BAN113353	43%	96.0%	95.8%
EFA200239	BFR11486	35%	94.7%	95.7%
EFA200239	BFR10152	35%	90.7%	96.4%
EFA200239	BPT102621	41%	98.1%	97.3%
EFA200239	BCE112181	40%	97.5%	96.7%
EFA200239	BFU100682	39%	98.4%	97.6%
EFA200239	BMA103928	41%	97.5%	96.7%
EFA200239	CJU100297	40%	98.1%	96.9%
EFA200239	CPN200454	37%	98.1%	96.1%
EFA200239	CTR200503	37%	98.1%	98.5%
EFA200239	CAC101231	45%	98.8%	98.5%
EFA200239	CBO102871	43%	96.6%	96.0%
EFA200239	CDF101767	42%	98.4%	97.9%
EFA200239	EBC100408	40%	96.9%	99.7%
EFA200239	EFA200239	100%	100%	100%
EFA200239	EFM200290	62%	100%	100%
EFA200239	ECO101064	39%	98.4%	99.1%
EFA200239	HIN100150	39%	98.1%	98.7%
EFA200239	HPY100199	39%	99.4%	98.5%
EFA200239	KPN300926	39%	98.4%	99.1%
EFA200239	LPN101178	41%	99.4%	99.4%
EFA200239	LMO102110	38%	98.1%	98.1%
EFA200239	MCA101964	28%	80.7%	71.9%
EFA200239	MAV100667	34%	96.3%	93.1%
EFA200239	MBV104576	32%	74.8%	90.7%
EFA200239	MTU200530	30%	96.3%	93.1%
EFA200239	NGO101399	41%	98.4%	98.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200239	NME200499	42%	98.4%	98.8%
EFA200239	PMU101914	40%	98.4%	99.1%
EFA200239	PRT100179	39%	98.4%	99.1%
EFA200239	PAE203331	37%	95.6%	93.3%
EFA200239	PPU100970	28%	95.3%	99.0%
EFA200239	PSY100579	34%	99.4%	98.8%
EFA200239	SPA100961	38%	98.4%	99.1%
EFA200239	STY102530	38%	98.4%	99.1%
EFA200239	STM102718	38%	98.4%	99.1%
EFA200239	SAU800983	39%	95.6%	95.5%
EFA200239	SEP200204	38%	95.6%	95.5%
EFA200239	SHA101381	38%	95.6%	95.5%
EFA200239	SMU100549	60%	99.1%	99.4%
EFA200239	SPN400377	57%	99.1%	99.4%
EFA200239	SPY201352	59%	99.1%	99.4%
EFA200239	VCH101993	41%	98.4%	99.1%
EFA200239	YPS003123	40%	98.4%	99.1%
EFA200240	CJU100409	35%	90.7%	90.9%
EFA200240	CPN200457	43%	94.7%	92.4%
EFA200240	CTR200500	36%	93.3%	93.5%
EFA200240	CAC102446	41%	96%	94.7%
EFA200240	CBO100718	55%	96%	95.9%
EFA200240	EFA200240	100%	100%	100%
EFA200240	EFM201544	85%	98.7%	100%
EFA200240	MPN100432	48%	41.3%	36.9%
EFA200240	SMU100547	67%	94.7%	94.6%
EFA200240	SPN400378	66%	94.7%	94.6%
EFA200240	SPY201351	66%	94.7%	94.6%
EFA200245	ABA100122	52%	99.3%	98.7%
EFA200245	BAN102154	53%	96.7%	99.8%
EFA200245	BAN113444	58%	97.4%	98.7%
EFA200245	BFR11898	50%	97.8%	88.3%
EFA200245	BFR11613	52%	96.9%	87.5%
EFA200245	BPT100134	52%	96.7%	96.5%
EFA200245	BCE104481	52%	97.1%	96.9%
EFA200245	BFU115826	52%	97.1%	96.9%
EFA200245	BMA101045	51%	97.1%	96.9%
EFA200245	CJU101214	51%	96.1%	98.2%
EFA200245	CPN200575	54%	96.3%	96.5%
EFA200245	CTR200394	54%	96.3%	95.8%
EFA200245	CAC103617	62%	97.4%	99.1%
EFA200245	CBO103874	62%	98.5%	100%
EFA200245	CDF101399	54%	98.0%	98.5%
EFA200245	CDP100825	44%	93.2%	71.2%
EFA200245	EBC102634	50%	64.9%	93.0%
EFA200245	EFA200245	100%	100%	100%
EFA200245	EFM201807	84%	99.6%	98.9%
EFA200245	ECO103186	52%	97.4%	98.4%
EFA200245	HIN100951	52%	97.4%	98.7%
EFA200245	HPY100366	49%	97.4%	96.5%
EFA200245	KPN308876	52%	97.4%	98.4%
EFA200245	LPN102993	52%	97.4%	98.9%
EFA200245	LMO101165	59%	99.3%	99.8%
EFA200245	MCA102208	53%	94.3%	95.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200245	MAV103606	49%	96.9%	62.3%
EFA200245	MBV101167	47%	97.4%	68.0%
EFA200245	MLP100439	44%	95.2%	72.1%
EFA200245	MTU202464	47%	97.4%	68.0%
EFA200245	NGO101616	52%	97.1%	97.4%
EFA200245	NME200552	52%	97.1%	97.4%
EFA200245	PMU101091	53%	97.4%	98.7%
EFA200245	PRT100504	51%	97.4%	98.7%
EFA200245	PAE204843	54%	97.4%	98.4%
EFA200245	PPU108141	54%	96.5%	97.1%
EFA200245	PSY108097	53%	97.1%	98.7%
EFA200245	SPA101601	52%	97.4%	99.5%
EFA200245	STY101665	52%	97.4%	98.4%
EFA200245	STM102307	52%	97.4%	98.4%
EFA200245	SAU801526	58%	98.2%	99.3%
EFA200245	SEP200908	58%	96.7%	97.6%
EFA200245	SHA100988	59%	96.7%	97.8%
EFA200245	SMU100533	75%	97.1%	98.4%
EFA200245	SPN400385	73%	98.9%	99.3%
EFA200245	SPY201344	73%	99.3%	100%
EFA200245	VCH100291	54%	97.4%	98.9%
EFA200245	YPS003128	52%	97.4%	98.4%
EFA200246	ABA101266	44%	85.1%	83.2%
EFA200246	BAN103283	54%	96.5%	94.1%
EFA200246	BFR11611	26%	77.1%	90.2%
EFA200246	BFR11899	24%	64.2%	34.0%
EFA200246	BFR11219	28%	69.8%	36.9%
EFA200246	BPT100791	42%	94.1%	94.2%
EFA200246	BCE105100	57%	43.8%	92.6%
EFA200246	BFU114977	42%	94.8%	95.5%
EFA200246	BMA103750	41%	94.1%	94.8%
EFA200246	CJU100116	48%	90.3%	95%
EFA200246	CPN200705	50%	85.8%	81.5%
EFA200246	CTR200558	49%	89.2%	92.2%
EFA200246	CAC103552	58%	98.3%	100%
EFA200246	CBO102220	60%	89.2%	46.7%
EFA200246	CDF101011	48%	96.5%	96.5%
EFA200246	CDP100046	39%	76.4%	43.5%
EFA200246	EBC101249	45%	81.6%	94.8%
EFA200246	EFA200246	100%	100%	100%
EFA200246	EFM200144	77%	99.7%	98.6%
EFA200246	ECO102274	45%	89.2%	85.9%
EFA200246	HIN101232	45%	90.3%	89.2%
EFA200246	HPY100934	47%	90.3%	91.0%
EFA200246	KPN302817	45%	89.2%	85.3%
EFA200246	LPN101645	54%	63.9%	84.0%
EFA200246	LMO101514	54%	89.6%	88.1%
EFA200246	MCA101005	48%	59.7%	91.5%
EFA200246	MAV105603	43%	74.3%	43.3%
EFA200246	MBV105423	42%	71.9%	41.4%
EFA200246	MLP100443	27%	75.3%	86.2%
EFA200246	MTU200895	42%	71.9%	41.4%
EFA200246	NGO100954	45%	88.5%	89.3%
EFA200246	NME200815	43%	94.1%	94.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200246	PMU100636	45%	92.0%	88.5%
EFA200246	PRT100424	45%	89.6%	81.9%
EFA200246	PAE203110	47%	89.2%	90%
EFA200246	PPU105860	46%	88.9%	87.5%
EFA200246	PSY101722	47%	88.9%	85.0%
EFA200246	SPA100127	40%	47.2%	61.8%
EFA200246	STY101011	46%	89.2%	85.9%
EFA200246	SAU801701	53%	96.5%	95.1%
EFA200246	SEP201705	51%	96.5%	95.1%
EFA200246	SHA100922	52%	96.5%	94.1%
EFA200246	SMU100531	67%	97.9%	98.6%
EFA200246	SPN400386	68%	97.9%	98.3%
EFA200246	SPY201343	66%	97.9%	98.6%
EFA200246	VCH100983	45%	89.6%	85.1%
EFA200246	YPS002401	45%	89.2%	85.9%
EFA200247	ABA100308	49%	96.6%	92.3%
EFA200247	BAN105768	56%	96.9%	78.4%
EFA200247	BPT101398	51%	99.2%	81.0%
EFA200247	BCE106451	51%	96.9%	78.6%
EFA200247	BFU100947	49%	96.9%	78.6%
EFA200247	BMA107589	50%	96.9%	78.6%
EFA200247	CJU100411	48%	95.4%	80.1%
EFA200247	CPN200335	49%	95.8%	77.5%
EFA200247	CTR200529	49%	95.8%	77.5%
EFA200247	CAC100492	62%	96.2%	92.0%
EFA200247	CDF101403	55%	97.7%	81.5%
EFA200247	EBC102554	53%	96.9%	79.6%
EFA200247	EFA200247	100%	100%	100%
EFA200247	EFM200190	76%	98.9%	99.2%
EFA200247	ECO100185	52%	96.9%	79.6%
EFA200247	HIN100386	54%	96.9%	80.6%
EFA200247	HPY100550	48%	94.3%	78.5%
EFA200247	KPN301921	53%	96.9%	79.6%
EFA200247	LPN101352	51%	95.8%	93.0%
EFA200247	LMO100159	56%	98.1%	80.8%
EFA200247	MCA100190	49%	96.6%	98.8%
EFA200247	NGO100369	51%	99.2%	81.5%
EFA200247	NME201237	51%	99.2%	81.5%
EFA200247	PMU100292	55%	96.9%	80.1%
EFA200247	PRT101241	54%	96.9%	79.6%
EFA200247	PRT100667	54%	97.3%	79.7%
EFA200247	PAE203637	54%	96.9%	80.4%
EFA200247	PPU101171	53%	98.5%	81.9%
EFA200247	PSY108491	51%	98.5%	81.4%
EFA200247	SPA100816	47%	96.9%	90.0%
EFA200247	STY103916	53%	96.9%	79.6%
EFA200247	STM103628	53%	96.9%	79.6%
EFA200247	SAU801700	53%	96.6%	80.6%
EFA200247	SEP201704	53%	96.9%	80.9%
EFA200247	SHA100923	54%	96.6%	80.3%
EFA200247	SMU100529	71%	95.4%	96.1%
EFA200247	SPN400387	66%	96.9%	98.0%
EFA200247	SPY201342	69%	95.4%	96.1%
EFA200247	VCH102210	52%	100%	83.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200247	YPS001157	55%	96.9%	79.6%
EFA200266	ABA102500	41%	99.4%	98.9%
EFA200266	BAN108871	62%	94.9%	96.9%
EFA200266	BAN105353	66%	98.8%	98.9%
EFA200266	BFR103141	48%	80.2%	99.4%
EFA200266	BPT101956	43%	98.9%	97.8%
EFA200266	BBU100719	41%	85.9%	94.3%
EFA200266	BCE105528	43%	99.4%	99.7%
EFA200266	BFU105096	43%	99.5%	97.8%
EFA200266	BMA106934	44%	99.4%	99.7%
EFA200266	CJU100194	40%	94.6%	99.8%
EFA200266	CPN201046	38%	97.2%	96.9%
EFA200266	CTR200859	39%	99.5%	99.1%
EFA200266	CAC102528	47%	98.9%	98.7%
EFA200266	CBO100249	47%	99.2%	95.0%
EFA200266	CDF102396	46%	99.2%	93.3%
EFA200266	CDP100262	40%	89.1%	87.3%
EFA200266	EBC102990	41%	99.2%	98.6%
EFA200266	EFA200266	100%	100%	100%
EFA200266	EFM200127	89%	99.7%	99.5%
EFA200266	ECO101687	41%	99.2%	98.6%
EFA200266	HIN101333	42%	95.0%	94.2%
EFA200266	HPY100121	40%	91.5%	94.6%
EFA200266	KPN300773	40%	96.4%	98.9%
EFA200266	LPN100924	46%	95.2%	99.7%
EFA200266	LMO102823	75%	99.1%	99.7%
EFA200266	MCA103158	40%	97.8%	97.5%
EFA200266	MAV102514	41%	89.3%	87.3%
EFA200266	MBV100785	42%	89.3%	85.7%
EFA200266	MLP100282	41%	89.3%	85.0%
EFA200266	MTU202577	42%	89.3%	86.3%
EFA200266	MGE100386	39%	81.9%	92.7%
EFA200266	MPN100289	38%	82.9%	94.0%
EFA200266	NGO101849	43%	99.2%	97.4%
EFA200266	NME200854	43%	98.9%	98.7%
EFA200266	PMU100593	42%	98.9%	98.1%
EFA200266	PRT105628	39%	99.2%	98.6%
EFA200266	PAE202742	41%	99.4%	98.9%
EFA200266	PPU103710	40%	99.4%	98.9%
EFA200266	PSY102599	41%	99.4%	98.9%
EFA200266	SPA100654	41%	75.2%	96.1%
EFA200266	STY101132	41%	99.2%	98.6%
EFA200266	STM103445	41%	99.2%	98.6%
EFA200266	SAU801683	67%	98.9%	98.6%
EFA200266	SEP201666	68%	96.9%	96.7%
EFA200266	SHA100279	69%	75.0%	98.8%
EFA200266	SMU101079	73%	99.7%	99.1%
EFA200266	SPN401471	72%	99.7%	97.4%
EFA200266	SPY200371	74%	99.7%	99.1%
EFA200266	TPA100828	43%	85.4%	92.4%
EFA200266	UUR100540	44%	88.2%	98.1%
EFA200266	VCH103018	42%	98.6%	98.1%
EFA200266	YPS003070	39%	99.2%	98.6%
EFA200290	ABA102360	24%	95.2%	94.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200290	BAN100998	46%	16.0%	98.9%
EFA200290	BAN106237	58%	68.9%	86.2%
EFA200290	BAN106908	59%	99.3%	100%
EFA200290	BFR10875	29%	98.9%	98.0%
EFA200290	BPT101508	23%	96.1%	95.7%
EFA200290	BBU100593	26%	96.4%	94.4%
EFA200290	BCE100461	26%	95.2%	93.8%
EFA200290	BFU103077	26%	95.2%	93.6%
EFA200290	BMA100457	26%	95.2%	93.6%
EFA200290	CJU101100	22%	97.7%	98.9%
EFA200290	CPN200176	31%	92.5%	92.0%
EFA200290	CTR200729	32%	96.1%	94.8%
EFA200290	CAC101790	48%	100%	100%
EFA200290	CBO100741	51%	100%	100%
EFA200290	CDF104545	52%	97.2%	97.2%
EFA200290	CDP100057	24%	95.4%	94.2%
EFA200290	EBC100321	33%	51.0%	98.4%
EFA200290	EFA200290	100%	100%	100%
EFA200290	EFM201011	80%	100%	100%
EFA200290	ECO101844	31%	100%	100%
EFA200290	HIN101550	34%	90.6%	90.6%
EFA200290	HPY100315	22%	98.0%	97.6%
EFA200290	KPN301304	31%	100%	100%
EFA200290	LPN101161	27%	97.0%	96.6%
EFA200290	LMO101656	27%	95.7%	94.4%
EFA200290	MCA100331	31%	97.7%	99.1%
EFA200290	MAV106525	25%	95.4%	94.2%
EFA200290	MBV105559	25%	95.2%	94%
EFA200290	MLP100693	23%	95.2%	94%
EFA200290	MTU201275	25%	95.2%	94%
EFA200290	MGE100389	19%	80.3%	81.0%
EFA200290	MPN100286	21%	98.2%	98.7%
EFA200290	NGO100228	34%	95.4%	95.6%
EFA200290	NME201566	33%	95.4%	95.6%
EFA200290	PMU100551	31%	96.1%	98.6%
EFA200290	PRT100545	33%	95.7%	95.8%
EFA200290	PAE205046	33%	95.2%	94.7%
EFA200290	PPU109126	33%	99.5%	99.1%
EFA200290	PSY103569	32%	99.5%	99.1%
EFA200290	SPA103053	29%	95.7%	95.8%
EFA200290	STY102666	32%	95.7%	95.8%
EFA200290	STM102429	32%	95.7%	95.8%
EFA200290	SAU800607	24%	99.5%	98.7%
EFA200290	SEP200171	25%	96.8%	95.8%
EFA200290	SHA101545	26%	96.8%	95.8%
EFA200290	SMU101264	60%	100%	100%
EFA200290	SPN401887	62%	100%	100%
EFA200290	SPY201643	62%	100%	100%
EFA200290	TPA100822	30%	95.4%	94.6%
EFA200290	UUR100280	22%	99.6%	98%
EFA200290	VCH102042	31%	89.5%	87.0%
EFA200290	YPS003380	33%	92.2%	92.2%
EFA200307	BAN107067	51%	98.5%	99.1%
EFA200307	BAN107697	53%	98.0%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200307	BFR103658	37%	99.0%	83.1%
EFA200307	BFR100902	38%	98.3%	99.5%
EFA200307	BPT102537	37%	97.1%	91.4%
EFA200307	BCE105218	36%	98.8%	99.7%
EFA200307	BFU100843	37%	98.6%	99.5%
EFA200307	BMA100378	37%	98.8%	93.2%
EFA200307	CAC103600	49%	98.1%	81.4%
EFA200307	CBO103824	48%	99.2%	82.7%
EFA200307	CDF101265	45%	98.6%	83.3%
EFA200307	EBC103961	41%	99.3%	97.5%
EFA200307	EFA200307	100%	100%	100%
EFA200307	EFM200383	60%	98.3%	98.5%
EFA200307	ECO103734	41%	99.0%	96.9%
EFA200307	HIN100708	40%	98.3%	95.5%
EFA200307	KPN303551	42%	99.0%	97.4%
EFA200307	LPN102588	45%	66.0%	99.2%
EFA200307	LMO101490	59%	98.0%	98.1%
EFA200307	NGO101892	37%	97.8%	93.8%
EFA200307	NME202048	37%	98.8%	88.6%
EFA200307	PMU101427	40%	98.6%	93.7%
EFA200307	PRT106116	42%	99.5%	99.5%
EFA200307	PAE203342	39%	98.0%	83.3%
EFA200307	PPU100810	39%	98.0%	83.1%
EFA200307	PSY104559	38%	92.5%	83.1%
EFA200307	SPA101175	40%	99.0%	98.7%
EFA200307	STY102015	41%	99.0%	97.2%
EFA200307	STM101102	41%	99.0%	96.3%
EFA200307	SAU800721	45%	98.8%	99.3%
EFA200307	SEP200775	43%	98.8%	99.5%
EFA200307	SHA101682	42%	98.8%	99.5%
EFA200307	VCH100194	41%	98.5%	95.2%
EFA200307	YPS001354	43%	98.3%	96.7%
EFA200309	BAN104824	46%	74.3%	80.6%
EFA200309	BAN106622	48%	74.3%	78.9%
EFA200309	EFA200309	100%	100%	100%
EFA200309	EFM200093	69%	97.0%	98%
EFA200309	LMO100844	52%	74.3%	80.6%
EFA200309	SAU801112	37%	77.2%	85.7%
EFA200309	SEP200833	40%	74.3%	82.4%
EFA200309	SHA101109	35%	67.3%	74.7%
EFA200310	ABA103723	29%	97.5%	93.2%
EFA200310	BAN104393	37%	92.3%	97.5%
EFA200310	BAN108260	37%	92.3%	97.2%
EFA200310	BFR100762	26%	92.3%	86.3%
EFA200310	BPT103003	28%	95.3%	93.7%
EFA200310	BCE103498	31%	92.0%	95.5%
EFA200310	BFU100816	29%	93.3%	86.2%
EFA200310	BMA109411	31%	92.0%	83.7%
EFA200310	CJU100966	28%	92.3%	97.9%
EFA200310	CPN200946	28%	89.8%	89.4%
EFA200310	CTR200136	32%	90.5%	85.3%
EFA200310	CAC100555	30%	94.5%	97.8%
EFA200310	CBO101485	33%	93.3%	92.0%
EFA200310	CDF103581	31%	94.0%	95.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200310	CDP101270	28%	95.0%	74.7%
EFA200310	EBC102569	31%	95.0%	88.2%
EFA200310	EFA200310	100%	100%	100%
EFA200310	EFM200911	63%	97.0%	99.5%
EFA200310	ECO100089	30%	92.0%	85.3%
EFA200310	HIN101111	31%	92.5%	90.1%
EFA200310	HPY101537	27%	92.3%	97.9%
EFA200310	KPN301852	31%	92.0%	83.3%
EFA200310	LPN100221	35%	74.9%	95.7%
EFA200310	LMO101232	37%	92.3%	91.5%
EFA200310	MCA103455	28%	93.0%	93.4%
EFA200310	MAV103648	32%	92.3%	57.2%
EFA200310	MBV100525	31%	90.8%	71.0%
EFA200310	MLP100568	32%	92.3%	65.4%
EFA200310	MTU202120	31%	90.8%	66.2%
EFA200310	NGO100588	32%	92.3%	91.7%
EFA200310	NME201907	31%	91.8%	89.0%
EFA200310	PMU100141	30%	94.8%	92.4%
EFA200310	PRT102637	31%	92.0%	90.9%
EFA200310	PAE204411	32%	98.0%	95.2%
EFA200310	PPU112591	31%	95.3%	90.8%
EFA200310	PSY103847	31%	95.3%	90.8%
EFA200310	SPA102524	27%	92.3%	93.0%
EFA200310	STY103175	31%	92.0%	85.3%
EFA200310	STM102887	31%	92.0%	85.3%
EFA200310	SAU801113	34%	86.6%	91.7%
EFA200310	SEP200834	34%	95.3%	92.9%
EFA200310	SHA101706	35%	93.3%	99.5%
EFA200310	SMU101535	50%	97.0%	94.1%
EFA200310	SPN400973	48%	97.0%	97.1%
EFA200310	SPY200440	46%	99.0%	94.0%
EFA200310	TPA100383	26%	96.5%	96.9%
EFA200310	VCH102367	30%	89.6%	86.4%
EFA200310	YPS001012	31%	91.0%	87%
EFA200317	BAN108934	43%	96.2%	98.4%
EFA200317	BAN112613	64%	99.7%	99.3%
EFA200317	CAC103250	52%	99.6%	99.5%
EFA200317	CBO103581	51%	99.7%	99.7%
EFA200317	CDF100269	51%	99.6%	99.5%
EFA200317	CDP100823	45%	99.8%	98.7%
EFA200317	EFA200317	100%	100%	100%
EFA200317	EFM202099	82%	100%	100%
EFA200317	LPN100100	46%	39.8%	94.9%
EFA200317	LMO100679	67%	99.7%	99.5%
EFA200317	MAV103158	46%	99.7%	99.8%
EFA200317	MBV103377	47%	99.6%	99.6%
EFA200317	MTU202929	47%	99.6%	99.6%
EFA200317	SAU801114	58%	99.9%	99.5%
EFA200317	SEP200837	57%	53.4%	100%
EFA200317	SHA101707	57%	53.4%	100%
EFA200326	ABA103427	35%	64.2%	53.2%
EFA200326	BAN105404	37%	99.5%	99.6%
EFA200326	BAN112023	46%	99.5%	99.6%
EFA200326	BFR11479	43%	59.9%	57.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200326	BPT102081	32%	81.7%	67.2%
EFA200326	BBU100460	36%	60.2%	63.2%
EFA200326	BCE106024	40%	56.5%	68.8%
EFA200326	BFU105306	41%	56.5%	57.0%
EFA200326	BMA107161	40%	56.5%	40.4%
EFA200326	CJU101082	41%	49.1%	56.2%
EFA200326	CPN200723	39%	61.3%	78.3%
EFA200326	CTR200603	36%	60.9%	74.4%
EFA200326	CAC103441	45%	61.1%	66.4%
EFA200326	CBO102854	34%	100%	99.4%
EFA200326	CDF100130	47%	60.8%	64.9%
EFA200326	EBC103996	39%	60.6%	55.3%
EFA200326	EFA200326	100%	100%	100%
EFA200326	EFM202154	77%	49.1%	98.3%
EFA200326	ECO100461	39%	60.6%	55.2%
EFA200326	HIN101201	38%	60.6%	51.0%
EFA200326	HPY100707	36%	49.7%	50%
EFA200326	KPN303900	32%	89.6%	81.1%
EFA200326	LMO101248	48%	99.8%	100%
EFA200326	MCA102344	35%	60.4%	47.3%
EFA200326	MAV103129	33%	71.7%	67.2%
EFA200326	MBV105819	36%	60.1%	67.1%
EFA200326	MLP101393	36%	59.9%	58.6%
EFA200326	MTU203667	36%	60.1%	62.1%
EFA200326	MGE100430	43%	39.6%	89.6%
EFA200326	MPN100224	33%	73.0%	64.8%
EFA200326	NGO100173	43%	56.5%	46.7%
EFA200326	NME201516	43%	56.5%	46.5%
EFA200326	PMU100364	39%	60.6%	49.2%
EFA200326	PRT105815	46%	36.2%	100%
EFA200326	PAE201531	33%	83.4%	71.4%
EFA200326	PPU104995	43%	55.5%	46.9%
EFA200326	PSY101776	41%	55.5%	44.1%
EFA200326	SPA100619	33%	43.3%	48.9%
EFA200326	STY100818	37%	63.7%	58.1%
EFA200326	STM100530	37%	63.7%	58.1%
EFA200326	SAU800478	42%	100%	99.8%
EFA200326	SEP201796	43%	100%	99.8%
EFA200326	SHA102047	42%	100%	99.8%
EFA200326	SMU101072	44%	93.5%	95.9%
EFA200326	SPN400769	43%	93.3%	96.7%
EFA200326	SPY201046	43%	93.5%	96.4%
EFA200326	TPA100995	40%	60.9%	62.4%
EFA200326	UUR100085	37%	63.0%	63.7%
EFA200326	VCH101035	32%	76.3%	63.9%
EFA200326	YPS001746	38%	60.6%	54.0%
EFA200357	ABA105065	31%	84.2%	83.4%
EFA200357	BCE107325	31%	84.4%	86.6%
EFA200357	BFU104800	29%	93.5%	89.6%
EFA200357	BMA103965	31%	85.5%	85.8%
EFA200357	CAC102908	32%	83.7%	85.5%
EFA200357	CDF102112	32%	97.6%	99.3%
EFA200357	EBC101322	33%	82.9%	84.8%
EFA200357	EFA200357	100%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200357	ECO102819	30%	83.7%	83.4%
EFA200357	KPN301122	34%	82.9%	83.0%
EFA200357	LPN100461	27%	83.7%	86.7%
EFA200357	PAE201520	31%	88.3%	88.7%
EFA200357	PPU107264	31%	93.5%	93.1%
EFA200357	PSY103885	31%	84.4%	84.4%
EFA200358	ABA102501	58%	99.2%	99.2%
EFA200358	BAN104202	58%	99.2%	99.2%
EFA200358	BAN110178	77%	99.2%	100%
EFA200358	BFR104064	55%	97.5%	100%
EFA200358	BPT100292	55%	99.2%	99.2%
EFA200358	BBU100187	49%	89.1%	92.2%
EFA200358	BCE102715	51%	99.2%	99.2%
EFA200358	BFU102443	52%	99.2%	99.2%
EFA200358	BMA107401	51%	99.2%	99.2%
EFA200358	CJU100217	63%	98.3%	100%
EFA200358	CPN200847	43%	98.3%	96.7%
EFA200358	CTR200218	45%	98.3%	95.1%
EFA200358	CAC101951	60%	99.2%	99.2%
EFA200358	CDF102735	55%	99.2%	100%
EFA200358	CDP100976	58%	98.3%	92.1%
EFA200358	EBC102984	60%	99.2%	100%
EFA200358	EFA200358	100%	100%	100%
EFA200358	EFM201307	93%	100%	100%
EFA200358	ECO101684	60%	99.2%	100%
EFA200358	HIN101286	61%	98.3%	100%
EFA200358	HPY100124	58%	96.6%	99.1%
EFA200358	KPN301692	59%	99.2%	100%
EFA200358	LPN101410	57%	99.2%	99.2%
EFA200358	LMO100743	80%	100%	100%
EFA200358	MAV106548	52%	98.3%	89.3%
EFA200358	MBV101274	52%	98.3%	90.7%
EFA200358	MLP100866	54%	98.3%	90.7%
EFA200358	MTU201622	52%	98.3%	90.7%
EFA200358	MGE100200	47%	98.3%	94.4%
EFA200358	MPN100037	47%	98.3%	92.1%
EFA200358	NGO101855	59%	99.2%	99.2%
EFA200358	NME200857	59%	99.2%	99.2%
EFA200358	PMU100604	62%	98.3%	100%
EFA200358	PRT101306	59%	99.2%	100%
EFA200358	PAE202739	63%	99.2%	100%
EFA200358	PPU111376	64%	99.2%	100%
EFA200358	PSY109131	63%	99.2%	100%
EFA200358	SPA100657	57%	100%	99.2%
EFA200358	STY101118	60%	99.2%	100%
EFA200358	STM103448	60%	99.2%	100%
EFA200358	SAU801678	71%	98.3%	99.2%
EFA200358	SEP201662	71%	98.3%	99.2%
EFA200358	SHA100082	69%	98.3%	99.2%
EFA200358	SMU100912	83%	100%	100%
EFA200358	SPN400863	84%	100%	100%
EFA200358	SPY200598	84%	100%	100%
EFA200358	TPA100839	45%	89.1%	86.9%
EFA200358	UUR100231	49%	92.4%	96.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200358	VCH103020	60%	98.3%	100%
EFA200358	YPS003061	59%	99.2%	100%
EFA200359	CBO100286	45%	98.2%	96.2%
EFA200359	EFA200359	100%	100%	100%
EFA200360	BAN104855	78%	98.8%	98.8%
EFA200360	BAN100961	82%	99.4%	98.8%
EFA200360	CAC101058	80%	99.4%	98.8%
EFA200360	EFA200360	100%	100%	100%
EFA200360	EFM202638	91%	100%	100%
EFA200360	HPY100841	85%	100%	99.4%
EFA200360	SAU801337	77%	99.4%	99.4%
EFA200360	SEP201995	76%	99.4%	99.4%
EFA200360	SHA100019	76%	89.8%	99.0%
EFA200360	SPN401127	75%	98.8%	97.3%
EFA200360	SPY200862	78%	99.4%	98.2%
EFA200366	BAN104659	56%	86.6%	88.1%
EFA200366	BAN106664	68%	95.2%	96.8%
EFA200366	BBU100333	53%	78.7%	96.2%
EFA200366	BFU106797	48%	85.2%	88.6%
EFA200366	BMA102072	53%	77.6%	83.3%
EFA200366	CTR200062	39%	90.9%	99.4%
EFA200366	CAC101738	58%	93.2%	96.8%
EFA200366	CAC101883	58%	92.6%	96.2%
EFA200366	CBO100432	54%	92.6%	93.7%
EFA200366	EFA200366	100%	100%	100%
EFA200366	EFM201140	84%	98.9%	97.8%
EFA200366	ECO101217	49%	87.8%	91.1%
EFA200366	HIN101094	51%	83.5%	90.7%
EFA200366	HPY100297	57%	72.7%	89.9%
EFA200366	KPN301634	49%	87.2%	90.5%
EFA200366	LMO102091	72%	96.9%	95.5%
EFA200366	MCA100669	55%	94.6%	96.0%
EFA200366	MGE100081	44%	93.8%	91.3%
EFA200366	MPN100614	47%	95.2%	87.9%
EFA200366	PMU101907	52%	84.4%	89.7%
EFA200366	PRT104091	50%	86.4%	92.4%
EFA200366	PAE201806	53%	72.2%	97.4%
EFA200366	SPA100463	46%	87.2%	91.0%
EFA200366	STY103006	50%	87.2%	91.0%
EFA200366	SAU800988	65%	94.9%	93.3%
EFA200366	SEP200209	64%	98.0%	96.7%
EFA200366	SHA101386	66%	94.9%	93.6%
EFA200366	SMU101518	64%	96.0%	96.3%
EFA200366	SPN401702	54%	94.9%	94.9%
EFA200366	SPY200218	57%	94.9%	94.7%
EFA200366	UUR100566	44%	98.3%	69.6%
EFA200366	VCH101075	51%	82.4%	89.2%
EFA200366	YPS000805	53%	83.0%	87.4%
EFA200381	BAN101878	90%	75.9%	97.8%
EFA200381	BAN111500	92%	96.6%	98.2%
EFA200381	BFR101607	40%	81.0%	60.3%
EFA200381	BPT103142	56%	86.2%	71.4%
EFA200381	BBU100255	44%	96.6%	81.2%
EFA200381	BCE106500	56%	86.2%	71.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200381	BFU102600	52%	94.8%	78.6%
EFA200381	BMA102838	56%	86.2%	71.4%
EFA200381	CJU100338	42%	86.2%	71.4%
EFA200381	CPN200733	44%	93.1%	93.1%
EFA200381	CTR200610	46%	93.1%	93.1%
EFA200381	CAC101256	73%	96.6%	96.6%
EFA200381	CBO102486	69%	96.6%	96.6%
EFA200381	CDF100846	63%	94.8%	93.2%
EFA200381	EBC104303	60%	82.8%	73.8%
EFA200381	EFA200381	100%	100%	100%
EFA200381	EFM103017	96%	55.2%	100%
EFA200381	ECO102999	62%	86.2%	70.4%
EFA200381	HIN100510	62%	86.2%	70.4%
EFA200381	HPY100555	38%	86.2%	71.4%
EFA200381	KPN204459	62%	86.2%	70.4%
EFA200381	LPN101208	64%	53.4%	54.4%
EFA200381	LMO101512	94%	96.6%	98.2%
EFA200381	MCA101455	50%	98.3%	80.3%
EFA200381	NGO103576	60%	69.0%	72.7%
EFA200381	NME200467	56%	86.2%	71.4%
EFA200381	PMU101239	62%	86.2%	70.4%
EFA200381	PRT103336	58%	86.2%	70.4%
EFA200381	PAE200578	60%	94.8%	77.5%
EFA200381	PSY102551	60%	94.8%	77.5%
EFA200381	SPA100115	62%	86.2%	70.4%
EFA200381	STY100808	62%	86.2%	70.4%
EFA200381	STM101264	62%	86.2%	70.4%
EFA200381	SAU801575	92%	96.6%	96.6%
EFA200381	SEP203226	92%	96.6%	96.6%
EFA200381	SHA101643	92%	96.6%	96.6%
EFA200381	SMU102404	96%	100%	87.9%
EFA200381	SPN401270	91%	100%	87.9%
EFA200381	SPY200574	96%	100%	100%
EFA200381	TPA100750	43%	94.8%	79.7%
EFA200381	UUR100279	36%	81.0%	81.8%
EFA200381	VCH100511	62%	86.2%	70.4%
EFA200381	YPS001963	62%	86.2%	70.4%
EFA200382	ABA100747	40%	97.3%	98.0%
EFA200382	BAN101433	47%	32.2%	68.6%
EFA200382	BAN103496	59%	98.0%	99.3%
EFA200382	BFR105454	37%	98.0%	99.3%
EFA200382	BPT100546	34%	97.3%	96.1%
EFA200382	BCE109876	43%	98.0%	98.6%
EFA200382	BFU102599	45%	98.0%	98.6%
EFA200382	BMA100917	43%	99.3%	100%
EFA200382	CJU100534	35%	98.7%	100%
EFA200382	CAC102981	49%	98.0%	98.0%
EFA200382	CBO101104	43%	99.3%	100%
EFA200382	CDF100102	34%	75.2%	100%
EFA200382	CDF102772	42%	98.7%	98%
EFA200382	CDP101689	36%	96.6%	97.4%
EFA200382	EFA200382	100%	100%	100%
EFA200382	EFM101005	76%	98.7%	99.3%
EFA200382	HIN101254	29%	71.8%	22.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200382	LPN100867	41%	98.0%	99.3%
EFA200382	LMO101122	57%	98.0%	99.3%
EFA200382	MCA103674	34%	98.0%	98.6%
EFA200382	MAV103815	35%	71.8%	89.3%
EFA200382	MBV103944	36%	88.6%	100%
EFA200382	MTU203634	36%	96.6%	98.1%
EFA200382	NGO101314	38%	98.0%	81.1%
EFA200382	NME200466	39%	98.0%	98.6%
EFA200382	PAE200577	35%	94.0%	94.0%
EFA200382	VCH100510	36%	98.0%	99.3%
EFA200400	ABA103575	35%	69.4%	98.8%
EFA200400	BPT101206	39%	100%	100%
EFA200400	BCE104446	59%	28.9%	89.2%
EFA200400	BFU105313	59%	29.4%	88.9%
EFA200400	BMA109515	60%	28.9%	76.0%
EFA200400	CJU101159	35%	69.1%	98.6%
EFA200400	CPN200896	36%	98.5%	97.8%
EFA200400	CTR200173	35%	98.9%	98.4%
EFA200400	CDF104028	40%	69.1%	98.4%
EFA200400	EBC104560	61%	29.3%	97.7%
EFA200400	EFA200400	100%	100%	100%
EFA200400	EFM200195	76%	98.4%	99.9%
EFA200400	ECO103481	35%	69.7%	99.4%
EFA200400	HIN100903	34%	69.7%	99.4%
EFA200400	HPY100944	56%	27.9%	92.4%
EFA200400	KPN305504	61%	29.3%	97.7%
EFA200400	LPN102108	35%	54.8%	99.4%
EFA200400	LMO101909	49%	69.5%	99.0%
EFA200400	MCA101554	35%	69.4%	99.1%
EFA200400	NGO101359	35%	69.4%	98.8%
EFA200400	NME200487	35%	69.4%	98.8%
EFA200400	PMU101102	35%	69.7%	99.4%
EFA200400	PRT101495	61%	29.1%	97.7%
EFA200400	PAE200009	63%	28.8%	91.7%
EFA200400	PPU103628	62%	28.8%	91.7%
EFA200400	PSY103530	61%	29.2%	82.5%
EFA200400	SPA100735	61%	29.3%	97.7%
EFA200400	STY100713	35%	69.7%	99.4%
EFA200400	SMU101427	61%	98.8%	100%
EFA200400	SPN401327	54%	69.2%	98.5%
EFA200400	SPY201298	51%	69.7%	99.3%
EFA200400	VCH100020	34%	69.7%	99.4%
EFA200400	YPS003356	35%	69.5%	99.1%
EFA200412	ABA104190	29%	96.5%	95.3%
EFA200412	BAN105171	44%	98.8%	100%
EFA200412	BAN102576	45%	99.2%	98.0%
EFA200412	BFR11285	31%	95.0%	95.3%
EFA200412	BPT101144	28%	97.7%	97.3%
EFA200412	BCE101162	30%	97.7%	96.5%
EFA200412	BFU105740	31%	97.7%	96.2%
EFA200412	BMA107144	31%	97.7%	95.8%
EFA200412	CPN200219	25%	94.6%	94.0%
EFA200412	CTR200673	32%	54.3%	52.5%
EFA200412	CAC101882	34%	97.3%	96.6%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200412	CBO101930	37%	95.7%	96.1%
EFA200412	CDF103571	32%	96.5%	95.8%
EFA200412	CDP100979	28%	93.8%	90.8%
EFA200412	EFA200412	100%	100%	100%
EFA200412	EFM200394	59%	98.4%	100%
EFA200412	LMO100578	43%	97.7%	98.4%
EFA200412	MCA101753	29%	72.9%	82.4%
EFA200412	MAV106532	30%	91.5%	90.5%
EFA200412	MBV103890	32%	91.5%	91.5%
EFA200412	MLP100867	30%	91.5%	91.9%
EFA200412	MTU201623	31%	91.5%	91.5%
EFA200412	NGO100361	35%	97.7%	96.6%
EFA200412	NME201239	34%	97.7%	96.6%
EFA200412	SAU801137	43%	98.8%	99.6%
EFA200412	SEP200862	42%	97.7%	98.4%
EFA200412	SHA100177	39%	98.8%	99.6%
EFA200412	SMU100505	41%	86.0%	98.6%
EFA200412	SPN401786	43%	98.1%	96.8%
EFA200412	SPY200257	43%	96.5%	98.0%
EFA200412	UUR100329	31%	97.7%	98.1%
EFA200412	VCH100789	29%	97.3%	93.8%
EFA200418	ABA104000	49%	85.4%	89.2%
EFA200418	BAN100446	70%	71.3%	99.5%
EFA200418	BAN110084	74%	88.9%	99.6%
EFA200418	BFR104950	45%	93.1%	86.7%
EFA200418	BPT101108	47%	93.1%	97.6%
EFA200418	BBU100122	49%	95.0%	98.8%
EFA200418	BCE101166	44%	98.9%	98.0%
EFA200418	BFU101939	52%	84.7%	88.4%
EFA200418	BMA101604	45%	98.1%	98.8%
EFA200418	CJU101107	51%	99.2%	98.9%
EFA200418	CPN200048	48%	84.3%	79.1%
EFA200418	CTR200051	44%	98.1%	89.7%
EFA200418	CAC101756	67%	88.5%	99.6%
EFA200418	CBO103187	69%	88.5%	99.6%
EFA200418	CDF101764	69%	89.7%	98.7%
EFA200418	CDP101120	52%	99.6%	97.7%
EFA200418	EBC103098	50%	91.2%	99.2%
EFA200418	EFA200418	100%	100%	100%
EFA200418	ECO100169	51%	91.2%	99.2%
EFA200418	HIN100892	50%	90.0%	93.6%
EFA200418	HPY101531	48%	96.2%	92.0%
EFA200418	KPN301398	50%	86.6%	99.1%
EFA200418	LPN100646	46%	93.9%	97.6%
EFA200418	LMO100442	74%	93.1%	100%
EFA200418	MCA101251	51%	85.4%	82.3%
EFA200418	MAV106404	59%	86.6%	81.9%
EFA200418	MBV102282	54%	96.2%	86.4%
EFA200418	MLP100973	58%	86.6%	81.6%
EFA200418	MTU202852	54%	96.2%	86.4%
EFA200418	MGE100072	36%	93.9%	84.9%
EFA200418	MPN100623	36%	93.9%	82.0%
EFA200418	NGO100393	44%	89.7%	95.5%
EFA200418	NME200306	44%	89.7%	95.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200418	PMU101984	51%	91.6%	94.4%
EFA200418	PRT105507	51%	89.3%	96.3%
EFA200418	PAE203654	49%	92.3%	97.6%
EFA200418	PPU107884	47%	91.6%	97.1%
EFA200418	PSY108183	48%	94.6%	92.1%
EFA200418	SPA101195	50%	91.6%	100%
EFA200418	STY103848	51%	91.2%	99.2%
EFA200418	STM103561	51%	91.2%	99.2%
EFA200418	SAU801256	70%	95.0%	99.6%
EFA200418	SEP201549	69%	96.6%	98.9%
EFA200418	SHA100713	63%	74.3%	96.6%
EFA200418	SMU100628	75%	99.2%	100%
EFA200418	SPN402017	76%	98.9%	100%
EFA200418	SPY201599	75%	98.5%	99.6%
EFA200418	TPA100599	55%	98.9%	88.3%
EFA200418	UUR100024	40%	84.7%	63.6%
EFA200418	VCH102226	50%	89.7%	96.7%
EFA200418	YPS001127	50%	91.2%	99.2%
EFA200421	ABA106144	42%	98.0%	97.3%
EFA200421	BAN110110	53%	96.6%	99.0%
EFA200421	BAN103067	64%	98.6%	98.3%
EFA200421	BFR10353	34%	91.5%	77.6%
EFA200421	BPT101109	43%	98.0%	97.3%
EFA200421	BBU100121	29%	91.5%	96.1%
EFA200421	BCE107064	42%	99.3%	97.6%
EFA200421	BFU100280	42%	99.3%	97.6%
EFA200421	BMA107429	42%	99.3%	97.6%
EFA200421	CJU101106	33%	99.3%	100%
EFA200421	CPN200047	33%	93.2%	99.6%
EFA200421	CTR200050	34%	93.2%	99.6%
EFA200421	CAC101812	46%	98.6%	98.7%
EFA200421	CBO101301	43%	98.3%	98.4%
EFA200421	CDF101762	50%	99.7%	100%
EFA200421	CDP101115	35%	93.5%	99.6%
EFA200421	EBC103096	41%	99.7%	99.3%
EFA200421	EFA200421	100%	100%	100%
EFA200421	ECO100170	41%	99.7%	99.3%
EFA200421	HIN100893	44%	98.0%	97.2%
EFA200421	HPY101532	35%	99.7%	100%
EFA200421	KPN301399	41%	99.7%	99.3%
EFA200421	LPN100716	42%	99.7%	99.7%
EFA200421	LMO102014	62%	99.7%	99.7%
EFA200421	MCA101252	45%	98.0%	96.9%
EFA200421	MAV106405	38%	93.5%	99.6%
EFA200421	MBV102285	35%	93.5%	99.6%
EFA200421	MLP100972	34%	93.5%	99.6%
EFA200421	MTU202851	35%	93.5%	99.6%
EFA200421	MGE100443	36%	97.6%	98.0%
EFA200421	MPN100211	37%	97.6%	98.0%
EFA200421	NGO100890	43%	99.7%	99.6%
EFA200421	NME200305	44%	99.7%	99.6%
EFA200421	PMU101985	43%	99.7%	99.6%
EFA200421	PRT104501	45%	99.7%	100%
EFA200421	PAE203653	44%	99.3%	98.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200421	PPU107887	43%	99.3%	98.3%
EFA200421	PSY104373	44%	99.3%	98.3%
EFA200421	SPA101193	41%	99.7%	99.3%
EFA200421	STY103870	41%	99.7%	99.3%
EFA200421	STM103563	41%	99.7%	99.3%
EFA200421	SAU801257	62%	99.7%	100%
EFA200421	SEP201550	62%	98.6%	99.3%
EFA200421	SHA100714	64%	98.6%	99.3%
EFA200421	SMU100627	47%	99.3%	98.3%
EFA200421	SPN402016	43%	99.3%	98.3%
EFA200421	SPY201600	43%	99.3%	98.3%
EFA200421	TPA100598	30%	91.5%	95.9%
EFA200421	UUR100520	40%	98.0%	98.6%
EFA200421	VCH102225	43%	98.6%	98.9%
EFA200421	YPS001128	43%	99.7%	99.3%
EFA200454	ABA100529	48%	98.3%	99.8%
EFA200454	BAN100354	53%	98.3%	99.5%
EFA200454	BAN103931	58%	98.8%	99.8%
EFA200454	BFR100495	25%	38.1%	7.0%
EFA200454	BPT102439	45%	98.6%	99.5%
EFA200454	BCE111561	56%	38.6%	99.5%
EFA200454	BFU106495	45%	98.1%	98.3%
EFA200454	BMA104091	45%	95.8%	96.0%
EFA200454	CJU100505	41%	97.4%	99.6%
EFA200454	CPN200251	39%	97.0%	98.1%
EFA200454	CTR200662	37%	97.4%	96.5%
EFA200454	CAC100467	49%	96.0%	95.8%
EFA200454	CBO100123	31%	98.8%	99.4%
EFA200454	CDF100404	42%	13.6%	83.0%
EFA200454	CDF100250	46%	97.4%	97.2%
EFA200454	CDP100483	40%	98.4%	99.0%
EFA200454	EBC102546	46%	97.4%	98.4%
EFA200454	EFA200454	100%	100%	100%
EFA200454	EFM201684	83%	99.0%	99.5%
EFA200454	ECO100194	47%	95.8%	96.7%
EFA200454	HIN100709	46%	98.3%	99.0%
EFA200454	HPY100234	41%	97.6%	98.3%
EFA200454	KPN301911	47%	93.7%	98.4%
EFA200454	LPN102483	50%	16.3%	98.9%
EFA200454	LMO100624	63%	98.6%	99.3%
EFA200454	MCA101839	42%	97.4%	99.3%
EFA200454	MAV102826	41%	96.0%	97.1%
EFA200454	MBV103229	41%	96.0%	97.1%
EFA200454	MTU202807	41%	96.3%	96.7%
EFA200454	MGE100289	28%	18.4%	22.4%
EFA200454	MPN100436	25%	79.4%	56.7%
EFA200454	NGO100106	44%	99.0%	99.8%
EFA200454	NME201412	44%	99.0%	99.8%
EFA200454	PMU101370	47%	98.1%	98.9%
EFA200454	PRT101177	46%	95.8%	96.8%
EFA200454	PAE200955	47%	98.3%	99.1%
EFA200454	PPU108855	47%	91.4%	95.3%
EFA200454	PSY105509	45%	94.8%	95.6%
EFA200454	SPA100809	44%	95.8%	98.2%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200454	STY103990	47%	95.8%	96.7%
EFA200454	SAU801263	56%	98.3%	98.8%
EFA200454	SEP201556	56%	98.6%	99.1%
EFA200454	SHA101150	56%	98.6%	99.1%
EFA200454	SMU101082	60%	99.0%	100%
EFA200454	SPN400243	60%	98.6%	99.5%
EFA200454	SPY201510	59%	98.6%	99.4%
EFA200454	TPA100158	39%	93.5%	94.2%
EFA200454	UUR100457	29%	23.4%	29.2%
EFA200454	VCH100859	45%	97.4%	98.4%
EFA200454	YPS002005	47%	97.4%	98.3%
EFA200457	BAN108834	45%	80.1%	87.5%
EFA200457	BAN108033	60%	99.8%	99.9%
EFA200457	CAC101590	43%	98.1%	98.9%
EFA200457	CBO102746	45%	95.4%	95.9%
EFA200457	CDF103797	43%	99.7%	99.9%
EFA200457	EFA200457	100%	100%	100%
EFA200457	EFM200946	82%	100%	100%
EFA200457	LMO102727	62%	99.7%	99.7%
EFA200457	MAV103787	34%	13.0%	86.1%
EFA200457	MBV104672	32%	13.0%	30.8%
EFA200457	MTU202157	32%	13.0%	30.4%
EFA200457	MGE100031	38%	84.0%	84.8%
EFA200457	MPN100120	38%	83.9%	85.4%
EFA200457	SAU801264	54%	99.9%	99.9%
EFA200457	SEP201557	54%	99.6%	99.7%
EFA200457	SHA103204	54%	99.8%	99.6%
EFA200457	SMU101474	55%	99.4%	99.7%
EFA200457	SPN400251	54%	99.4%	99.7%
EFA200457	SPY201509	54%	99.4%	99.7%
EFA200457	UUR100379	37%	86.7%	88.6%
EFA200478	ABA100930	30%	98.9%	97.0%
EFA200478	BAN107253	28%	69.4%	72.2%
EFA200478	BAN102625	46%	30.2%	56.8%
EFA200478	BAN103946	46%	30.2%	81.2%
EFA200478	BAN106298	40%	98.7%	98.9%
EFA200478	BFR103444	39%	43.1%	84.7%
EFA200478	BPT104540	29%	75.5%	10.4%
EFA200478	BBU100303	27%	92.1%	92.2%
EFA200478	BCE104414	25%	82.3%	97.9%
EFA200478	BFU100824	27%	93.2%	90.9%
EFA200478	BMA104638	27%	93.2%	91.2%
EFA200478	CJU100734	20%	72.9%	65.3%
EFA200478	CPN200950	28%	93.9%	94.4%
EFA200478	CTR200132	27%	93.2%	92.9%
EFA200478	CAC101153	33%	99.3%	98.9%
EFA200478	CBO102608	35%	93.2%	92.6%
EFA200478	CDF103288	30%	93.9%	94.1%
EFA200478	CDP101279	28%	99.6%	99.4%
EFA200478	EBC102572	31%	95.0%	94.7%
EFA200478	EFA200478	100%	100%	100%
EFA200478	BFM201777	58%	99.3%	99.1%
EFA200478	ECO100086	30%	98.2%	98.0%
EFA200478	HIN101108	29%	100%	99.1%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200478	HPY100728	25%	63.7%	56.2%
EFA200478	KPN301858	28%	98.2%	98.0%
EFA200478	LMO101402	40%	100%	100%
EFA200478	MCA100820	31%	91.9%	90.9%
EFA200478	MAV103997	23%	59.7%	91.1%
EFA200478	MLP100565	26%	93.4%	92.3%
EFA200478	MTU202123	27%	93.4%	91.6%
EFA200478	NGO100600	31%	94.7%	98.6%
EFA200478	NME201912	31%	94.7%	95.1%
EFA200478	PMU100138	28%	99.8%	98.9%
EFA200478	PRT102642	29%	99.1%	97.6%
EFA200478	PAE204414	29%	94.5%	93.7%
EFA200478	PPU111733	31%	94.5%	93.6%
EFA200478	PSY103854	29%	94.5%	94.5%
EFA200478	SPA102755	30%	95.2%	94.9%
EFA200478	STY103172	31%	95.2%	94.9%
EFA200478	STM102864	31%	95.2%	94.9%
EFA200478	SAU802082	42%	94.1%	94.2%
EFA200478	SEP201343	42%	94.1%	94.5%
EFA200478	SHA100952	41%	94.1%	94.5%
EFA200478	SMU100741	49%	99.3%	99.6%
EFA200478	SPN401513	46%	99.3%	98.9%
EFA200478	SPY201087	49%	99.6%	97.8%
EFA200478	TPA100382	31%	100%	99.6%
EFA200478	VCH102370	30%	95.2%	95.1%
EFA200478	YPS000994	30%	95.2%	93.9%
EFA200495	BFR101164	51%	100%	46.1%
EFA200495	CDP100056	26%	24.5%	26.6%
EFA200495	EFA200495	100%	100%	100%
EFA200515	ABA100815	30%	89.0%	79.9%
EFA200515	BPT103008	29%	87.6%	81.8%
EFA200515	BCE112921	29%	29.3%	75.1%
EFA200515	BCE112214	38%	33.8%	83.8%
EFA200515	BCE114431	36%	48.9%	67.4%
EFA200515	BCE111221	29%	87.2%	88.9%
EFA200515	BCE105983	33%	88.7%	86.6%
EFA200515	BFU102806	31%	87.2%	82.5%
EFA200515	BMA100434	30%	89.0%	82.8%
EFA200515	BMA105823	31%	87.6%	85.8%
EFA200515	EBC101455	29%	90.5%	81.2%
EFA200515	EFA200515	100%	100%	100%
EFA200515	KPN305645	28%	90.5%	81.4%
EFA200515	MBV105656	30%	90.1%	76.3%
EFA200515	MLP100958	29%	88.7%	73.8%
EFA200515	MTU202299	30%	90.1%	74.3%
EFA200515	PRT100665	33%	88.5%	78.6%
EFA200515	PAE201315	29%	88.7%	76.8%
EFA200515	SPA102628	28%	90.5%	81.2%
EFA200515	STY103797	29%	90.5%	81.2%
EFA200515	SAU202063	29%	87.6%	75.9%
EFA200515	SHA102166	29%	87.2%	85.5%
EFA200515	YPS000055	29%	88.3%	82.3%
EFA200538	ABA105508	40%	99.5%	98.9%
EFA200538	BAN102826	75%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200538	BFR10298	46%	99.8%	99.9%
EFA200538	BPT102350	38%	99.5%	99.4%
EFA200538	BBU100250	49%	99.5%	99.4%
EFA200538	BCE103321	39%	99.5%	99.4%
EFA200538	BMA109061	38%	99.5%	94.1%
EFA200538	CJU101017	39%	99.8%	99.8%
EFA200538	CPN200606	49%	99.8%	99.9%
EFA200538	CTR200474	51%	99.8%	99.9%
EFA200538	CAC101070	45%	99.8%	99.8%
EFA200538	CBO100961	47%	99.1%	99.1%
EFA200538	CDF103555	46%	99.5%	99.4%
EFA200538	CDP101454	44%	99.0%	97.0%
EFA200538	EBC100539	38%	53.0%	99.6%
EFA200538	EFA200538	100%	100%	100%
EFA200538	EFM200610	87%	100%	100%
EFA200538	ECO100632	42%	99.5%	99.3%
EFA200538	HIN100900	42%	99.5%	99.2%
EFA200538	HPY101524	40%	98.9%	99.1%
EFA200538	KPN300581	40%	16.3%	79.3%
EFA200538	KPN302684	42%	99.5%	99.5%
EFA200538	LPN103327	44%	99.6%	99.4%
EFA200538	LMO100611	75%	100%	100%
EFA200538	MCA102972	39%	99.5%	98.6%
EFA200538	MAV103767	44%	98.9%	94.2%
EFA200538	MBV104696	44%	98.9%	96.2%
EFA200538	MLP100028	43%	98.9%	96.4%
EFA200538	MTU200041	44%	98.9%	96.4%
EFA200538	MGE100272	41%	99.5%	99.5%
EFA200538	MPN100453	41%	99.5%	99.4%
EFA200538	NGO100059	42%	99.5%	99.2%
EFA200538	NME200518	40%	99.5%	99.5%
EFA200538	PMU101214	40%	99.6%	99.4%
EFA200538	PRT102887	41%	99.5%	99.3%
EFA200538	PAE203984	41%	99.8%	99.5%
EFA200538	PPU108817	42%	99.8%	99.5%
EFA200538	PSY105072	42%	99.8%	99.5%
EFA200538	SPA100430	45%	62.3%	97.8%
EFA200538	STY101466	42%	99.5%	99.3%
EFA200538	SAU801760	72%	99.9%	99.9%
EFA200538	SEP202121	71%	99.9%	99.9%
EFA200538	SHA100631	73%	99.9%	99.9%
EFA200538	SMU100492	70%	99.5%	99.4%
EFA200538	SPN400235	70%	99.5%	99.4%
EFA200538	SPY200128	71%	99.5%	99.4%
EFA200538	TPA100579	50%	99.8%	99.9%
EFA200538	UUR100373	52%	99.5%	99.8%
EFA200538	VCH100940	44%	99.8%	95.5%
EFA200538	YPS001199	42%	99.5%	99.3%
EFA200544	ABA102927	27%	94.4%	93.3%
EFA200544	BAN107304	34%	90.3%	92.1%
EFA200544	BFR104340	26%	74.5%	70.1%
EFA200544	BPT104317	32%	75.5%	61.0%
EFA200544	BCE102893	24%	63.9%	75.3%
EFA200544	BMA103625	33%	34.7%	33.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200544	CAC100597	37%	46.3%	33.8%
EFA200544	CBO103870	29%	81.9%	98.9%
EFA200544	CDF100442	30%	71.8%	57.1%
EFA200544	EBC102841	28%	63.4%	69.8%
EFA200544	EFA200544	100%	100%	100%
EFA200544	EFM201387	50%	95.4%	94.5%
EFA200544	ECO100817	25%	68.1%	74.2%
EFA200544	HIN100201	35%	44.0%	39.0%
EFA200544	HPY100346	29%	89.4%	85.1%
EFA200544	HPY100838	35%	89.4%	86.8%
EFA200544	KPN302156	36%	33.3%	32.0%
EFA200544	LPN100696	25%	87.0%	27.4%
EFA200544	LMO100669	36%	93.1%	94.0%
EFA200544	MAV102855	34%	64.8%	49.5%
EFA200544	MLP100064	31%	49.1%	53.1%
EFA200544	PMU100676	34%	31.5%	28.2%
EFA200544	PRT100154	38%	38.9%	35.3%
EFA200544	PAE204008	29%	76.4%	38.7%
EFA200544	PPU107569	28%	84.7%	41.1%
EFA200544	PSY105067	31%	91.7%	45.0%
EFA200544	SPA102202	25%	72.2%	75%
EFA200544	STY102442	24%	72.2%	83.2%
EFA200544	SAU801417	30%	84.7%	92.6%
EFA200544	SEP200350	32%	84.7%	92.6%
EFA200544	SHA100392	30%	87.0%	93.7%
EFA200544	SMU100446	39%	100%	100%
EFA200544	SPN400434	40%	100%	100%
EFA200544	SPY200272	43%	99.5%	99.1%
EFA200544	TPA100545	27%	54.6%	41.7%
EFA200544	VCH102452	38%	41.7%	48.3%
EFA200544	YPS001142	40%	18.5%	22.2%
EFA200562	ABA100383	63%	98.7%	98.7%
EFA200562	BAN108106	75%	98.2%	98.0%
EFA200562	BFR103242	51%	98.2%	98.8%
EFA200562	BPT100493	61%	97.5%	97.7%
EFA200562	BBU100375	49%	97.7%	96.7%
EFA200562	BCE104520	63%	97.5%	97.9%
EFA200562	BFU106887	62%	97.5%	92.4%
EFA200562	BMA102515	62%	98.5%	96.7%
EFA200562	CJU101022	41%	98.5%	99.7%
EFA200562	CAC100015	70%	98.7%	99.7%
EFA200562	CDF101475	69%	98.0%	98.0%
EFA200562	CDP100317	58%	98.5%	97.1%
EFA200562	EBC106045	62%	97.7%	99.5%
EFA200562	EFA200562	100%	100%	100%
EFA200562	EFM102997	89%	14.2%	100%
EFA200562	ECO102877	63%	98.0%	97.9%
EFA200562	HIN101146	59%	97.7%	97.7%
EFA200562	HPY100194	57%	99.0%	99.0%
EFA200562	KPN303051	62%	98.0%	97.9%
EFA200562	LPN103398	60%	99.5%	100%
EFA200562	LMO101989	76%	98.0%	97.7%
EFA200562	MCA100501	60%	98.2%	99.0%
EFA200562	MAV103344	60%	99.5%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200562	MBV103088	60%	98.2%	97.8%
EFA200562	MLP100335	59%	99.5%	100%
EFA200562	MTU201374	60%	99.5%	100%
EFA200562	MGE100047	40%	97.0%	95.6%
EFA200562	MPN100094	39%	97.2%	95.0%
EFA200562	NGO101704	64%	98.2%	98.5%
EFA200562	NME200613	64%	98.2%	98.5%
EFA200562	PMU101027	61%	98.5%	98.4%
EFA200562	PRT101183	60%	97.7%	97.7%
EFA200562	PAE200545	58%	98.7%	98.7%
EFA200562	PPU109309	57%	98.7%	98.7%
EFA200562	PSY103013	58%	99.2%	99.2%
EFA200562	SPA102476	63%	97.7%	98.2%
EFA200562	STY104545	62%	98.0%	97.9%
EFA200562	STM100571	62%	98.0%	97.9%
EFA200562	SAU801790	72%	98.7%	98.5%
EFA200562	SEP202182	73%	98.0%	97.5%
EFA200562	SHA101199	72%	98.0%	97.7%
EFA200562	SMU101066	76%	99.5%	99.5%
EFA200562	SPN400671	76%	99.5%	99.7%
EFA200562	SPY201042	74%	98.5%	98.0%
EFA200562	TPA100786	58%	96.2%	94.4%
EFA200562	UUR100416	46%	98.5%	98.7%
EFA200562	VCH100467	62%	98.7%	98.4%
EFA200562	YPS000215	61%	98.0%	97.9%
EFA200590	ABA101280	48%	89.7%	97.7%
EFA200590	BAN110913	44%	99.4%	100%
EFA200590	BAN103692	62%	99.6%	99.6%
EFA200590	BFR11725	41%	5.6%	7.2%
EFA200590	BPT102975	47%	100%	100%
EFA200590	BBU100153	42%	95.7%	95.9%
EFA200590	BCE111466	53%	65.9%	93.5%
EFA200590	BFU106498	47%	99.4%	99.4%
EFA200590	BMA103047	46%	99.4%	99.4%
EFA200590	CJU100872	48%	98.8%	97.7%
EFA200590	CPN201009	44%	5.6%	17.6%
EFA200590	CTR200074	43%	4.4%	16.6%
EFA200590	CAC100650	56%	98.5%	98.5%
EFA200590	CBO100098	55%	98.6%	98.0%
EFA200590	CDF101445	44%	98.5%	98.8%
EFA200590	CDF100803	54%	90.8%	97.2%
EFA200590	CDP100932	48%	94.4%	99.1%
EFA200590	EBC107179	56%	43.1%	95.7%
EFA200590	EFA200590	100%	100%	100%
EFA200590	EFM100280	86%	26.4%	100%
EFA200590	ECO100098	47%	98.2%	98.1%
EFA200590	HIN100888	46%	98.3%	98.1%
EFA200590	HPY100773	48%	97.6%	96.5%
EFA200590	KPN300997	47%	98.2%	98.0%
EFA200590	LPN103376	48%	99.6%	99.6%
EFA200590	LMO101013	66%	100%	100%
EFA200590	MCA100812	44%	98.7%	98.5%
EFA200590	MAV101468	47%	94.3%	91.5%
EFA200590	MBV103337	48%	94.9%	91.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200590	MLP100475	49%	89.5%	86.4%
EFA200590	MTU203197	48%	96.2%	91.5%
EFA200590	MGE100074	45%	91.1%	94.8%
EFA200590	MPN100621	45%	91.1%	94.6%
EFA200590	NGO100323	47%	100%	99.9%
EFA200590	NME201594	47%	100%	99.9%
EFA200590	PMU101219	47%	98.2%	97.9%
EFA200590	PRT105129	47%	98.5%	98.3%
EFA200590	PAE204401	47%	99.6%	99.6%
EFA200590	PPU107707	46%	99.6%	96.6%
EFA200590	PSY103871	47%	97.4%	99.6%
EFA200590	SPA100472	43%	64.0%	84.7%
EFA200590	STY103214	47%	98.2%	98.1%
EFA200590	STM102926	47%	98.2%	98.1%
EFA200590	SAU800753	56%	99.4%	99.8%
EFA200590	SEP201381	56%	99.4%	99.6%
EFA200590	SHA101267	56%	99.4%	99.5%
EFA200590	SMU101178	69%	99.8%	99.6%
EFA200590	SPN401543	68%	99.8%	99.8%
EFA200590	SPY201389	68%	100%	99.8%
EFA200590	TPA100375	44%	98.3%	98.4%
EFA200590	UUR100118	44%	91.0%	91.6%
EFA200590	VCH102359	48%	99.8%	99.7%
EFA200590	YPS001804	48%	98.2%	98.1%
EFA200613	EFA200613	100%	100%	100%
EFA200613	SAU800898	31%	94.1%	85.0%
EFA200613	SPY200749	38%	92.9%	95.7%
EFA200621	ABA104593	47%	77.0%	67.2%
EFA200621	BAN113310	48%	18.3%	4.4%
EFA200621	BAN110029	66%	14.1%	1.5%
EFA200621	BFR11714	43%	89.2%	73.4%
EFA200621	BPT100248	48%	81.0%	70.9%
EFA200621	BBU100800	45%	77.5%	71.5%
EFA200621	BCE101969	46%	87.2%	94.9%
EFA200621	BFU100867	52%	75.9%	59.9%
EFA200621	BMA109716	44%	93.0%	80.7%
EFA200621	CJU100125	44%	17.3%	4.1%
EFA200621	CPN200434	39%	89.1%	77.8%
EFA200621	CTR200365	40%	87.4%	74.3%
EFA200621	CAC100425	55%	15.6%	1.9%
EFA200621	CBO103185	53%	12.1%	2.6%
EFA200621	CDF102888	56%	17.3%	4.3%
EFA200621	CDP100479	49%	73.4%	97.7%
EFA200621	EBC101431	42%	100%	88.4%
EFA200621	EFA200621	100%	100%	100%
EFA200621	EFM201052	79%	92.4%	99.9%
EFA200621	ECO103100	44%	95.1%	82.6%
EFA200621	HIN101252	50%	78.8%	75.2%
EFA200621	HPY101031	38%	98.4%	83.5%
EFA200621	KPN301426	45%	92.5%	85.6%
EFA200621	LPN102343	54%	54.2%	97.9%
EFA200621	LMO100282	60%	99.9%	98.5%
EFA200621	MCA100802	47%	76.4%	72.1%
EFA200621	MAV100286	48%	73.1%	96.1%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200621	MBV104310	50%	54.2%	98.2%
EFA200621	MLP100953	46%	17.6%	26.7%
EFA200621	MTU202801	47%	3.4%	11.2%
EFA200621	MGE100144	42%	77.7%	97.4%
EFA200621	MPN100676	41%	77.0%	97.9%
EFA200621	NGO101494	43%	95.7%	93.9%
EFA200621	NME201748	46%	88.7%	72.2%
EFA200621	PMU100759	42%	100%	94.8%
EFA200621	PRT102425	42%	99.1%	83.4%
EFA200621	PAE204740	42%	95.7%	91.4%
EFA200621	PPU108488	46%	78.4%	72.0%
EFA200621	PSY104832	49%	69.5%	98.4%
EFA200621	SPA101256	53%	57.6%	98.1%
EFA200621	STY101473	44%	93.0%	85.1%
EFA200621	SAU801269	62%	1.6%	10.2%
EFA200621	SEP201562	55%	100%	97.5%
EFA200621	SHA100514	54%	100%	97.5%
EFA200621	SMU100784	60%	21.4%	1.7%
EFA200621	SPN400481	64%	20.9%	4.9%
EFA200621	SPY201321	62%	17.8%	1.2%
EFA200621	TPA100881	48%	80.1%	74.7%
EFA200621	UUR100322	48%	75.8%	97.6%
EFA200621	VCH100631	50%	78.8%	68.8%
EFA200621	YPS001051	42%	99.0%	87.8%
EFA200624	ABA103925	34%	99.5%	82.8%
EFA200624	BAN104708	56%	83.5%	94.4%
EFA200624	BAN102313	66%	86.0%	92.9%
EFA200624	BFR10840	33%	82.2%	86.6%
EFA200624	BPT100246	35%	98.7%	81.7%
EFA200624	BBU100799	35%	92.0%	75.1%
EFA200624	BCE107342	38%	93.7%	77.8%
EFA200624	BFU100866	41%	89.0%	71.9%
EFA200624	BMA107734	39%	93.7%	77.8%
EFA200624	CJU100425	30%	88.7%	97.8%
EFA200624	CPN200435	34%	92.0%	84.8%
EFA200624	CTR200366	35%	88.7%	81.8%
EFA200624	CAC100279	52%	85.7%	97.7%
EFA200624	CBO102108	48%	99.5%	91.0%
EFA200624	CDF102471	52%	96.2%	100%
EFA200624	CDP100481	39%	84.5%	98.5%
EFA200624	EBC101239	34%	100%	79.8%
EFA200624	EFA200624	100%	100%	100%
EFA200624	EFM201833	85%	97.2%	98.7%
EFA200624	ECO103101	35%	100%	79.0%
EFA200624	HIN101251	34%	99.0%	82.2%
EFA200624	HPY101493	27%	91.5%	99.0%
EFA200624	KPN300994	35%	100%	79.0%
EFA200624	LPN100039	35%	99.7%	82.7%
EFA200624	LMO100131	63%	93.0%	99.5%
EFA200624	MCA100801	34%	100%	86.6%
EFA200624	MAV103287	30%	48.1%	96.7%
EFA200624	MBV103220	40%	84.0%	92.5%
EFA200624	MLP100955	40%	86.7%	95.7%
EFA200624	MTU202803	40%	84.0%	92.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200624	MGE100143	28%	99.0%	76.8%
EFA200624	MPN100677	30%	85.7%	65.4%
EFA200624	NGO101492	36%	88.5%	72.2%
EFA200624	NME201747	37%	94.0%	75.0%
EFA200624	PMU100760	35%	99.0%	82.4%
EFA200624	PRT102427	37%	100%	79.3%
EFA200624	PAE204741	34%	91.2%	74.2%
EFA200624	PPU108490	39%	71.9%	65.5%
EFA200624	PSY104834	36%	93.7%	77.5%
EFA200624	SPA101734	33%	91.2%	73.7%
EFA200624	STY101474	35%	91.2%	73.8%
EFA200624	SAU801266	57%	97.5%	99.0%
EFA200624	SEP201559	56%	97.5%	95.8%
EFA200624	SHA101153	60%	89.5%	94.7%
EFA200624	SMU100777	53%	97.7%	100%
EFA200624	SPN400478	54%	91.5%	100%
EFA200624	SPY201324	52%	94.2%	99.7%
EFA200624	TPA100882	37%	87.5%	71.3%
EFA200624	UUR100320	24%	98.5%	88.6%
EFA200624	VCH100630	34%	100%	79.0%
EFA200624	YPS001052	35%	100%	79.0%
EFA200660	ABA105585	47%	88.6%	93.3%
EFA200660	BAN110583	71%	92.4%	96.1%
EFA200660	BAN103323	71%	92.4%	96.1%
EFA200660	BFR100885	55%	86.1%	75.6%
EFA200660	BPT101387	50%	88.6%	77.8%
EFA200660	BBU100113	68%	63.3%	52.1%
EFA200660	BCE105745	51%	97.5%	84.6%
EFA200660	BFU105922	46%	97.5%	84.6%
EFA200660	BMA104982	51%	97.5%	84.6%
EFA200660	CJU100998	49%	100%	88.4%
EFA200660	CPN200890	50%	94.9%	90.2%
EFA200660	CTR200180	50%	94.9%	91.4%
EFA200660	CAC102549	54%	89.9%	82.2%
EFA200660	CBO100272	56%	92.4%	91.2%
EFA200660	CDF103531	55%	87.3%	92%
EFA200660	CDP100127	49%	84.8%	81.7%
EFA200660	EBC103610	51%	88.6%	93.3%
EFA200660	EFA200660	100%	100%	100%
EFA200660	EFM100455	93%	98.7%	100%
EFA200660	ECO104092	51%	88.6%	93.3%
EFA200660	HIN100524	52%	88.6%	93.3%
EFA200660	HPY101227	51%	73.4%	68.2%
EFA200660	KPN300649	51%	88.6%	93.3%
EFA200660	LPN101987	50%	82.3%	86.7%
EFA200660	LMO102748	70%	100%	100%
EFA200660	MCA101348	52%	88.6%	93.3%
EFA200660	MAV101549	53%	84.8%	78.6%
EFA200660	MBV106246	52%	84.8%	78.6%
EFA200660	MLP101583	53%	84.8%	78.6%
EFA200660	MTU200055	52%	84.8%	78.6%
EFA200660	MGE100094	48%	70.9%	51.4%
EFA200660	MPN100601	51%	70.9%	51.9%
EFA200660	NGO100183	51%	88.6%	92.1%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200660	NME201394	51%	88.6%	92.1%
EFA200660	PMU101178	51%	88.6%	93.3%
EFA200660	PRT102061	51%	88.6%	93.3%
EFA200660	PAE204929	53%	82.3%	85.5%
EFA200660	PPU106680	50%	82.3%	85.5%
EFA200660	PSY101038	50%	82.3%	85.5%
EFA200660	SPA102211	51%	88.6%	93.3%
EFA200660	STY103813	51%	88.6%	93.3%
EFA200660	STM103619	51%	88.6%	93.3%
EFA200660	SAU800367	76%	94.9%	93.8%
EFA200660	SEP201354	77%	94.9%	93.8%
EFA200660	SHA101080	78%	93.7%	92.5%
EFA200660	SMU101249	81%	98.7%	100%
EFA200660	SPN401393	81%	98.7%	100%
EFA200660	SPY201406	78%	98.7%	100%
EFA200660	TPA100060	62%	67.1%	53.5%
EFA200660	UUR100558	52%	91.1%	91.1%
EFA200660	VCH100363	51%	88.6%	93.3%
EFA200660	YPS002204	50%	88.6%	93.3%
EFA200661	ABA105929	28%	99.5%	98.4%
EFA200661	BAN105418	54%	100%	100%
EFA200661	BAN102675	59%	100%	100%
EFA200661	BFR100085	33%	54.3%	66.9%
EFA200661	BFR10599	40%	62.8%	76.3%
EFA200661	BPT100946	30%	63.8%	69.8%
EFA200661	BBU100114	33%	58.5%	75.2%
EFA200661	BCE112892	31%	99.5%	98.4%
EFA200661	BFU103395	30%	99.5%	98.3%
EFA200661	BMA103994	33%	70.7%	73.4%
EFA200661	CJU100997	37%	85.1%	79.8%
EFA200661	CPN200363	22%	95.7%	95.6%
EFA200661	CTR200309	23%	96.8%	95%
EFA200661	CAC102955	46%	55.9%	96.4%
EFA200661	CAC103317	54%	54.8%	77.4%
EFA200661	CAC101327	45%	91.0%	100%
EFA200661	CBO103395	38%	55.9%	92.9%
EFA200661	CBO103707	53%	72.9%	89.9%
EFA200661	CDF104218	32%	57.4%	79.0%
EFA200661	CDF103030	43%	58.0%	76.4%
EFA200661	CDP100636	34%	75%	90.1%
EFA200661	CDP100782	34%	98.4%	96.9%
EFA200661	EBC104214	30%	88.8%	95.5%
EFA200661	EFA200661	100%	100%	100%
EFA200661	EFM202042	61%	100%	100%
EFA200661	ECO103953	30%	88.8%	95.5%
EFA200661	HIN100237	30%	99.5%	98.2%
EFA200661	HPY101228	28%	100%	100%
EFA200661	KPN308310	32%	88.8%	95.4%
EFA200661	KPN301041	30%	75.5%	89.9%
EFA200661	LPN103463	27%	58.0%	78.6%
EFA200661	LMO100923	54%	100%	100%
EFA200661	LMO101733	58%	100%	100%
EFA200661	MCA100569	29%	99.5%	99.2%
EFA200661	MAV101548	38%	60.1%	73.2%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200661	MBV106247	34%	76.1%	93.9%
EFA200661	MLP101584	37%	60.1%	73.2%
EFA200661	MTU200054	34%	76.1%	93.9%
EFA200661	MGE100093	23%	58.5%	66.2%
EFA200661	MPN100602	22%	58.5%	66.3%
EFA200661	NGO100403	30%	67.0%	73.6%
EFA200661	NME201532	28%	99.5%	98.9%
EFA200661	PMU101950	30%	91.0%	98.2%
EFA200661	PRT100733	26%	93.1%	90.3%
EFA200661	PRT101487	31%	88.8%	95.4%
EFA200661	PAE204230	34%	58.0%	69.7%
EFA200661	PPU104550	29%	99.5%	97.8%
EFA200661	PSY105770	30%	99.5%	97.9%
EFA200661	STY102437	33%	60.6%	65.7%
EFA200661	STY102277	29%	88.8%	95.5%
EFA200661	STM102829	29%	88.8%	95.5%
EFA200661	SAU800366	51%	100%	100%
EFA200661	SAU801983	44%	100%	100%
EFA200661	SAU800864	54%	78.7%	95.7%
EFA200661	SEP201353	52%	100%	100%
EFA200661	SHA101079	51%	100%	100%
EFA200661	SMU101251	62%	100%	100%
EFA200661	SPN401394	54%	100%	100%
EFA200661	SPY201407	61%	100%	100%
EFA200661	TPA100061	30%	95.2%	96.0%
EFA200661	UUR100559	32%	97.3%	98.8%
EFA200661	VCH100392	30%	88.8%	95.5%
EFA200661	YPS002815	32%	88.8%	95.6%
EFA200662	ABA101593	29%	93%	70.9%
EFA200662	BAN105775	63%	94%	96.8%
EFA200662	BAN110631	65%	94%	95.8%
EFA200662	BFR100626	24%	94%	80.7%
EFA200662	BPT101390	25%	93%	71.4%
EFA200662	BCE111148	30%	93%	72.6%
EFA200662	BFU105918	30%	93%	66.2%
EFA200662	BMA108586	30%	93%	72.6%
EFA200662	CJU100996	30%	93%	72.8%
EFA200662	CPN200891	26%	94%	82.1%
EFA200662	CTR200179	30%	94%	82.1%
EFA200662	CAC102614	42%	94%	96.8%
EFA200662	CBO100194	39%	94%	94.8%
EFA200662	CDF103506	37%	90%	94.6%
EFA200662	CDP100784	34%	91%	93.7%
EFA200662	EBC103612	26%	93%	68.7%
EFA200662	EFA200662	100%	100%	100%
EFA200662	EFM100453	85%	98%	99.0%
EFA200662	ECO104090	26%	93%	68.7%
EFA200662	HIN100526	28%	90%	69.6%
EFA200662	HPY101229	28%	94%	64.8%
EFA200662	KPN302207	27%	93%	69.8%
EFA200662	LPN101590	32%	89%	76.8%
EFA200662	LMO102694	69%	95%	96.9%
EFA200662	MCA101349	27%	91%	66.2%
EFA200662	MAV101547	31%	93%	94.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200662	MBV100941	34%	93%	94.8%
EFA200662	MLP101585	30%	93%	94.8%
EFA200662	MTU200053	34%	93%	94.8%
EFA200662	NGO100178	30%	93%	73.8%
EFA200662	NME201396	29%	93%	73.8%
EFA200662	PMU101180	29%	93%	72%
EFA200662	PRT104507	27%	93%	68.7%
EFA200662	PAE204930	28%	91%	63.3%
EFA200662	PPU106677	28%	91%	62.4%
EFA200662	PSY101040	28%	91%	62.4%
EFA200662	STY103809	26%	93%	68.7%
EFA200662	STM103613	26%	93%	68.7%
EFA200662	SAU800365	62%	91%	91.8%
EFA200662	SEP201352	60%	91%	91.8%
EFA200662	SHA101078	55%	88%	94.6%
EFA200662	SMU101253	70%	95%	97.9%
EFA200662	SPN401395	72%	95%	97.9%
EFA200662	SPY201408	74%	95%	97.9%
EFA200662	UUR100560	34%	94%	56.9%
EFA200662	VCH100361	26%	94%	74.6%
EFA200662	YPS002210	29%	93%	69.2%
EFA200674	ABA100992	48%	96.6%	97.0%
EFA200674	BAN111688	50%	94.5%	97.5%
EFA200674	BAN103655	71%	99.5%	99.1%
EFA200674	BFR10422	52%	99.4%	99.5%
EFA200674	BPT100120	49%	92.8%	99.7%
EFA200674	BBU100435	53%	98.9%	100%
EFA200674	BCE109504	49%	99.5%	98.7%
EFA200674	BFU102072	50%	99.4%	99.8%
EFA200674	BMA101322	53%	100%	100%
EFA200674	CJU100003	52%	98.2%	99.7%
EFA200674	CPN200477	55%	98.9%	100%
EFA200674	CTR200455	56%	98.9%	100%
EFA200674	CAC101093	61%	98.9%	100%
EFA200674	CBO101275	61%	98.8%	99.7%
EFA200674	CDF100210	60%	98.2%	99.7%
EFA200674	CDP100030	50%	98.0%	98.5%
EFA200674	EBC104360	55%	98.3%	99.9%
EFA200674	EFA200674	100%	100%	100%
EFA200674	EFM200514	89%	99.5%	99.7%
EFA200674	ECO103620	55%	98.3%	99.9%
EFA200674	HIN100546	53%	97.8%	99.0%
EFA200674	HPY100496	50%	98.2%	99.9%
EFA200674	KPN301149	53%	63.5%	98.3%
EFA200674	LPN102764	61%	17.6%	95.1%
EFA200674	LMO100884	72%	100%	100%
EFA200674	MCA101384	51%	96.8%	97.2%
EFA200674	MAV100554	51%	98.8%	99.4%
EFA200674	MBV104294	49%	98.8%	94.0%
EFA200674	MLP100005	50%	98.8%	99.4%
EFA200674	MTU200005	49%	98.8%	94.0%
EFA200674	MGE100003	52%	99.5%	99.8%
EFA200674	MPN100151	53%	98.5%	99.2%
EFA200674	NGO100713	51%	99.1%	91.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200674	NME200053	51%	98.5%	99.5%
EFA200674	PMU101476	50%	98.2%	99.3%
EFA200674	PRT102211	54%	97.8%	99.5%
EFA200674	PAB200004	54%	97.8%	99.3%
EFA200674	PPU109146	53%	98.0%	99.4%
EFA200674	PSY100091	53%	98.0%	99.4%
EFA200674	SPA101583	52%	83.7%	89.7%
EFA200674	STY103968	55%	98.3%	99.9%
EFA200674	SAU800005	66%	97.7%	97.8%
EFA200674	SEP201276	67%	97.7%	98.0%
EFA200674	SHA102259	67%	97.7%	97.7%
EFA200674	SMU100247	77%	100%	100%
EFA200674	SPN400715	78%	100%	100%
EFA200674	SPY200532	76%	100%	100%
EFA200674	TPA100996	55%	98.0%	99.5%
EFA200674	UUR100079	54%	98.9%	99.7%
EFA200674	VCH100015	54%	98.3%	99.9%
EFA200674	YPS003447	55%	97.8%	99.5%
EFA200677	ABA100983	47%	79.2%	76.3%
EFA200677	BAN112286	19%	14.8%	48.4%
EFA200677	BAN110545	49%	93.3%	97.0%
EFA200677	BAN102589	54%	99.6%	99.8%
EFA200677	BFR101484	31%	98.0%	96.0%
EFA200677	BPT100629	38%	98.9%	99.6%
EFA200677	BBU100436	31%	99.1%	99.0%
EFA200677	BCE108826	45%	75.8%	90.9%
EFA200677	BFU100017	46%	69.4%	88.8%
EFA200677	BMA102755	46%	75.8%	63.4%
EFA200677	CJU100001	36%	86.4%	88.0%
EFA200677	CPN200324	37%	97.5%	93.6%
EFA200677	CTR200540	37%	98.0%	96.0%
EFA200677	CAC102789	50%	98.0%	97.5%
EFA200677	CBO101747	51%	98.2%	97.8%
EFA200677	CDF100209	58%	74.0%	91.7%
EFA200677	CDP100027	44%	84.1%	69.0%
EFA200677	EBC104357	49%	77.2%	78.0%
EFA200677	EFA200677	100%	100%	100%
EFA200677	EFM201887	28%	22.4%	39.3%
EFA200677	EFM202229	25%	21.9%	39.3%
EFA200677	ECO103623	42%	98.9%	99.4%
EFA200677	HIN100974	38%	99.6%	99.8%
EFA200677	HPY101507	36%	75.8%	74.0%
EFA200677	KPN301146	42%	98.7%	99.4%
EFA200677	LPN101463	41%	87.9%	98.8%
EFA200677	LMO100513	54%	99.3%	98.4%
EFA200677	MCA100098	33%	98.7%	95.3%
EFA200677	MAV100561	43%	94.0%	90.0%
EFA200677	MBV103652	43%	94.0%	89.9%
EFA200677	MLP100001	42%	94.0%	86.6%
EFA200677	MTU200001	43%	94.0%	89.9%
EFA200677	MGE100479	29%	98.7%	99.5%
EFA200677	MPN100156	29%	98.7%	99.5%
EFA200677	NGO100049	45%	75.4%	67.1%
EFA200677	NME200512	45%	75.4%	65.1%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200677	PMU101161	40%	99.6%	99.3%
EFA200677	PRT103054	40%	66.9%	98.5%
EFA200677	PAE200001	50%	75.4%	64.8%
EFA200677	PPU102202	44%	93.7%	83.4%
EFA200677	PSY103554	48%	81.9%	71.2%
EFA200677	SPA101587	49%	54.1%	100%
EFA200677	STY103948	42%	98.9%	99.4%
EFA200677	SAU800001	50%	98.0%	98.0%
EFA200677	SEP201279	51%	98.0%	98.0%
EFA200677	SHA102255	50%	98.0%	98.0%
EFA200677	SMU100027	44%	97.8%	97.8%
EFA200677	SPN400001	45%	98.0%	98.5%
EFA200677	SPY200001	44%	97.8%	97.8%
EFA200677	TPA100001	36%	98.2%	97.2%
EFA200677	UUR100001	31%	74.5%	75.1%
EFA200677	VCH100012	41%	98.9%	98.3%
EFA200677	YPS003458	42%	98.9%	99.4%
EFA200698	BPT101006	36%	95.3%	91.1%
EFA200698	BCE100250	30%	52.2%	98.0%
EFA200698	BFU106928	32%	93.6%	94.2%
EFA200698	BFU108046	31%	93.9%	98.3%
EFA200698	BFU110913	32%	93.2%	95.9%
EFA200698	BFU101670	34%	94.6%	97.8%
EFA200698	BFU102611	35%	94.6%	94.2%
EFA200698	BFU114233	31%	94.2%	97.3%
EFA200698	BMA106862	27%	95.9%	94.0%
EFA200698	CDP100121	25%	94.2%	94.9%
EFA200698	EBC102104	58%	97.3%	98.6%
EFA200698	EFA200698	100%	100%	100%
EFA200698	ECO100606	55%	95.6%	92.2%
EFA200698	HIN100022	59%	95.6%	97.3%
EFA200698	KPN302601	31%	26.1%	15.0%
EFA200698	MCA100880	25%	93.6%	97.0%
EFA200698	MAV100316	32%	99.0%	97.3%
EFA200698	MBV101161	31%	87.5%	87.9%
EFA200698	MTU202461	31%	87.5%	87.9%
EFA200698	PRT106096	29%	92.5%	95.0%
EFA200698	PAE200882	30%	94.6%	96.4%
EFA200698	PSY105164	21%	77.6%	74.4%
EFA200698	SPA101729	54%	89.5%	98.5%
EFA200698	STY101151	55%	95.6%	97.6%
EFA200698	STM100866	55%	95.6%	97.6%
EFA200698	SMU100150	81%	100%	98.3%
EFA200698	SPY200907	83%	100%	100%
EFA200698	VCH100784	59%	93.9%	93.9%
EFA200698	YPS002471	30%	94.6%	95.4%
EFA200699	BFR102889	30%	15.5%	16.2%
EFA200699	BFU101081	28%	26.1%	28.6%
EFA200699	CDF103732	21%	48.8%	59.3%
EFA200699	EBC102105	55%	91.0%	87.1%
EFA200699	EFA200699	100%	100%	100%
EFA200699	ECO100605	54%	94.7%	94.9%
EFA200699	HIN100021	56%	91.6%	93.4%
EFA200699	KPN201812	54%	97.1%	92.9%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200699	MAV106467	28%	34.1%	86.3%
EFA200699	MAV105815	28%	35.1%	44.2%
EFA200699	MAV105306	23%	44.1%	55.3%
EFA200699	NGO100728	23%	40.6%	73.5%
EFA200699	NME200226	22%	52.7%	96.0%
EFA200699	PSY103268	28%	30.8%	39.7%
EFA200699	SPA100333	55%	91.6%	95.7%
EFA200699	STY101418	55%	95.1%	95.5%
EFA200699	STM100867	53%	97.1%	97.8%
EFA200699	SMU100152	83%	100%	100%
EFA200699	SPY200908	84%	100%	100%
EFA200699	VCH100785	53%	96.3%	92.7%
EFA200731	ABA100331	31%	58.8%	76.3%
EFA200731	BAN110824	33%	98.7%	99.4%
EFA200731	BAN102960	45%	98.7%	99.3%
EFA200731	BFR104661	25%	67.5%	87.5%
EFA200731	BPT101402	31%	59.8%	84.9%
EFA200731	BBU100419	28%	42.5%	17.4%
EFA200731	BCE113044	28%	59.8%	67.9%
EFA200731	BFU111080	26%	67.6%	91.1%
EFA200731	BMA100367	27%	59.8%	81.0%
EFA200731	CJU101147	27%	35.8%	50.8%
EFA200731	CPN200162	22%	55.1%	85.6%
EFA200731	CAC103503	30%	98.2%	100%
EFA200731	CBO100338	29%	95.8%	98.8%
EFA200731	CDF103795	30%	68.8%	97.2%
EFA200731	EBC101910	28%	58.7%	78.9%
EFA200731	EFA200731	100%	100%	100%
EFA200731	EFM202051	76%	99.0%	99.5%
EFA200731	ECO100392	29%	60.6%	82.4%
EFA200731	KPN304908	28%	60.6%	82.4%
EFA200731	LPN101514	24%	60.5%	88%
EFA200731	LPN102152	33%	36.6%	75.1%
EFA200731	LMO102502	46%	98.5%	99.2%
EFA200731	MCA100492	33%	54.9%	93.4%
EFA200731	MAV103023	37%	39.2%	57.7%
EFA200731	MBV102357	30%	59.6%	87.8%
EFA200731	MLP101453	35%	40.7%	56.7%
EFA200731	MTU200488	30%	59.6%	87.8%
EFA200731	NGO101717	26%	68.1%	59.6%
EFA200731	NME200153	25%	74.2%	65.4%
EFA200731	PRT101269	31%	55.6%	75.3%
EFA200731	PAE205479	28%	97.9%	98.8%
EFA200731	PPU102000	32%	67.8%	70.0%
EFA200731	PSY103050	30%	69.0%	71.4%
EFA200731	SPA101180	28%	60.6%	83.5%
EFA200731	STY100357	28%	60.6%	82.4%
EFA200731	STM100029	28%	60.6%	82.4%
EFA200731	SAU800019	42%	98.5%	98.8%
EFA200731	SEP201242	42%	98.5%	98.9%
EFA200731	SHA101256	41%	98.5%	98.7%
EFA200731	SMU100503	53%	62.6%	95.2%
EFA200731	SPN401105	51%	70.6%	96.7%
EFA200731	SPY200379	52%	63.7%	87.6%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200731	VCH100707	29%	58.5%	79.9%
EFA200731	YPS002602	31%	55.6%	74.0%
EFA200733	ABA101702	39%	96.6%	93.7%
EFA200733	BAN102017	65%	99.6%	99.1%
EFA200733	BAN108755	74%	99.6%	98.7%
EFA200733	BFR10442	44%	95.7%	96.1%
EFA200733	BPT101404	43%	95.3%	94.4%
EFA200733	BCE115095	46%	99.1%	85.3%
EFA200733	BFU109627	47%	98.3%	92.7%
EFA200733	BMA100321	42%	96.2%	96.6%
EFA200733	CJU101186	32%	97.4%	99.1%
EFA200733	CJU101152	38%	97.4%	99.1%
EFA200733	CAC100510	55%	96.2%	95.7%
EFA200733	CBO101454	53%	96.6%	96.6%
EFA200733	CDF103771	49%	95.7%	97.4%
EFA200733	CDP100744	47%	96.6%	98.2%
EFA200733	EBC104489	42%	97.4%	98.3%
EFA200733	EFA200733	100%	100%	100%
EFA200733	EFM200129	90%	100%	89.7%
EFA200733	ECO103818	43%	97.4%	98.3%
EFA200733	HIN100817	39%	97.4%	99.1%
EFA200733	KPN302148	44%	99.6%	97.9%
EFA200733	LMO101754	81%	99.6%	98.7%
EFA200733	MCA101884	43%	96.2%	96.2%
EFA200733	MAV103024	47%	97.4%	99.1%
EFA200733	MBV102356	47%	97.4%	97.8%
EFA200733	MLP100469	47%	96.2%	95.6%
EFA200733	MTU200489	47%	97.4%	99.1%
EFA200733	PMU101887	38%	97.4%	98.3%
EFA200733	PRT100356	42%	97.4%	98.3%
EFA200733	PAE201156	40%	95.7%	94.9%
EFA200733	SPA101179	41%	96.2%	96.5%
EFA200733	STY103227	42%	97.4%	98.3%
EFA200733	STM100028	41%	96.2%	96.5%
EFA200733	SAU800018	70%	98.7%	98.3%
EFA200733	SEP201243	70%	97.4%	95.4%
EFA200733	SHA101255	71%	97.4%	95.8%
EFA200733	SMU100506	71%	98.3%	99.1%
EFA200733	SPN401106	70%	98.3%	92.4%
EFA200733	SPY200378	70%	98.3%	99.2%
EFA200733	YPS001580	43%	97.4%	98.3%
EFA200746	ABA104775	26%	35%	68.7%
EFA200746	BAN107854	29%	96.3%	99.8%
EFA200746	BAN111708	32%	88.5%	98.3%
EFA200746	EFA200746	100%	100%	100%
EFA200746	EFM202588	56%	100%	100%
EFA200746	LMO100335	36%	97.6%	96.8%
EFA200746	SAU800923	32%	96.7%	97.7%
EFA200746	SEP201474	31%	97.0%	97.9%
EFA200746	SHA100958	37%	50.9%	98.7%
EFA200746	SMU100022	37%	98.3%	98.6%
EFA200747	EFA200747	100%	100%	100%
EFA200747	EFM200896	82%	99.5%	100%
EFA200747	LMO100794	57%	98.1%	99.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200747	PAE203612	29%	18.1%	21.6%
EFA200747	SAU801275	46%	97.9%	98.9%
EFA200747	SEP201568	46%	97.9%	96.3%
EFA200747	SHA101100	46%	97.9%	97.0%
EFA200747	SMU100333	60%	97.5%	99.6%
EFA200747	SPN400538	60%	97.7%	99.8%
EFA200747	SPY200771	58%	97.5%	99.6%
EFA200747	VCH100261	25%	18.1%	20.7%
EFA200766	ABA105133	32%	92.5%	94.1%
EFA200766	BAN113695	40%	95.2%	95.9%
EFA200766	BAN110083	51%	97.6%	95.3%
EFA200766	BFR106048	33%	85.1%	86.2%
EFA200766	BMA108673	34%	73.3%	95.3%
EFA200766	CJU100651	36%	74.0%	73.1%
EFA200766	CAC103516	43%	98.1%	99.8%
EFA200766	CAC103116	43%	98.1%	99.5%
EFA200766	CBO101395	43%	98.1%	98.8%
EFA200766	CDF101858	45%	97.6%	97.6%
EFA200766	EBC107301	37%	65.8%	39.8%
EFA200766	EFA200766	100%	100%	100%
EFA200766	EFM201535	88%	98.8%	99.3%
EFA200766	ECO102040	34%	94.7%	94.3%
EFA200766	HIN100399	32%	95.2%	94.1%
EFA200766	HPY100166	33%	74.7%	73.5%
EFA200766	KPN300423	46%	11.3%	44.8%
EFA200766	KPN304482	34%	91.8%	91.6%
EFA200766	LMO102686	70%	98.6%	99.5%
EFA200766	MCA100567	31%	88.4%	92.0%
EFA200766	NGO100452	35%	92.3%	94.5%
EFA200766	NME201774	35%	92.3%	94.5%
EFA200766	PMU100233	32%	94.9%	94.1%
EFA200766	PRT102329	33%	91.6%	90.2%
EFA200766	PAE205435	34%	93.5%	88.8%
EFA200766	PPU111450	32%	95.7%	95.3%
EFA200766	PSY104961	36%	65.8%	38.9%
EFA200766	SPA104056	34%	91.8%	97.4%
EFA200766	STY104182	34%	95.7%	95.1%
EFA200766	STM103916	34%	95.7%	95.1%
EFA200766	SAU801612	51%	99.8%	98.1%
EFA200766	SEP201130	51%	99.8%	98.1%
EFA200766	SHA101196	50%	99.8%	99.5%
EFA200766	SMU100046	72%	98.6%	95.3%
EFA200766	SPN401281	67%	54.0%	92.5%
EFA200766	SPN401283	74%	99.8%	94.9%
EFA200766	SPY200427	72%	97.8%	94.6%
EFA200766	VCH100704	34%	91.3%	90.1%
EFA200766	YPS003165	32%	97.1%	94.0%
EFA200794	BAN112108	39%	82.3%	80.3%
EFA200794	BAN105533	40%	97.2%	97.6%
EFA200794	BPT101186	28%	52.8%	56%
EFA200794	CDF101053	32%	81.6%	77.5%
EFA200794	EFA200794	100%	100%	100%
EFA200794	EFM201900	59%	98.7%	99.7%
EFA200794	HIN100435	24%	83.9%	79.2%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200794	LPN103565	35%	48.1%	50.8%
EFA200794	LMO101540	38%	98.4%	99.1%
EFA200794	MCA101120	33%	67.1%	66.6%
EFA200794	NGO100045	31%	68.0%	68.6%
EFA200794	NME200903	36%	43.0%	44.9%
EFA200794	PMU101674	27%	71.5%	70.3%
EFA200794	PAE202959	35%	47.8%	45.7%
EFA200794	PPU104835	37%	48.1%	46.0%
EFA200794	PSY106959	33%	47.8%	45.7%
EFA200794	SPA100838	28%	57.0%	54.5%
EFA200794	SAU800484	27%	93.4%	97.7%
EFA200794	SEP201817	29%	93.4%	97.7%
EFA200794	SHA101458	29%	93.4%	97.7%
EFA200794	SMU100344	35%	96.2%	99.3%
EFA200794	SPN400836	35%	97.2%	98.6%
EFA200794	SPY200290	33%	95.9%	98.6%
EFA200794	VCH101985	32%	53.8%	52.8%
EFA200797	BFR101396	23%	34.6%	89.3%
EFA200797	BCE109516	30%	23.4%	55.2%
EFA200797	BFU110052	26%	32.9%	26.0%
EFA200797	EFA200797	100%	100%	100%
EFA200797	ECO101249	24%	17.7%	37.4%
EFA200797	KPN301095	26%	17.8%	36.6%
EFA200797	PRT105300	36%	13.6%	31.7%
EFA200797	SPA104362	24%	17.8%	37.5%
EFA200797	STY103053	26%	17.8%	37.4%
EFA200797	YPS000920	25%	18.2%	37.5%
EFA200805	ABA104003	47%	93.9%	99.2%
EFA200805	BAN107104	43%	82.4%	84.9%
EFA200805	BAN105134	73%	98.3%	99.7%
EFA200805	BFR12467	43%	91.2%	98.4%
EFA200805	BPT100051	47%	93.8%	98.5%
EFA200805	BBU100388	47%	94.5%	98.7%
EFA200805	BCE104307	45%	93.8%	99.1%
EFA200805	BFU100849	45%	80.6%	96.9%
EFA200805	BMA104886	45%	93.8%	99.1%
EFA200805	CJU100443	41%	94.3%	99.1%
EFA200805	CPN200682	47%	94.0%	98.7%
EFA200805	CTR200581	58%	7.3%	0.2%
EFA200805	CAC102610	65%	96.1%	94.8%
EFA200805	CBO100154	63%	99.1%	98.0%
EFA200805	CDF100552	62%	99.6%	98.2%
EFA200805	CDP100874	61%	0.9%	8.0%
EFA200805	EBC101233	47%	72.8%	93.7%
EFA200805	EFA200805	100%	100%	100%
EFA200805	EFM202205	94%	99.8%	99.5%
EFA200805	ECO103885	46%	94.1%	99.4%
EFA200805	HIN100494	45%	93.9%	99.3%
EFA200805	KPN302483	47%	89.2%	99.9%
EFA200805	LPN101720	65%	5.6%	95.7%
EFA200805	LMO101542	78%	96.0%	97.8%
EFA200805	MCA101003	44%	94.4%	99.3%
EFA200805	MAV102933	62%	1.7%	7.3%
EFA200805	MBV100910	61%	1.7%	7.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200805	MLP101145	61%	66.2%	71.4%
EFA200805	MTU200664	61%	1.7%	7.2%
EFA200805	MGE100350	48%	0.6%	6.2%
EFA200805	MPN100326	47%	0.5%	6.1%
EFA200805	NME200136	46%	93.8%	99.1%
EFA200805	PMU101737	45%	94.4%	99.4%
EFA200805	PAE204268	46%	93.9%	99.3%
EFA200805	PPU104497	44%	93.8%	99.1%
EFA200805	PSY103339	45%	93.8%	99.1%
EFA200805	SPA102792	59%	42.3%	78.8%
EFA200805	STY102671	46%	94.1%	99.4%
EFA200805	STM102058	46%	94.1%	99.4%
EFA200805	SAU800542	73%	98.1%	99.7%
EFA200805	SEP201886	73%	98.1%	99.7%
EFA200805	SHA101636	71%	93.8%	100%
EFA200805	SMU100556	77%	97.9%	99.4%
EFA200805	SPN401775	75%	99.5%	98.9%
EFA200805	SPY200071	76%	97.9%	99.3%
EFA200805	TPA100238	58%	2.1%	5.8%
EFA200805	UUR100187	45%	1.1%	7.5%
EFA200805	VCH100323	45%	94.1%	96.9%
EFA200805	YPS000489	46%	93.9%	99.3%
EFA200807	ABA100041	39%	11.1%	72.8%
EFA200807	ABA104621	52%	98.0%	97.3%
EFA200807	BAN107772	45%	98.2%	99.8%
EFA200807	BAN101907	76%	98.4%	99.8%
EFA200807	BFR102987	50%	96.7%	97.3%
EFA200807	BPT101163	52%	97.7%	96.4%
EFA200807	BBU100387	56%	97.6%	99.6%
EFA200807	BCE108518	62%	47.2%	96.7%
EFA200807	BFU100842	54%	80.2%	61.1%
EFA200807	BMA101246	52%	99.2%	97.7%
EFA200807	CJU100444	51%	97.1%	98.7%
EFA200807	CPN200681	51%	96.9%	96.9%
EFA200807	CTR200580	51%	96.9%	97.1%
EFA200807	CAC100576	63%	97.3%	98.1%
EFA200807	CBO100117	64%	98.3%	99.2%
EFA200807	CDF100550	63%	97.7%	99.8%
EFA200807	CDP100877	50%	5.7%	1.0%
EFA200807	EBC103916	49%	96.8%	96.2%
EFA200807	EFA200807	100%	100%	100%
EFA200807	EFM200070	89%	96.5%	100%
EFA200807	ECO103886	49%	99.4%	97.9%
EFA200807	HIN100493	52%	99.3%	98.1%
EFA200807	HPY101181	52%	96.7%	51.2%
EFA200807	KPN300484	41%	12.5%	88.9%
EFA200807	KPN302484	49%	96.8%	96.2%
EFA200807	LPN100508	65%	44.0%	98.7%
EFA200807	LMO101517	79%	98.8%	100%
EFA200807	MCA101004	52%	99.1%	97.0%
EFA200807	MAV102932	52%	6.0%	0.6%
EFA200807	MBV100906	52%	6.0%	0.6%
EFA200807	MLP101144	51%	6.0%	0.6%
EFA200807	MTU200665	52%	6.0%	0.6%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200807	MGE100349	46%	96.1%	97.2%
EFA200807	MPN100327	46%	96.1%	97.4%
EFA200807	NGO101637	54%	77.2%	38.2%
EFA200807	NME200135	51%	97.7%	98.1%
EFA200807	PMU101736	50%	98.8%	97.2%
EFA200807	PRT104687	55%	77.2%	41.2%
EFA200807	PAE204267	49%	98.8%	98.4%
EFA200807	PPU104498	49%	98.8%	97.7%
EFA200807	PSY103340	49%	98.8%	98.4%
EFA200807	SPA101954	39%	64.7%	100%
EFA200807	STY102668	48%	96.8%	96.2%
EFA200807	STM102060	48%	96.8%	96.2%
EFA200807	SAU800543	72%	98.8%	99.8%
EFA200807	SEP201887	73%	98.8%	100%
EFA200807	SHA100756	54%	6.7%	73.6%
EFA200807	SHA101637	73%	97.4%	98.5%
EFA200807	SMU100552	78%	99.0%	99.5%
EFA200807	SPN401774	77%	97.7%	97.1%
EFA200807	SPY200072	77%	99.3%	99.8%
EFA200807	TPA100239	56%	99.3%	99.1%
EFA200807	UUR100188	45%	96.2%	98.2%
EFA200807	VCH100324	52%	97.1%	96.8%
EFA200807	YPS000478	52%	99.4%	98.0%
EFA200811	ABA100676	55%	95.9%	98.6%
EFA200811	BAN101291	66%	97.3%	97.9%
EFA200811	BAN111521	66%	97.3%	97.9%
EFA200811	BFR11426	51%	97.9%	94.8%
EFA200811	BPT102861	51%	95.2%	97.9%
EFA200811	BBU100338	52%	92.5%	92.5%
EFA200811	BCE107311	58%	95.9%	79.5%
EFA200811	BFU103522	60%	95.9%	98.6%
EFA200811	BMA107182	59%	95.9%	78.2%
EFA200811	CJU101396	53%	91.1%	95.0%
EFA200811	CPN200505	44%	95.9%	94.6%
EFA200811	CTR200395	46%	95.2%	94%
EFA200811	CAC102148	52%	95.9%	97.2%
EFA200811	CBO103121	58%	95.9%	96.6%
EFA200811	CDF100062	54%	95.2%	97.2%
EFA200811	CDP100045	52%	95.9%	95.2%
EFA200811	EBC102180	58%	95.9%	98.6%
EFA200811	EFA200811	100%	100%	100%
EFA200811	EFM201491	95%	100%	83.0%
EFA200811	ECO103161	58%	95.9%	98.6%
EFA200811	HIN101412	59%	95.9%	98.6%
EFA200811	HPY100082	48%	91.1%	94.3%
EFA200811	KPN301994	56%	95.9%	98.6%
EFA200811	LPN102178	55%	95.9%	97.2%
EFA200811	LMO100177	76%	97.3%	97.9%
EFA200811	MCA103453	56%	96.6%	98.6%
EFA200811	MAV103415	60%	92.5%	91.8%
EFA200811	MBV101152	60%	92.5%	69.2%
EFA200811	MLP100232	59%	95.9%	95.2%
EFA200811	MTU203396	60%	92.5%	91.8%
EFA200811	MGE100428	42%	96.6%	97.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200811	MPN100225	45%	88.4%	88.4%
EFA200811	NGO101071	57%	95.9%	97.9%
EFA200811	NME200352	57%	95.9%	97.9%
EFA200811	PMU100520	56%	95.9%	98.6%
EFA200811	PRT100489	57%	95.9%	98.6%
EFA200811	PAE204431	58%	95.9%	98.6%
EFA200811	PFU105984	56%	95.9%	98.6%
EFA200811	PSY103838	58%	92.5%	95.1%
EFA200811	SPA100958	58%	95.9%	98.6%
EFA200811	STY101563	58%	95.9%	98.6%
EFA200811	SAU802218	69%	94.5%	95.2%
EFA200811	SEP202048	66%	94.5%	95.2%
EFA200811	SHA100040	74%	72.6%	94.6%
EFA200811	SMU101369	82%	100%	98.6%
EFA200811	SPN400271	82%	100%	98.6%
EFA200811	SPY201486	82%	100%	98.6%
EFA200811	TPA101015	48%	92.5%	95.1%
EFA200811	UUR100584	55%	89.0%	87.8%
EFA200811	VCH100560	57%	95.9%	98.6%
EFA200811	YPS002279	57%	95.9%	98.6%
EFA200812	ABA100673	53%	94.6%	96.1%
EFA200812	BAN112009	70%	100%	100%
EFA200812	BAN109246	71%	100%	100%
EFA200812	BFR11427	52%	93.1%	94.5%
EFA200812	BPT102858	52%	94.6%	94.6%
EFA200812	BBU100337	55%	94.6%	90.4%
EFA200812	BCE104886	52%	94.6%	94.6%
EFA200812	BFU103523	50%	94.6%	94.6%
EFA200812	BMA104857	52%	94.6%	94.6%
EFA200812	CJU101395	49%	93.8%	95.3%
EFA200812	CPN200506	54%	93.8%	91.8%
EFA200812	CTR200396	51%	93.8%	91.7%
EFA200812	CAC102494	64%	100%	100%
EFA200812	CBO103462	63%	100%	100%
EFA200812	CDF100063	61%	100%	100%
EFA200812	CDP100047	51%	93.1%	68.4%
EFA200812	EBC102179	52%	100%	100%
EFA200812	EFA200812	100%	100%	100%
EFA200812	EFM201820	96%	100%	100%
EFA200812	ECO103160	52%	100%	100%
EFA200812	HIN101411	50%	100%	100%
EFA200812	HPY100081	45%	93.8%	95.3%
EFA200812	KPN302005	52%	100%	100%
EFA200812	LPN102542	47%	96.9%	96.5%
EFA200812	LMO100441	74%	100%	100%
EFA200812	MCA100086	55%	94.6%	96.1%
EFA200812	MAV103416	54%	93.1%	72.9%
EFA200812	MBV101153	54%	93.1%	80.1%
EFA200812	MLP100233	53%	93.1%	79.1%
EFA200812	MTU203395	54%	93.1%	80.1%
EFA200812	MGE100427	44%	100%	100%
EFA200812	MPN100226	49%	100%	100%
EFA200812	NGO102668	58%	96.2%	96.2%
EFA200812	NME200353	58%	96.2%	96.2%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200812	PMU100521	53%	100%	100%
EFA200812	PRT100490	53%	100%	100%
EFA200812	PAE204430	54%	100%	100%
EFA200812	PPU105982	53%	100%	100%
EFA200812	PSY108021	54%	100%	100%
EFA200812	SPA100957	51%	100%	100%
EFA200812	STY101559	51%	100%	100%
EFA200812	SAU802217	72%	100%	100%
EFA200812	SEP202046	72%	100%	100%
EFA200812	SHA100041	73%	100%	100%
EFA200812	SMU101370	91%	100%	100%
EFA200812	SPN400272	89%	100%	100%
EFA200812	SPY201485	90%	100%	100%
EFA200812	TPA101014	54%	94.6%	95.3%
EFA200812	UUR100583	52%	97.7%	95.5%
EFA200812	VCH100561	51%	100%	100%
EFA200812	YPS002276	53%	100%	100%
EFA200829	ABA100810	27%	84.3%	85.6%
EFA200829	BAN105237	33%	94.7%	96.4%
EFA200829	BAN104566	51%	99.1%	99.3%
EFA200829	BFR11211	23%	79.3%	94.8%
EFA200829	BPT102727	25%	79%	82.6%
EFA200829	BBU100597	31%	92.3%	92.7%
EFA200829	BCE105021	34%	87%	92.9%
EFA200829	BFU110799	29%	46%	32.1%
EFA200829	BMA103015	26%	80%	78.7%
EFA200829	CJU101581	33%	61%	65.9%
EFA200829	CPN200851	34%	89.7%	87.5%
EFA200829	CTR200213	35%	92.3%	92.6%
EFA200829	CAC101781	47%	98.3%	96.7%
EFA200829	CBO101419	52%	95%	93.1%
EFA200829	CDF101126	43%	98%	93.1%
EFA200829	CDP100735	25%	87%	98.2%
EFA200829	EBC104194	28%	79.3%	83.9%
EFA200829	EFA200829	100%	100%	100%
EFA200829	EFM201956	74%	99.7%	96.1%
EFA200829	ECO103874	27%	82.3%	86.5%
EFA200829	HIN100255	27%	84.7%	88.9%
EFA200829	HPY101397	27%	78.7%	85.7%
EFA200829	KPN300758	27%	79.3%	83.9%
EFA200829	LPN101622	35%	96.7%	96.0%
EFA200829	LMO102057	57%	95.7%	96.3%
EFA200829	MCA100620	23%	78.3%	85.0%
EFA200829	MAV103805	24%	79.3%	82.0%
EFA200829	MBV102338	25%	79.3%	82.1%
EFA200829	MLP101458	24%	79.3%	81.7%
EFA200829	MTU200480	25%	79.3%	82.1%
EFA200829	NGO100898	27%	84.3%	89.0%
EFA200829	NME200943	27%	77.7%	83.2%
EFA200829	PMU101589	27%	89.3%	95.6%
EFA200829	PRT102712	27%	93.7%	96.5%
EFA200829	PAE202975	26%	86.7%	92.3%
EFA200829	PPU101791	26%	83.3%	89.4%
EFA200829	PSY101711	27%	86.7%	92.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200829	SPA103331	27%	81.3%	85.7%
EFA200829	STY102701	28%	81.3%	85.7%
EFA200829	STM102039	28%	81%	85.4%
EFA200829	SAU800738	52%	98.3%	96.1%
EFA200829	SEP200812	52%	99.3%	98.7%
EFA200829	SHA102002	55%	95.7%	93.5%
EFA200829	SMU100056	51%	99.7%	97.7%
EFA200829	SPN401246	55%	98.3%	93.4%
EFA200829	SPY200834	54%	98.3%	100%
EFA200829	TPA100089	28%	93.7%	92.9%
EFA200829	VCH100313	31%	60.7%	63.6%
EFA200829	YPS000538	26%	67.3%	72.2%
EFA200839	ABA106058	62%	100%	99.3%
EFA200839	BAN106044	77%	80.7%	99.1%
EFA200839	BFR10521	61%	100%	95.2%
EFA200839	BPT100048	59%	100%	98.6%
EFA200839	BBU100392	51%	98.6%	97.2%
EFA200839	BCE100591	60%	100%	98.6%
EFA200839	BFU104508	62%	100%	92.8%
EFA200839	BMA106139	61%	100%	98.6%
EFA200839	CJU100439	60%	97.9%	97.2%
EFA200839	CPN200686	61%	98.6%	97.9%
EFA200839	CTR200585	57%	98.6%	97.9%
EFA200839	CAC101038	72%	99.3%	98.6%
EFA200839	CBO102195	77%	100%	99.3%
EFA200839	CDF104047	78%	100%	99.3%
EFA200839	CDP100850	63%	98.6%	97.2%
EFA200839	EBC102886	65%	100%	99.3%
EFA200839	EFA200839	100%	100%	100%
EFA200839	ECO103881	65%	100%	99.3%
EFA200839	HIN100496	66%	100%	99.3%
EFA200839	HPY101185	61%	99.3%	98.6%
EFA200839	KPN300527	65%	100%	99.3%
EFA200839	LMO100036	84%	100%	99.3%
EFA200839	MCA100999	64%	100%	98.6%
EFA200839	MAV102318	68%	98.6%	97.2%
EFA200839	MBV103157	68%	98.6%	97.2%
EFA200839	MLP101154	66%	98.6%	97.2%
EFA200839	MTU200637	68%	98.6%	97.2%
EFA200839	MGE100083	50%	99.3%	98.5%
EFA200839	MPN100612	50%	99.3%	98.5%
EFA200839	NGO101667	59%	100%	97.9%
EFA200839	NME200140	59%	100%	97.9%
EFA200839	PMU101743	65%	100%	99.3%
EFA200839	PAE204272	62%	100%	98.6%
EFA200839	PPU104469	61%	100%	98.6%
EFA200839	PSY106552	60%	100%	95.9%
EFA200839	SPA107834	69%	62.9%	90.7%
EFA200839	STY102683	65%	100%	99.3%
EFA200839	STM102055	65%	100%	99.3%
EFA200839	SAU800537	85%	100%	100%
EFA200839	SEP201881	84%	100%	100%
EFA200839	SHA101488	84%	99.3%	98.6%
EFA200839	SMU101147	84%	99.3%	98.6%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200839	SPN400555	86%	99.3%	98.6%
EFA200839	SPY200329	85%	99.3%	98.6%
EFA200839	TPA100234	56%	98.6%	95.2%
EFA200839	UUR100547	49%	98.6%	89.3%
EFA200839	VCH100319	65%	100%	99.3%
EFA200839	YPS000498	66%	100%	99.3%
EFA200840	ABA104945	52%	98.3%	97.4%
EFA200840	BAN101496	74%	38.9%	94.7%
EFA200840	BAN103921	61%	98.3%	98.3%
EFA200840	BFR10522	50%	99.6%	98.3%
EFA200840	BPT100050	55%	99.6%	98.3%
EFA200840	BBU100391	47%	98.3%	98.2%
EFA200840	BCE101116	52%	99.6%	98.3%
EFA200840	BFU100848	53%	99.6%	98.3%
EFA200840	BMA108405	52%	99.6%	98.3%
EFA200840	CJU100440	54%	98.3%	96.6%
EFA200840	CPN200685	54%	98.3%	97.0%
EFA200840	CTR200584	54%	98.3%	97.0%
EFA200840	CAC102626	62%	96.1%	96.5%
EFA200840	CBO103496	63%	96.1%	96.5%
EFA200840	CDF100546	65%	99.1%	98.3%
EFA200840	CDP100852	56%	98.3%	95.7%
EFA200840	EBC102885	54%	99.1%	97.0%
EFA200840	EFA200840	100%	100%	100%
EFA200840	ECO103882	54%	99.1%	97.0%
EFA200840	HIN100495	52%	99.6%	99.6%
EFA200840	HPY101184	56%	98.3%	96.6%
EFA200840	KPN300590	57%	49.8%	91.1%
EFA200840	LMO100406	79%	99.6%	99.6%
EFA200840	MCA101000	51%	98.3%	96.6%
EFA200840	MAV102320	59%	98.3%	95.7%
EFA200840	MBV103159	58%	98.3%	99.1%
EFA200840	MLP101153	58%	98.3%	95.7%
EFA200840	MTU200638	59%	98.3%	95.7%
EFA200840	MGE100084	47%	97.8%	98.2%
EFA200840	MPN100611	50%	97.8%	98.2%
EFA200840	NGO101665	52%	99.6%	98.7%
EFA200840	NME200139	53%	99.6%	98.7%
EFA200840	PMU101742	51%	99.6%	99.6%
EFA200840	PAE204271	50%	99.6%	98.7%
EFA200840	PPU104471	50%	99.6%	98.7%
EFA200840	PSY103536	50%	99.6%	98.7%
EFA200840	SPA102795	54%	99.1%	97.0%
EFA200840	STY102680	54%	99.1%	97.0%
EFA200840	STM102056	54%	99.1%	97.0%
EFA200840	SAU800538	73%	100%	99.6%
EFA200840	SEP201882	72%	100%	99.1%
EFA200840	SHA101489	73%	100%	99.1%
EFA200840	SMU101145	75%	100%	100%
EFA200840	SPN400556	74%	98.3%	98.3%
EFA200840	SPY200330	75%	99.6%	99.6%
EFA200840	TPA100235	44%	96.9%	96.9%
EFA200840	UUR100546	48%	97.8%	97.8%
EFA200840	VCH100320	51%	98.7%	97.0%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200840	YPS000494	54%	99.1%	97.0%
EFA200841	ABA104908	38%	97.0%	97.0%
EFA200841	BAN101384	59%	95.8%	95.8%
EFA200841	BAN106254	59%	95.8%	95.8%
EFA200841	BFR101778	25%	89.8%	88.2%
EFA200841	BPT104548	37%	92.8%	87.9%
EFA200841	BBU100390	31%	96.4%	94.6%
EFA200841	BCE110567	39%	95.2%	95.2%
EFA200841	BFU104512	40%	93.4%	76.6%
EFA200841	BMA104533	39%	95.2%	85.3%
EFA200841	CJU100441	30%	94.6%	96.9%
EFA200841	CPN200684	26%	91.0%	89.4%
EFA200841	CTR200583	25%	91.0%	88.4%
EFA200841	CAC103420	43%	93.4%	92.3%
EFA200841	CBO103649	46%	93.4%	93.4%
EFA200841	CDF100545	45%	95.8%	90.9%
EFA200841	CDP100855	39%	87.3%	90.6%
EFA200841	EFA200841	100%	100%	100%
EFA200841	EFM100720	84%	98.2%	97.6%
EFA200841	ECO103883	34%	93.4%	94.5%
EFA200841	HIN100621	39%	95.2%	95.7%
EFA200841	HPY101183	33%	94.0%	93.9%
EFA200841	KPN304658	33%	93.4%	94.5%
EFA200841	LMO101102	63%	93.4%	93.4%
EFA200841	MCA101001	35%	95.2%	95.2%
EFA200841	MAV102938	41%	94.6%	85.2%
EFA200841	MBV100919	38%	97.6%	90.4%
EFA200841	MLP101148	39%	94.6%	94.4%
EFA200841	MTU200648	38%	97.6%	90.4%
EFA200841	MGE100371	36%	79.5%	82.1%
EFA200841	MPN100304	37%	91.6%	96.3%
EFA200841	NGO101663	37%	97.0%	97.6%
EFA200841	NME200138	37%	97.0%	97.6%
EFA200841	PMU101739	35%	95.2%	95.7%
EFA200841	PRT103043	34%	95.2%	95.8%
EFA200841	PAE204270	39%	95.2%	95.2%
EFA200841	PPU104473	36%	95.2%	81.0%
EFA200841	PSY103338	39%	95.2%	95.2%
EFA200841	SPA102794	33%	93.4%	94.5%
EFA200841	STY102677	33%	93.4%	94.5%
EFA200841	STM102057	33%	93.4%	94.5%
EFA200841	SAU800539	60%	98.2%	98.2%
EFA200841	SEP201883	60%	98.2%	98.2%
EFA200841	SHA101633	61%	98.2%	98.2%
EFA200841	SMU100974	73%	100%	99.4%
EFA200841	SPN401211	69%	100%	100%
EFA200841	SPY200814	71%	100%	100%
EFA200841	TPA100236	32%	98.8%	88.9%
EFA200841	UUR100008	38%	96.4%	96.4%
EFA200841	VCH100321	35%	93.4%	94.4%
EFA200841	YPS000491	32%	95.2%	95.8%
EFA200842	ABA105381	66%	69.7%	100%
EFA200842	BAN106592	60%	95.9%	97.5%
EFA200842	BAN112078	66%	95.9%	97.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200842	BFR106071	51%	97.5%	98.4%
EFA200842	BPT104549	65%	100%	100%
EFA200842	BBU100389	55%	100%	100%
EFA200842	BCE104254	67%	100%	100%
EFA200842	BFU104514	64%	100%	100%
EFA200842	BMA108492	66%	100%	100%
EFA200842	CJU100442	52%	100%	100%
EFA200842	CPN200683	45%	97.5%	95.3%
EFA200842	CTR200582	50%	97.5%	95.4%
EFA200842	CAC103770	61%	95.9%	97.6%
EFA200842	CBO100998	65%	95.9%	97.6%
EFA200842	CDF100554	64%	100%	99.2%
EFA200842	CDP100862	54%	98.4%	97.6%
EFA200842	EBC100455	60%	100%	100%
EFA200842	EFA200842	100%	100%	100%
EFA200842	EFM100721	87%	100%	100%
EFA200842	ECO103884	59%	100%	100%
EFA200842	HIN100622	63%	100%	100%
EFA200842	HPY101182	53%	100%	100%
EFA200842	KPN205542	57%	100%	100%
EFA200842	LMO102795	69%	100%	100%
EFA200842	MCA101002	60%	100%	100%
EFA200842	MAV102937	57%	98.4%	97.7%
EFA200842	MBV100917	56%	98.4%	97.7%
EFA200842	MLP101147	53%	98.4%	97.7%
EFA200842	MTU200649	56%	98.4%	97.7%
EFA200842	MGE100372	43%	98.4%	97.5%
EFA200842	MPN100303	44%	98.4%	97.5%
EFA200842	NGO101640	61%	100%	100%
EFA200842	NME200137	62%	100%	100%
EFA200842	PMU101738	55%	100%	100%
EFA200842	PRT100056	57%	100%	100%
EFA200842	PAE204269	65%	100%	100%
EFA200842	PPU104475	60%	100%	100%
EFA200842	PSY108092	68%	51.6%	98.4%
EFA200842	SPA107849	59%	100%	100%
EFA200842	STY102674	59%	100%	100%
EFA200842	STM107215	59%	100%	100%
EFA200842	SAU800540	64%	97.5%	98.4%
EFA200842	SEP201884	64%	97.5%	98.4%
EFA200842	SHA101634	63%	97.5%	98.4%
EFA200842	SMU100975	64%	100%	100%
EFA200842	SPN401210	68%	100%	96.1%
EFA200842	SPY200815	69%	100%	100%
EFA200842	TPA100237	52%	98.4%	97.7%
EFA200842	UUR100009	52%	95.9%	95.0%
EFA200842	VCH100322	65%	100%	100%
EFA200842	YPS005201	58%	95.9%	95.1%
EFA200894	BAN113200	65%	88.4%	99%
EFA200894	BAN103787	67%	94.2%	99.5%
EFA200894	CAC100985	55%	92.4%	79.0%
EFA200894	CBO102049	60%	88.4%	73.9%
EFA200894	CDF104297	57%	87.1%	70.7%
EFA200894	CDP101225	24%	74.6%	51.0%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200894	EFA200894	100%	100%	100%
EFA200894	LMO102016	70%	92.4%	93.2%
EFA200894	SAU801006	66%	90.2%	95.7%
EFA200894	SEP200232	64%	90.2%	95.7%
EFA200894	SHA100763	65%	90.2%	96.7%
EFA200894	SMU100221	64%	87.9%	89.1%
EFA200894	SPN401604	65%	89.7%	90.1%
EFA200894	SPY200855	64%	89.7%	90.1%
EFA200898	BAN108111	26%	40.4%	58.4%
EFA200898	BFR104427	29%	96.5%	98.4%
EFA200898	BPT102001	26%	98.2%	90.6%
EFA200898	BBU100379	30%	94.5%	95.8%
EFA200898	BFU108711	22%	25.8%	82%
EFA200898	BMA104773	26%	27.6%	77.3%
EFA200898	CPN200466	28%	88.5%	87.4%
EFA200898	CTR200459	27%	78.1%	74.5%
EFA200898	CAC103232	27%	49.4%	85.1%
EFA200898	CBO103653	29%	96.5%	96.9%
EFA200898	CDF103045	33%	96.2%	95.5%
EFA200898	CDP101052	28%	51.4%	51.9%
EFA200898	EBC100989	27%	89.8%	84.9%
EFA200898	EFA200898	100%	100%	100%
EFA200898	KPN301564	27%	91.4%	91.0%
EFA200898	MAV107258	23%	33.6%	47.1%
EFA200898	MAV107193	24%	52.3%	55.2%
EFA200898	MBV102187	31%	88.1%	90.4%
EFA200898	MTU200361	31%	88.1%	90.4%
EFA200898	NGO100524	29%	94.5%	88.2%
EFA200898	NME200413	30%	94.5%	88.2%
EFA200898	PRT101978	26%	94.9%	88.1%
EFA200898	PAE200912	25%	94.7%	89.2%
EFA200898	PPU101059	25%	96.2%	90.8%
EFA200898	PSY103108	25%	94.7%	91.5%
EFA200898	SAU801009	47%	99.8%	98.9%
EFA200898	SEP200235	48%	95.8%	94.4%
EFA200898	SHA100766	48%	96.9%	95.4%
EFA200898	TPA100907	31%	89.8%	93.8%
EFA200898	UUR100007	26%	80.1%	73.7%
EFA200898	VCH102497	27%	96.2%	96.0%
EFA200898	YPS003101	24%	97.6%	89.6%
EFA200916	BBU100585	20%	93.3%	93.1%
EFA200916	EFA200916	100%	100%	100%
EFA200916	ECO101716	26%	21.4%	23.9%
EFA200916	SMU101553	46%	100%	99.3%
EFA200916	SPN400540	38%	100%	99.8%
EFA200916	SPY200920	44%	99.0%	97.3%
EFA200958	ABA105050	36%	94.6%	97.5%
EFA200958	BAN105743	46%	83.1%	98.0%
EFA200958	BAN103527	57%	98.0%	99.3%
EFA200958	BPT101774	37%	95.6%	97.9%
EFA200958	BCE105719	38%	94.9%	94.0%
EFA200958	BFU103415	37%	95.6%	91.7%
EFA200958	BMA101496	38%	94.9%	95.6%
EFA200958	CAC100640	49%	94.9%	95.9%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA200958	CBO103526	48%	94.9%	95.9%
EFA200958	CDF101175	44%	96.3%	100%
EFA200958	CDP100284	40%	93.9%	94.2%
EFA200958	EBC104047	39%	95.9%	98.9%
EFA200958	EFA200958	100%	100%	100%
EFA200958	EFM102057	72%	17.3%	100%
EFA200958	ECO103135	39%	95.9%	98.9%
EFA200958	HIN101120	38%	98.3%	99.7%
EFA200958	KPN301883	38%	95.9%	98.9%
EFA200958	LMO101258	63%	97.3%	98.3%
EFA200958	MCA100868	38%	94.6%	95.6%
EFA200958	MAV100819	46%	94.9%	91.6%
EFA200958	MBV102154	44%	94.9%	93.4%
EFA200958	MLP100349	45%	94.9%	94.3%
EFA200958	MTU201402	44%	94.9%	93.4%
EFA200958	NGO101945	40%	94.6%	97.2%
EFA200958	NME200872	40%	94.6%	97.2%
EFA200958	PMU100169	40%	96.9%	98.6%
EFA200958	PRT101284	39%	95.9%	99.3%
EFA200958	PAE204463	40%	94.9%	99.0%
EFA200958	PPU103901	40%	94.9%	99.6%
EFA200958	PSY104751	40%	94.9%	99.3%
EFA200958	SPA101395	39%	95.9%	99.3%
EFA200958	STY101515	39%	95.9%	98.9%
EFA200958	STM101784	39%	95.9%	98.9%
EFA200958	SAU800765	50%	94.6%	93.4%
EFA200958	SEP201405	49%	94.6%	93.7%
EFA200958	SHA100647	48%	94.6%	94.6%
EFA200958	SMU100310	58%	99.3%	99.0%
EFA200958	SPN401423	58%	99.3%	99.0%
EFA200958	SPY200470	57%	99.3%	99.0%
EFA200958	VCH102495	39%	96.6%	99.7%
EFA200958	YPS002374	38%	96.3%	99.3%
EFA201009	ABA100755	39%	98.5%	92.7%
EFA201009	BAN102923	61%	97.6%	99.4%
EFA201009	BAN106149	63%	97.6%	97.6%
EFA201009	BFR12283	29%	90%	94.7%
EFA201009	BPT100880	37%	97.4%	96.6%
EFA201009	BBU100367	29%	90.9%	91.7%
EFA201009	BCE108622	30%	19.1%	84.4%
EFA201009	BCE112887	39%	97.1%	99.7%
EFA201009	BFU102699	39%	97.1%	97.6%
EFA201009	BMA100059	39%	84.4%	92.9%
EFA201009	CJU101121	31%	95%	98.0%
EFA201009	CPN200995	35%	97.9%	99.4%
EFA201009	CTR200087	34%	97.9%	99.4%
EFA201009	CAC100593	47%	97.6%	99.1%
EFA201009	CBO102206	48%	97.9%	97.3%
EFA201009	CDF103877	49%	97.9%	96.2%
EFA201009	CDP100269	43%	97.1%	97.6%
EFA201009	EBC103199	42%	96.8%	96.8%
EFA201009	EFA201009	100%	100%	100%
EFA201009	EFM202201	83%	99.4%	95.2%
EFA201009	ECO103530	42%	96.8%	96.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201009	HIN100585	42%	96.8%	97.9%
EFA201009	HPY100945	31%	95.6%	99.4%
EFA201009	KPN303398	41%	96.8%	96.8%
EFA201009	LPN100608	38%	97.6%	99.4%
EFA201009	LMO101105	58%	98.2%	98.8%
EFA201009	MCA100182	37%	97.9%	74.4%
EFA201009	MAV101851	38%	95%	93.8%
EFA201009	MBV102040	43%	96.8%	97.9%
EFA201009	MLP101025	40%	96.8%	96.3%
EFA201009	MTU202944	43%	96.8%	97.9%
EFA201009	NGO101070	39%	97.1%	99.7%
EFA201009	NME200349	39%	97.1%	99.7%
EFA201009	PMU101431	41%	96.8%	97.3%
EFA201009	PRT100958	41%	99.4%	100%
EFA201009	PAE201613	39%	98.5%	97.4%
EFA201009	PPU100025	40%	98.5%	97.1%
EFA201009	PSY106919	39%	98.5%	97.1%
EFA201009	SPA102938	41%	96.8%	96.8%
EFA201009	STY100361	41%	96.8%	96.8%
EFA201009	SAU801474	53%	97.1%	99.4%
EFA201009	SEP200460	54%	97.4%	99.7%
EFA201009	SHA101410	52%	97.1%	99.4%
EFA201009	SMU100645	62%	99.1%	99.4%
EFA201009	SPN401899	66%	98.8%	99.4%
EFA201009	SPY200164	63%	98.5%	99.1%
EFA201009	TPA100999	33%	94.7%	98.6%
EFA201009	UUR100385	27%	91.5%	95.4%
EFA201009	VCH102614	41%	97.1%	95.6%
EFA201009	YPS001566	43%	96.8%	96.8%
EFA201025	BAN101717	33%	70.4%	84.3%
EFA201025	BAN104028	48%	82.0%	96.7%
EFA201025	CAC101539	30%	82.0%	98.3%
EFA201025	CBO100610	30%	81.8%	98.3%
EFA201025	CDF100046	29%	81.8%	97.3%
EFA201025	CDP100495	31%	36.5%	38.9%
EFA201025	EBC101306	30%	65.7%	77.6%
EFA201025	EFA201025	100%	100%	100%
EFA201025	EFM100281	81%	73.5%	100%
EFA201025	ECO102045	27%	78.2%	90.6%
EFA201025	KPN304484	27%	73.8%	86.6%
EFA201025	LPN102533	26%	79.6%	96.7%
EFA201025	LMO101117	59%	84.0%	96.5%
EFA201025	MTU303433	30%	31.8%	36.8%
EFA201025	PRT102330	29%	65.7%	78.1%
EFA201025	PAE203021	30%	73.5%	85.1%
EFA201025	PPU103228	25%	73.5%	85.8%
EFA201025	PSY100248	30%	35.6%	92.6%
EFA201025	PSY102861	26%	82.0%	95.1%
EFA201025	SPA100769	25%	73.8%	86.9%
EFA201025	STM103922	26%	73.8%	87.0%
EFA201025	SAU801898	50%	84.8%	95.6%
EFA201025	SEP200546	50%	86.5%	97.2%
EFA201025	SHA101107	48%	90.6%	96.7%
EFA201025	SMU101024	59%	96.1%	96.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201025	SPY200551	61%	95.6%	97.6%
EFA201025	YPS003168	30%	73.5%	86.1%
EFA201028	ABA101192	49%	98.5%	96.9%
EFA201028	BAN113289	53%	97.1%	97.1%
EFA201028	BAN103118	72%	100%	100%
EFA201028	BPT102505	47%	99.4%	99.8%
EFA201028	BBU100340	40%	99.6%	99.6%
EFA201028	BCE113424	47%	75%	94.5%
EFA201028	BFU106894	46%	99.2%	98.6%
EFA201028	BMA107258	47%	98.9%	99.2%
EFA201028	CJU101122	45%	98.9%	99.6%
EFA201028	CPN200756	42%	99.6%	98.6%
EFA201028	CTR200267	41%	98.1%	97.1%
EFA201028	CAC103172	51%	100%	100%
EFA201028	CBO100777	54%	99.8%	99.8%
EFA201028	CDP100169	44%	99.2%	96.6%
EFA201028	EFA201028	100%	100%	100%
EFA201028	EFM100482	93%	22.9%	100%
EFA201028	HPY100650	45%	99.4%	99.6%
EFA201028	LPN102938	39%	99.4%	99.8%
EFA201028	LMO100253	77%	100%	100%
EFA201028	MCA100584	47%	98.5%	97.1%
EFA201028	MAV106350	41%	98.1%	95.0%
EFA201028	MBV101310	40%	98.5%	94.3%
EFA201028	MLP101041	39%	98.1%	93.9%
EFA201028	MTU202971	40%	98.5%	94.3%
EFA201028	MGE100102	34%	98.9%	98.5%
EFA201028	MPN100593	36%	98.9%	98.3%
EFA201028	NGO101113	46%	99.6%	100%
EFA201028	NME201429	46%	99.6%	100%
EFA201028	PAE204482	45%	99.4%	99.6%
EFA201028	PPU103969	45%	99.4%	99.6%
EFA201028	PSY104801	46%	99.4%	94.9%
EFA201028	STM101344	53%	5.9%	6.5%
EFA201028	SAU801899	72%	100%	100%
EFA201028	SEP200547	71%	100%	100%
EFA201028	SHA101106	71%	100%	100%
EFA201028	SMU101137	73%	99.8%	99.4%
EFA201028	SPN400393	68%	99.8%	99.2%
EFA201028	SPY201364	68%	99.8%	99.4%
EFA201028	TPA101011	37%	99.4%	94.9%
EFA201028	UUR100550	35%	99.6%	99.6%
EFA201041	ABA101195	48%	99.8%	99.8%
EFA201041	BAN102336	50%	97.8%	99.6%
EFA201041	BAN100349	65%	97.8%	99.0%
EFA201041	BPT102507	45%	97.1%	96.9%
EFA201041	BBU100341	38%	92.8%	91.9%
EFA201041	BCE103922	50%	98.0%	99.4%
EFA201041	BFU106893	51%	98.0%	99.4%
EFA201041	BMA103667	52%	98.0%	99.4%
EFA201041	CJU100987	47%	91.2%	95.1%
EFA201041	CPN200757	45%	99.0%	99.6%
EFA201041	CTR200266	45%	99.0%	98.6%
EFA201041	CAC102417	52%	97.8%	99.0%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201041	CBO102412	54%	95.7%	96.9%
EFA201041	CDP100148	48%	95.1%	96.4%
EFA201041	EBC101332	32%	96.5%	97.2%
EFA201041	EFA201041	100%	100%	100%
EFA201041	EFM100481	85%	98.6%	100%
EFA201041	HPY100817	47%	91.8%	98.2%
EFA201041	KPN302436	32%	95.9%	96.6%
EFA201041	LPN101348	47%	97.1%	98.3%
EFA201041	LMO101334	67%	98.0%	99.2%
EFA201041	MCA100258	49%	97.8%	98.4%
EFA201041	MAV101410	47%	96.9%	98.4%
EFA201041	MBV100289	47%	93.3%	94.7%
EFA201041	MLP101043	47%	93.9%	94.6%
EFA201041	MTU202973	47%	93.3%	94.7%
EFA201041	MGE100101	29%	97.8%	98.1%
EFA201041	MPN100594	32%	83.0%	86.4%
EFA201041	NGO101120	47%	97.1%	99.0%
EFA201041	NME201427	48%	97.1%	99.0%
EFA201041	PAE204481	51%	98.0%	99.2%
EFA201041	PPU101392	50%	98.0%	99.4%
EFA201041	PSY105880	48%	98.0%	99.4%
EFA201041	SAU801900	61%	96.5%	97.7%
EFA201041	SEP200550	62%	96.5%	97.7%
EFA201041	SHA100413	62%	75.9%	97.1%
EFA201041	SMU101138	69%	98.8%	99.0%
EFA201041	SPN400394	68%	99.0%	99.2%
EFA201041	SPY201365	69%	98.6%	98.8%
EFA201041	TPA101010	44%	84.3%	83.4%
EFA201041	UUR100551	30%	94.9%	97.3%
EFA201041	YPS002788	32%	95.3%	95.9%
EFA201047	ABA100577	42%	98.4%	98.8%
EFA201047	BAN102650	43%	96.6%	99.9%
EFA201047	BAN110615	59%	97.1%	99.1%
EFA201047	BFR102809	41%	96.0%	98.6%
EFA201047	BPT100689	42%	94.9%	96.7%
EFA201047	BBU100551	31%	96.2%	98.5%
EFA201047	BCE104345	47%	96.9%	97.5%
EFA201047	BFU101944	47%	97.9%	98.5%
EFA201047	BMA104881	46%	96.6%	97.3%
EFA201047	CJU100547	37%	94.1%	96.6%
EFA201047	CPN200612	40%	95.9%	97.7%
EFA201047	CTR200416	39%	95.6%	97.6%
EFA201047	CAC101086	38%	96.5%	99.1%
EFA201047	CAC101820	39%	95.7%	97.5%
EFA201047	CBO101063	39%	95.7%	98.2%
EFA201047	CDF103325	47%	96.5%	96.8%
EFA201047	CDP100142	38%	96.0%	97.3%
EFA201047	EBC101052	44%	96.0%	98.7%
EFA201047	EFA201047	100%	100%	100%
EFA201047	EFM100886	71%	31.4%	100%
EFA201047	ECO102362	45%	96.0%	98.4%
EFA201047	HIN101074	45%	96.9%	97.9%
EFA201047	HPY100608	38%	95.3%	97.3%
EFA201047	KPN300317	39%	24.0%	92.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201047	KPN301038	45%	96.0%	98.4%
EFA201047	LPN101707	43%	95.7%	97.8%
EFA201047	LMO102553	60%	96.5%	98.1%
EFA201047	MCA101464	43%	95.5%	94.5%
EFA201047	MAV101428	41%	95.2%	95.1%
EFA201047	MBV102830	40%	95.2%	95.4%
EFA201047	MLP101046	39%	95.2%	95.0%
EFA201047	MTU202976	40%	95.2%	95.4%
EFA201047	MGE100258	37%	95.5%	98.5%
EFA201047	MPN100479	39%	96.0%	99.2%
EFA201047	NGO100904	42%	96.5%	99.1%
EFA201047	NME200800	43%	96.9%	96.9%
EFA201047	PMU101716	45%	95.2%	97.0%
EFA201047	PRT102270	46%	96.5%	98.4%
EFA201047	PAE201528	44%	97.2%	98.6%
EFA201047	PPU107257	44%	96.9%	98.8%
EFA201047	PSY103902	41%	87.8%	97.9%
EFA201047	SPA103528	44%	96.0%	98.5%
EFA201047	STY101179	45%	96.3%	98.7%
EFA201047	SAU801904	56%	96.5%	98.4%
EFA201047	SEP200563	56%	96.2%	98.3%
EFA201047	SHA100321	56%	95.6%	99.7%
EFA201047	SMU101026	56%	95.5%	98.6%
EFA201047	SPN401024	56%	95.5%	98.6%
EFA201047	SPY200550	55%	95.5%	98.6%
EFA201047	TPA100627	28%	97.5%	78.1%
EFA201047	UUR100120	40%	95.0%	97.3%
EFA201047	VCH100955	44%	96.5%	99.0%
EFA201047	YPS000606	45%	96.0%	98.4%
EFA201084	ABA102248	39%	98.4%	57.7%
EFA201084	BAN113590	48%	99.3%	99.8%
EFA201084	BAN102128	63%	99.3%	99.6%
EFA201084	BPT101969	38%	97.4%	93.1%
EFA201084	BBU100557	36%	98.8%	97.9%
EFA201084	BCE105897	39%	94.4%	91.4%
EFA201084	BFU102716	39%	94.4%	91.5%
EFA201084	BMA107198	39%	94.4%	92.3%
EFA201084	CPN200725	25%	97.7%	96.1%
EFA201084	CTR200605	27%	97.0%	95.8%
EFA201084	CAC102388	51%	93.6%	99.3%
EFA201084	CBO103848	54%	93.6%	99.3%
EFA201084	CDF100789	55%	98.6%	98.8%
EFA201084	CDP100363	32%	96.3%	95.4%
EFA201084	EBC101637	49%	99.1%	99.6%
EFA201084	EFA201084	100%	100%	100%
EFA201084	EFM201634	93%	44.5%	99.2%
EFA201084	ECO102367	49%	99.1%	98.8%
EFA201084	HIN101677	50%	99.1%	98.8%
EFA201084	HPY100119	26%	66.1%	48.4%
EFA201084	KPN300705	49%	99.1%	98.8%
EFA201084	LPN100853	34%	93.6%	70.0%
EFA201084	LMO101249	69%	99.8%	99.7%
EFA201084	MCA100687	27%	65.7%	49.2%
EFA201084	MGE100439	45%	99.0%	98.1%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201084	MPN100215	48%	99.3%	98.4%
EFA201084	NGO101819	38%	94.1%	92.2%
EFA201084	NME200366	36%	99.5%	97.3%
EFA201084	PMU100897	49%	99.1%	98.8%
EFA201084	PRT102260	49%	99.5%	99.1%
EFA201084	PAE203560	39%	99.0%	57.7%
EFA201084	PPU109910	38%	99.0%	58%
EFA201084	PSY105138	39%	98.8%	57.7%
EFA201084	SPA101201	41%	99.1%	98.8%
EFA201084	STY104022	31%	96.3%	73.5%
EFA201084	STM101237	49%	99.1%	98.8%
EFA201084	SAU801084	63%	100%	100%
EFA201084	SEP200784	64%	100%	100%
EFA201084	SHA101356	65%	93.4%	100%
EFA201084	SMU100862	77%	99.7%	99.3%
EFA201084	SPN401062	78%	99.7%	99.3%
EFA201084	SPY201054	76%	99.7%	99.3%
EFA201084	VCH100949	48%	99.1%	99.1%
EFA201084	YPS000626	49%	99.3%	99.7%
EFA201087	ABA104415	31%	76.1%	75.3%
EFA201087	BAN108284	62%	97.7%	98.9%
EFA201087	BAN113302	63%	97.7%	98.9%
EFA201087	BPT101967	38%	87.5%	65.3%
EFA201087	BBU100556	36%	94.3%	100%
EFA201087	BCE109463	43%	92.0%	91.0%
EFA201087	BFU102715	41%	92.0%	91.0%
EFA201087	BMA101428	41%	92.0%	91.0%
EFA201087	CPN200726	39%	60.2%	49.1%
EFA201087	CTR200606	29%	84.1%	71.2%
EFA201087	CAC100614	46%	93.2%	95.3%
EFA201087	CBO101012	43%	93.2%	96.6%
EFA201087	CDF100787	43%	90.9%	93.0%
EFA201087	CDP100378	31%	89.8%	93.2%
EFA201087	EFA201087	100%	100%	100%
EFA201087	EFM100206	89%	100%	100%
EFA201087	HIN101678	37%	93.2%	100%
EFA201087	KPN300336	42%	95.5%	33.0%
EFA201087	LPN103186	41%	92.0%	91.0%
EFA201087	LMO101585	63%	100%	100%
EFA201087	MGE100041	46%	94.3%	95.5%
EFA201087	MPN100101	40%	94.3%	95.5%
EFA201087	NGO102690	38%	92.0%	91.0%
EFA201087	NME200365	39%	92.0%	91.0%
EFA201087	PMU100898	37%	93.2%	100%
EFA201087	PRT102262	40%	92.0%	95.3%
EFA201087	PPU103902	34%	92.0%	91.1%
EFA201087	PSY104754	34%	95.5%	94.4%
EFA201087	SPA100416	41%	95.5%	29.7%
EFA201087	STM101235	37%	92.0%	95.3%
EFA201087	SAU801083	64%	100%	100%
EFA201087	SEP200782	67%	100%	100%
EFA201087	SHA101355	68%	100%	100%
EFA201087	SMU103189	79%	98.9%	100%
EFA201087	SPN401063	79%	98.9%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201087	SPY201055	78%	98.9%	100%
EFA201087	TPA100582	42%	95.5%	95.5%
EFA201087	UUR100594	33%	97.7%	98.9%
EFA201087	VCH100950	34%	94.3%	97.6%
EFA201122	BCE109468	25%	26.3%	37.7%
EFA201122	CBO103578	59%	95.6%	97.2%
EFA201122	CDF103357	56%	96.0%	70.4%
EFA201122	EFA201122	100%	100%	100%
EFA201122	EFM200703	44%	95.3%	70.6%
EFA201122	KPN301965	58%	95.6%	99.3%
EFA201122	SPA103916	57%	95.6%	99.3%
EFA201122	STY100944	58%	95.6%	93.9%
EFA201122	STM101392	58%	95.6%	93.9%
EFA201122	SMU101447	69%	98.3%	99.4%
EFA201124	CBO101731	41%	98.7%	94.7%
EFA201124	EBC102987	29%	96.8%	97.1%
EFA201124	EFA201124	100%	100%	100%
EFA201124	ECO102127	32%	98.4%	97.8%
EFA201124	KPN300446	44%	36.0%	88.6%
EFA201124	KPN301962	37%	98.1%	98.7%
EFA201124	SPA103914	38%	98.7%	99.3%
EFA201124	STY100943	37%	98.7%	99.3%
EFA201124	STM101389	37%	98.7%	99.3%
EFA201124	SMU101446	56%	99.4%	99.0%
EFA201124	YPS001092	33%	93.8%	93.3%
EFA201155	ABA100567	46%	97.7%	99.8%
EFA201155	BAN113732	60%	71.0%	100%
EFA201155	BAN108180	68%	73.1%	100%
EFA201155	BFR10168	50%	81.1%	99.0%
EFA201155	BPT101335	47%	94.7%	97.9%
EFA201155	BBU100693	40%	91.9%	97.1%
EFA201155	BCE112884	46%	68.2%	99.1%
EFA201155	BFU115323	47%	93.9%	99.1%
EFA201155	BMA100755	46%	95.8%	99.3%
EFA201155	CJU100659	42%	93.6%	98.2%
EFA201155	CPN200646	39%	91.3%	96.2%
EFA201155	CTR200289	40%	94.1%	98.9%
EFA201155	CAC101092	55%	93.2%	98.4%
EFA201155	CBO101744	58%	95.8%	99.6%
EFA201155	CDF103672	59%	77.5%	95.1%
EFA201155	CDP101160	50%	100%	89.6%
EFA201155	EBC100407	51%	73.9%	94.6%
EFA201155	EFA201155	100%	100%	100%
EFA201155	EFM202293	90%	82.2%	99.7%
EFA201155	ECO102557	50%	95.1%	99.8%
EFA201155	HIN100105	50%	94.9%	97.6%
EFA201155	HPY101135	41%	90.9%	94.4%
EFA201155	KPN301264	51%	73.9%	94.4%
EFA201155	LPN101209	46%	96.4%	98.5%
EFA201155	LMO100196	62%	96.2%	97.8%
EFA201155	MCA100840	46%	95.6%	99.1%
EFA201155	MAV103395	50%	99.4%	89.6%
EFA201155	MBV102321	50%	95.8%	87.6%
EFA201155	MLP100989	48%	99.4%	88.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201155	MTU202878	50%	95.8%	87.6%
EFA201155	MGE100048	39%	90.5%	95.3%
EFA201155	MPN100093	40%	94.9%	98.7%
EFA201155	NGO101772	47%	95.3%	98.5%
EFA201155	NME202026	48%	95.3%	98.5%
EFA201155	PMU101183	51%	96.0%	99.1%
EFA201155	PRT100858	47%	95.1%	99.8%
EFA201155	PAE203743	49%	94.5%	99.1%
EFA201155	PPU107798	49%	95.3%	99.8%
EFA201155	PSY103783	48%	95.3%	99.8%
EFA201155	SPA101887	46%	74.4%	100%
EFA201155	STY102223	50%	95.1%	99.8%
EFA201155	STM103011	23%	19.9%	21.7%
EFA201155	SAU801237	58%	97.9%	98.7%
EFA201155	SEP201530	58%	97.9%	98.7%
EFA201155	SMU100253	65%	100%	99.2%
EFA201155	SPN401165	64%	100%	99.6%
EFA201155	SPY200915	64%	100%	99.6%
EFA201155	TPA100412	43%	90.5%	95.1%
EFA201155	UUR100090	43%	89.6%	94.2%
EFA201155	VCH100550	49%	95.6%	98.5%
EFA201155	YPS003448	50%	95.1%	99.8%
EFA201163	ABA100463	48%	81.3%	91.6%
EFA201163	BFR103669	58%	100%	42.9%
EFA201163	BPT101149	44%	79.1%	86.0%
EFA201163	BBU100694	54%	93.4%	98.8%
EFA201163	BCE101287	50%	81.3%	89.3%
EFA201163	BFU106133	50%	81.3%	68.2%
EFA201163	BMA105933	50%	81.3%	89.3%
EFA201163	CJU100660	51%	79.1%	96%
EFA201163	CPN200645	39%	83.5%	63.0%
EFA201163	CTR200290	35%	100%	79.3%
EFA201163	CAC102507	62%	87.9%	98.8%
EFA201163	CBO102241	60%	90.1%	96.5%
EFA201163	CDF104187	55%	98.9%	96.8%
EFA201163	CDP101155	43%	90.1%	52.2%
EFA201163	EFA201163	100%	100%	100%
EFA201163	ECO102556	47%	81.3%	92.7%
EFA201163	HIN100194	52%	81.3%	92.7%
EFA201163	HPY101134	45%	79.1%	94.7%
EFA201163	KPN203248	50%	74.7%	95.9%
EFA201163	LPN102433	47%	81.3%	88.4%
EFA201163	LMO101675	71%	95.6%	96.7%
EFA201163	MCA100471	51%	79.1%	90.2%
EFA201163	MAV103402	46%	90.1%	48.2%
EFA201163	MBV102277	43%	90.1%	50.6%
EFA201163	MLP100988	42%	90.1%	51.2%
EFA201163	MTU202871	43%	90.1%	50.6%
EFA201163	MGE100455	46%	91.2%	93.3%
EFA201163	MPN100182	45%	86.8%	89.8%
EFA201163	NGO102008	49%	82.4%	95.1%
EFA201163	NME200735	49%	82.4%	95.1%
EFA201163	PRT100822	54%	74.7%	72.9%
EFA201163	PAE203742	48%	79.1%	89.2%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201163	PPU107799	52%	81.3%	69.7%
EFA201163	PSY103786	43%	91.2%	92.9%
EFA201163	SPA101888	46%	81.3%	74.5%
EFA201163	STY102221	46%	81.3%	92.7%
EFA201163	SAU801238	65%	98.9%	100%
EFA201163	SEP201531	64%	98.9%	100%
EFA201163	SHA102521	80%	46.2%	82.4%
EFA201163	SMU100800	76%	100%	100%
EFA201163	SPN400682	80%	95.6%	96.7%
EFA201163	SPY200625	78%	95.6%	96.7%
EFA201163	TPA100895	56%	81.3%	61.0%
EFA201163	UUR100575	48%	97.8%	86.1%
EFA201163	VCH100551	52%	79.1%	90.2%
EFA201163	YPS003446	49%	82.4%	92.7%
EFA201165	BBU100695	39%	91.4%	90.2%
EFA201165	CJU100661	26%	91.4%	93.8%
EFA201165	CPN200025	43%	96.3%	100%
EFA201165	CTR200030	48%	93.8%	97.4%
EFA201165	CAC101280	38%	92.6%	100%
EFA201165	CBO100415	44%	92.6%	100%
EFA201165	CDF104379	48%	96.3%	100%
EFA201165	EFA201165	100%	100%	100%
EFA201165	HPY101133	28%	67.9%	48.7%
EFA201165	LMO100358	56%	93.8%	100%
EFA201165	MAV103400	28%	93.8%	91.2%
EFA201165	MBV102280	29%	96.3%	93.8%
EFA201165	MLP100987	27%	93.8%	91.2%
EFA201165	MTU202870	29%	96.3%	93.8%
EFA201165	SMU101983	53%	100%	97.5%
EFA201165	SPN400683	49%	100%	100%
EFA201165	SPY200626	53%	100%	100%
EFA201165	TPA100896	36%	92.6%	93.8%
EFA201204	ABA100431	36%	97.1%	98.7%
EFA201204	BAN104776	58%	98.4%	97.9%
EFA201204	BFU113278	34%	97.1%	89.7%
EFA201204	CTR200096	38%	95.5%	93.4%
EFA201204	CAC103133	47%	97.5%	97.5%
EFA201204	CBO100292	54%	96.7%	98.3%
EFA201204	CDF102819	53%	97.5%	97.9%
EFA201204	EBC102915	40%	95.5%	96.6%
EFA201204	EFA201204	100%	100%	100%
EFA201204	EFM200797	64%	98.0%	100%
EFA201204	ECO102142	41%	95.5%	98.3%
EFA201204	HIN101215	39%	96.7%	99.1%
EFA201204	KPN301779	41%	98.4%	97.9%
EFA201204	LMO101945	62%	98.0%	100%
EFA201204	MCA103178	36%	96.3%	99.6%
EFA201204	NGO100244	33%	92.6%	97.0%
EFA201204	NME201373	33%	92.6%	97.0%
EFA201204	PMU100003	39%	95.5%	97.8%
EFA201204	PRT101140	39%	96.7%	98.3%
EFA201204	PAE200732	38%	95.5%	98.7%
EFA201204	PPU103373	37%	95.5%	98.7%
EFA201204	SPA100233	41%	95.5%	98.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201204	STY104331	41%	95.5%	98.3%
EFA201204	SAU801753	47%	98.0%	100%
EFA201204	SEP202114	45%	97.1%	99.6%
EFA201204	SHA101326	48%	97.1%	99.6%
EFA201204	SPN400256	56%	97.1%	98.3%
EFA201204	SPY201026	53%	97.5%	97.1%
EFA201204	VCH101608	43%	96.7%	99.1%
EFA201204	YPS000335	40%	95.5%	96.6%
EFA201208	ABA100927	25%	89.2%	90.8%
EFA201208	BAN109007	28%	92.3%	97.5%
EFA201208	BAN102528	30%	79.3%	93.5%
EFA201208	BAN108968	31%	89.8%	94.1%
EFA201208	BAN109347	31%	92.3%	94.7%
EFA201208	BFR11372	28%	91.5%	94.8%
EFA201208	BBU100200	26%	86.8%	88.2%
EFA201208	BCE108649	27%	71.7%	92.6%
EFA201208	BFU100823	27%	87.8%	89.0%
EFA201208	BMA100072	29%	75.6%	75.7%
EFA201208	CJU101547	29%	81.7%	90.6%
EFA201208	CPN200331	32%	87.8%	90.9%
EFA201208	CTR200533	28%	82.3%	84.2%
EFA201208	CAC101131	27%	87.6%	91.3%
EFA201208	CAC103376	36%	91.9%	94.8%
EFA201208	CBO100064	33%	88.2%	91.7%
EFA201208	CDF102952	30%	88.8%	92.1%
EFA201208	CDP101281	29%	90.6%	95.5%
EFA201208	EBC102573	27%	82.7%	85.7%
EFA201208	EFA201208	100%	100%	100%
EFA201208	EFM201835	62%	99.6%	100%
EFA201208	ECO100085	27%	91.1%	94.7%
EFA201208	HIN101107	27%	91.7%	96.3%
EFA201208	HPY101473	28%	76.0%	83.9%
EFA201208	KPN301847	26%	82.7%	85.7%
EFA201208	LPN100418	39%	25.8%	79.6%
EFA201208	LMO101113	29%	88.2%	90.8%
EFA201208	MCA100819	27%	76.6%	73.7%
EFA201208	MAV104018	33%	79.5%	76.9%
EFA201208	MBV100072	32%	65.2%	74.5%
EFA201208	MLP100564	29%	83.3%	79.1%
EFA201208	MTU202124	32%	78.3%	73.6%
EFA201208	NGO100606	28%	81.3%	82.9%
EFA201208	NME201913	28%	81.3%	82.9%
EFA201208	PMU100137	26%	91.5%	95.1%
EFA201208	PRT102626	28%	89.8%	94.7%
EFA201208	PAE204415	28%	89.6%	93.0%
EFA201208	PPU105954	30%	88.4%	91.7%
EFA201208	PSY107311	29%	89.6%	93.0%
EFA201208	SPA102754	25%	89.0%	92.7%
EFA201208	STY103171	28%	89.0%	92.5%
EFA201208	STM102863	28%	89.0%	92.5%
EFA201208	SAU801018	27%	92.5%	94.5%
EFA201208	SEP200270	27%	92.1%	94.1%
EFA201208	SHA101090	27%	91.9%	93.9%
EFA201208	SMU100386	52%	90.9%	91.9%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201208	SPN401383	49%	98.8%	99.8%
EFA201208	SPY200283	50%	98.8%	99.8%
EFA201208	TPA100923	27%	86.8%	89.1%
EFA201208	VCH102371	26%	94.1%	93.2%
EFA201208	YPS000993	27%	88.6%	93.1%
EFA201312	ABA100914	31%	100%	95.4%
EFA201312	BAN112047	50%	93.8%	96.0%
EFA201312	BAN107884	51%	100%	100%
EFA201312	BFR11934	34%	99.0%	96.7%
EFA201312	BPT102002	31%	100%	92.9%
EFA201312	BBU100444	26%	92.4%	88.0%
EFA201312	BCE111090	32%	97.6%	92.3%
EFA201312	BFU111409	33%	100%	92.7%
EFA201312	BMA102172	32%	97.6%	92.3%
EFA201312	CJU100558	29%	99.0%	96.9%
EFA201312	CAC101944	58%	99.3%	99.7%
EFA201312	CBO101667	38%	99.3%	99.0%
EFA201312	CDF100408	37%	99.7%	99.6%
EFA201312	CDF101639	38%	100%	97.9%
EFA201312	CDP101376	28%	91.7%	91.3%
EFA201312	EBC103878	36%	99.7%	97.6%
EFA201312	EFA201312	100%	100%	100%
EFA201312	EFM201881	91%	59.5%	82.7%
EFA201312	ECO103069	37%	99.7%	99.0%
EFA201312	HIN100503	26%	96.5%	94.7%
EFA201312	HPY100173	36%	99.0%	99.3%
EFA201312	KPN306125	42%	99.0%	99.3%
EFA201312	LMO100774	51%	100%	100%
EFA201312	MCA100353	32%	100%	95.4%
EFA201312	MAV105904	30%	19.0%	17.6%
EFA201312	MBV102190	29%	92.0%	91.6%
EFA201312	MLP100198	29%	97.9%	96.2%
EFA201312	MTU200362	29%	92.0%	91.6%
EFA201312	MGE100023	51%	96.9%	97.2%
EFA201312	MPN100129	53%	99.3%	99.7%
EFA201312	NGO101574	32%	91.7%	86.2%
EFA201312	NME200544	32%	92.0%	86.4%
EFA201312	PMU101373	33%	100%	98.0%
EFA201312	PRT102752	37%	94.1%	94.0%
EFA201312	PAE200554	30%	100%	92.9%
EFA201312	PPU104672	31%	100%	94.3%
EFA201312	PSY100210	32%	100%	92.9%
EFA201312	SPA103912	38%	94.1%	94.0%
EFA201312	STY100942	38%	94.1%	94.0%
EFA201312	STM101386	38%	94.1%	94.0%
EFA201312	SAU802125	48%	100%	99.7%
EFA201312	SEP201915	48%	100%	99.7%
EFA201312	SHA101918	48%	100%	99.6%
EFA201312	SMU101408	69%	100%	100%
EFA201312	SPN400530	71%	100%	100%
EFA201312	SPY201455	70%	100%	100%
EFA201312	TPA100654	33%	99.3%	97.6%
EFA201312	UUR100603	50%	99.3%	98.6%
EFA201312	VCH100473	27%	95.5%	93.9%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201312	YPS000084	39%	99.7%	99.6%
EFA201375	ABA105021	27%	57.4%	76.1%
EFA201375	BAN112531	51%	72.1%	91.1%
EFA201375	BAN105862	50%	72.1%	93.6%
EFA201375	EFA201375	100%	100%	100%
EFA201375	EFM101838	71%	70.6%	100%
EFA201375	LMO102887	54%	72.1%	87.6%
EFA201375	SAU801446	40%	73.5%	96.5%
EFA201375	SEP200408	42%	73.5%	96.4%
EFA201375	SHA102651	40%	73.5%	96.4%
EFA201375	SMU101487	50%	77.9%	100%
EFA201375	SPN400332	46%	76.5%	91.2%
EFA201375	SPY201268	52%	77.9%	100%
EFA201379	ABA102299	53%	98.7%	98.5%
EFA201379	BAN109892	62%	98.7%	99.6%
EFA201379	BAN105788	76%	100%	100%
EFA201379	BFR11358	51%	98.7%	99.1%
EFA201379	BPT101706	51%	100%	99.3%
EFA201379	BBU100574	44%	98.5%	99.1%
EFA201379	BCE101396	52%	100%	99.3%
EFA201379	BFU102359	51%	100%	98.4%
EFA201379	BMA102378	51%	100%	99.1%
EFA201379	CJU100027	52%	98.7%	98.5%
EFA201379	CPN200516	48%	98.5%	97.8%
EFA201379	CTR200448	47%	98.5%	97.8%
EFA201379	CAC102177	62%	99.4%	99.4%
EFA201379	CBO103313	63%	99.3%	99.6%
EFA201379	EBC102296	54%	98.5%	98.0%
EFA201379	EFA201379	100%	100%	100%
EFA201379	EFM200622	90%	100%	100%
EFA201379	ECO102720	53%	98.5%	98.0%
EFA201379	HIN101052	55%	99.1%	98.5%
EFA201379	HPY100345	48%	98.7%	98.9%
EFA201379	KPN305112	54%	98.5%	92.9%
EFA201379	LPN101405	54%	100%	99.4%
EFA201379	LMO100139	73%	99.4%	100%
EFA201379	MCA101097	51%	99.6%	99.6%
EFA201379	MAV102050	54%	99.3%	92.8%
EFA201379	MBV105357	53%	92.7%	93.2%
EFA201379	MLP100845	53%	99.8%	92.2%
EFA201379	MTU201678	54%	99.3%	92.3%
EFA201379	NGO101273	51%	99.8%	100%
EFA201379	NME201601	51%	99.8%	100%
EFA201379	PMU101872	55%	99.4%	99.4%
EFA201379	PRT105301	56%	98.5%	98.0%
EFA201379	PAE203635	52%	98.9%	98.9%
EFA201379	PPU101175	53%	99.4%	99.4%
EFA201379	PSY108013	52%	99.6%	99.4%
EFA201379	SPA104183	52%	91.2%	100%
EFA201379	STY103510	54%	98.5%	98.0%
EFA201379	SAU802127	67%	100%	100%
EFA201379	SEP201917	67%	98.9%	99.1%
EFA201379	SHA101916	67%	98.7%	98.9%
EFA201379	SMU101407	78%	99.8%	99.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201379	SPN400438	79%	99.1%	99.3%
EFA201379	SPY201457	78%	99.3%	99.6%
EFA201379	TPA100302	45%	99.4%	99.1%
EFA201379	UUR100286	41%	99.6%	98.0%
EFA201379	VCH102412	54%	98.5%	98.0%
EFA201379	YPS000130	54%	98.5%	98.0%
EFA201401	ABA103339	32%	63.1%	63.4%
EFA201401	BAN112582	58%	100%	98.0%
EFA201401	BAN103160	70%	100%	97.1%
EFA201401	BFR104214	34%	44.2%	82.7%
EFA201401	BPT100459	33%	60.9%	61.5%
EFA201401	BCE103325	33%	60.9%	61.1%
EFA201401	BFU107045	33%	60.9%	61.1%
EFA201401	BMA103602	34%	60.9%	61.1%
EFA201401	CAC102377	54%	98.3%	96.6%
EFA201401	CBO103048	55%	99.1%	97.5%
EFA201401	CDF100334	54%	99.6%	97.5%
EFA201401	EBC102483	34%	61.8%	62.0%
EFA201401	EFA201401	100%	100%	100%
EFA201401	EFM200481	60%	100%	100%
EFA201401	ECO100166	34%	61.8%	62.0%
EFA201401	HIN101600	33%	61.8%	56.1%
EFA201401	KPN304185	33%	61.8%	62.2%
EFA201401	LPN101240	31%	60.9%	60.9%
EFA201401	LMO101801	67%	100%	98.7%
EFA201401	MCA102141	33%	63.9%	64.1%
EFA201401	NGO101587	32%	72.1%	74.7%
EFA201401	NME201990	32%	72.1%	74.7%
EFA201401	PMU100658	33%	61.8%	62.0%
EFA201401	PRT101208	33%	61.8%	62.0%
EFA201401	PAE203850	32%	51.1%	58.5%
EFA201401	PSY104618	36%	52.8%	54.0%
EFA201401	SPA102652	33%	61.8%	62.3%
EFA201401	STY103844	34%	61.8%	62.0%
EFA201401	SAU801397	62%	100%	97.5%
EFA201401	SEP202107	61%	100%	97.1%
EFA201401	SHA100970	62%	100%	97.5%
EFA201401	SMU100640	61%	100%	97.8%
EFA201401	SPN401904	62%	100%	97.8%
EFA201401	VCH100907	45%	40.3%	66.4%
EFA201401	YPS001119	34%	61.8%	62.0%
EFA201433	ABA103721	36%	77.8%	78.9%
EFA201433	BAN108866	41%	90.5%	100%
EFA201433	BAN105656	48%	97.1%	98.9%
EFA201433	BAN100164	48%	91.6%	90.6%
EFA201433	BAN103658	58%	97.1%	98.9%
EFA201433	BFR102236	37%	94.9%	95.7%
EFA201433	BPT101248	21%	45.1%	52.0%
EFA201433	BBU100100	24%	71.3%	72.8%
EFA201433	BCE107277	34%	70.5%	92.3%
EFA201433	BFU109172	32%	84.7%	90.7%
EFA201433	BMA106607	32%	93.5%	88.6%
EFA201433	CJU101558	34%	91.3%	98%
EFA201433	CAC101362	35%	79.6%	85.2%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201433	CBO102188	33%	79.3%	83.5%
EFA201433	CDF101024	42%	96.4%	98.5%
EFA201433	CDP101353	45%	92.4%	95.1%
EFA201433	EBC101695	31%	77.8%	83.1%
EFA201433	EFA201433	100%	100%	100%
EFA201433	EFM201002	70%	98.5%	97.8%
EFA201433	ECO103873	30%	77.8%	74.7%
EFA201433	HIN101705	34%	76.7%	78.8%
EFA201433	HPY100542	35%	90.5%	98.4%
EFA201433	KPN308897	30%	74.9%	86.0%
EFA201433	LPN100405	38%	96.7%	95.0%
EFA201433	LMO101688	57%	96.4%	99.2%
EFA201433	MCA100045	32%	85.5%	83.9%
EFA201433	MAV103533	42%	90.9%	92%
EFA201433	MBV101876	40%	94.5%	95.6%
EFA201433	MLP100726	40%	94.5%	96.0%
EFA201433	MTU201321	40%	94.5%	95.6%
EFA201433	NGO101679	37%	97.5%	98.9%
EFA201433	NME201872	38%	97.5%	98.9%
EFA201433	PMU100917	32%	82.5%	84.8%
EFA201433	PRT105607	31%	77.1%	74.7%
EFA201433	PAE204659	34%	89.1%	91.7%
EFA201433	PPU109719	34%	88.7%	91.3%
EFA201433	PSY106535	37%	77.8%	77.8%
EFA201433	SPA103848	43%	16%	35.5%
EFA201433	STY102718	31%	77.8%	83.1%
EFA201433	STM102035	31%	77.8%	76.3%
EFA201433	SAU801151	50%	91.3%	94.4%
EFA201433	SEP200875	50%	91.6%	94.4%
EFA201433	SHA100464	49%	91.6%	94.7%
EFA201433	SMU100491	61%	90.5%	93.9%
EFA201433	SPN401694	58%	90.5%	93.9%
EFA201433	SPY200261	59%	90.5%	93.9%
EFA201433	TPA100402	27%	72.4%	75%
EFA201433	VCH100156	33%	93.5%	91.7%
EFA201433	YPS001748	31%	77.1%	74.6%
EFA201457	ABA102495	35%	90.6%	100%
EFA201457	BAN109820	36%	78.7%	80.6%
EFA201457	BAN101919	46%	100%	99.9%
EFA201457	BFR11118	37%	100%	100%
EFA201457	BPT100285	31%	99.3%	99.1%
EFA201457	BBU100513	23%	36.1%	48.8%
EFA201457	BCE101979	32%	97.4%	97.4%
EFA201457	BFU107151	28%	43.4%	99.2%
EFA201457	BMA101914	31%	99.3%	99.1%
EFA201457	CJU100827	27%	98.9%	99.0%
EFA201457	CPN200152	27%	95.5%	95.1%
EFA201457	CTR200749	29%	98.1%	97.7%
EFA201457	CAC101148	34%	100%	100%
EFA201457	CBO103321	37%	100%	99.9%
EFA201457	CDF100484	38%	32.8%	100%
EFA201457	CDF103760	35%	100%	99.7%
EFA201457	CDP100987	31%	97.4%	97.4%
EFA201457	EBC102988	36%	72.2%	99.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201457	EFA201457	100%	100%	100%
EFA201457	EFM200867	72%	100%	100%
EFA201457	ECO101681	35%	100%	99.9%
EFA201457	HIN101278	36%	100%	99.9%
EFA201457	HPY100398	26%	100%	99.9%
EFA201457	KPN301695	35%	100%	99.9%
EFA201457	LPN100643	33%	100%	99.9%
EFA201457	LMO101759	47%	100%	100%
EFA201457	MCA100197	35%	100%	99.9%
EFA201457	MAV106542	29%	100%	99.9%
EFA201457	MBV101271	29%	74.3%	93.7%
EFA201457	MLP100870	28%	99.3%	99.0%
EFA201457	MTU201629	28%	99.3%	99.2%
EFA201457	MGE100197	23%	89.6%	89.6%
EFA201457	MPN100048	24%	98.9%	99.8%
EFA201457	NGO101903	36%	98.4%	98.3%
EFA201457	NME200861	35%	98.4%	98.3%
EFA201457	PMU100629	36%	100%	99.9%
EFA201457	PRT101304	34%	100%	99.9%
EFA201457	PAE202737	34%	100%	99.9%
EFA201457	PPU103715	33%	100%	99.9%
EFA201457	PSY100068	32%	100%	99.9%
EFA201457	SPA100516	35%	77.3%	98.9%
EFA201457	STY101114	35%	100%	99.9%
EFA201457	STM103450	35%	100%	99.9%
EFA201457	SAU801139	45%	99.6%	99.8%
EFA201457	SEP200864	45%	100%	100%
EFA201457	SHA100442	48%	62.5%	94.9%
EFA201457	SMU100476	60%	5.7%	100%
EFA201457	SMU100483	56%	100%	100%
EFA201457	SPN400509	57%	100%	100%
EFA201457	SPY200565	55%	100%	100%
EFA201457	TPA100014	25%	38.5%	49.5%
EFA201457	UUR100462	23%	92.2%	93.0%
EFA201457	VCH101201	34%	98.9%	98.7%
EFA201457	YPS003055	34%	100%	99.9%
EFA201460	ABA105548	22%	68.7%	69.3%
EFA201460	BAN111196	33%	97.8%	99.9%
EFA201460	BAN105909	37%	98.7%	99.9%
EFA201460	BBU100632	22%	67.9%	69.1%
EFA201460	BMA105524	21%	93.2%	91.2%
EFA201460	CTR200007	23%	94.9%	95.4%
EFA201460	CAC103739	31%	97.7%	99.4%
EFA201460	CBO101540	33%	97.2%	99.1%
EFA201460	CDF102097	31%	97.1%	99.2%
EFA201460	EBC102605	22%	18.9%	17.3%
EFA201460	EFA201460	100%	100%	100%
EFA201460	EFM200194	56%	98.3%	99.6%
EFA201460	ECO102757	21%	67.3%	66.9%
EFA201460	KPN305144	22%	21.4%	21.4%
EFA201460	LPN101834	24%	22.1%	34.4%
EFA201460	LMO102657	38%	98.8%	99.7%
EFA201460	PRT102297	21%	67.3%	65.6%
EFA201460	PAE204282	22%	67.7%	67.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201460	PPU101093	22%	67.7%	67.2%
EFA201460	PSY102740	23%	67.7%	67.4%
EFA201460	SAU800967	32%	98.2%	99.8%
EFA201460	SEP200182	32%	98.3%	99.3%
EFA201460	SHA101673	32%	97.1%	98.0%
EFA201460	SMU100467	32%	97.1%	97.0%
EFA201460	SPN401040	33%	96.9%	96.9%
EFA201460	SPY200572	30%	97.7%	97.6%
EFA201506	BAN101235	49%	100%	100%
EFA201506	BAN102202	70%	100%	98.8%
EFA201506	BFR11955	43%	100%	100%
EFA201506	BBU100503	43%	99.2%	99.8%
EFA201506	CJU101134	44%	99.8%	100%
EFA201506	CAC102280	58%	99.2%	98.8%
EFA201506	CBO100216	48%	45.2%	99.1%
EFA201506	CDF100051	80%	21.8%	93.4%
EFA201506	CDF100869	59%	99.4%	97.7%
EFA201506	EFA201506	100%	100%	100%
EFA201506	EFM100483	88%	97.9%	100%
EFA201506	ECO201319	29%	18.0%	31.4%
EFA201506	ECO201260	31%	15.8%	35.8%
EFA201506	HPY100747	38%	84.4%	93.5%
EFA201506	LMO101581	73%	100%	99.6%
EFA201506	MGE100132	29%	46.3%	49.8%
EFA201506	MPN100564	24%	68.3%	70.4%
EFA201506	PSY102419	23%	25.1%	40.5%
EFA201506	SAU801286	65%	99.8%	99.6%
EFA201506	SEP201589	64%	99.8%	99.6%
EFA201506	SHA101288	65%	99.8%	99.6%
EFA201506	SMU101495	61%	99.8%	100%
EFA201506	SPN401582	59%	99.8%	99.6%
EFA201506	SPY201258	60%	99.8%	100%
EFA201506	TPA101008	47%	100%	100%
EFA201506	UUR100083	32%	84.6%	92.2%
EFA201507	BAN112473	63%	37.7%	100%
EFA201507	BAN113311	51%	58.5%	100%
EFA201507	BAN107300	64%	100%	100%
EFA201507	BBU100504	38%	96.6%	97.7%
EFA201507	EFA201507	100%	100%	100%
EFA201507	EFM201335	81%	100%	100%
EFA201507	LMO102094	66%	99.2%	98.9%
EFA201507	MGE100250	37%	98.1%	94.0%
EFA201507	MPN100487	36%	98.9%	94.7%
EFA201507	SAU801288	59%	99.2%	98.9%
EFA201507	SEP201596	58%	99.6%	99.6%
EFA201507	SHA101290	58%	100%	100%
EFA201507	UUR100505	38%	97.7%	99.6%
EFA201512	ABA100157	49%	95.7%	100%
EFA201512	BAN112499	75%	46.1%	97.4%
EFA201512	BAN106136	50%	97.2%	99.4%
EFA201512	BAN101660	70%	98.5%	99.7%
EFA201512	BFR10407	48%	94.1%	95.8%
EFA201512	BPT100617	54%	95.0%	97.2%
EFA201512	BBU100543	29%	87.6%	76.6%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201512	BCE112713	54%	98.5%	99.1%
EFA201512	BFU100079	55%	95.7%	97.2%
EFA201512	BMA100055	56%	95.7%	97.2%
EFA201512	CJU100848	52%	95.4%	98.4%
EFA201512	CAC100050	58%	96.0%	97.2%
EFA201512	CBO100851	61%	96.0%	97.5%
EFA201512	CDF100459	64%	95.7%	97.8%
EFA201512	CDP100215	45%	96.0%	95.4%
EFA201512	EBC101345	50%	96.6%	99.4%
EFA201512	EFA201512	100%	100%	100%
EFA201512	EFM200023	93%	100%	100%
EFA201512	ECO101180	50%	96.6%	99.4%
EFA201512	HIN101576	51%	96.3%	99.4%
EFA201512	HPY100730	51%	95.4%	95.6%
EFA201512	KPN303464	50%	96.6%	99.4%
EFA201512	LPN101587	49%	95.7%	98.4%
EFA201512	LMO100583	75%	98.8%	100%
EFA201512	MCA100701	47%	96.0%	98.7%
EFA201512	MAV105952	45%	98.8%	99.1%
EFA201512	MBV105572	45%	95.4%	98.7%
EFA201512	MLP100179	44%	96.0%	95.4%
EFA201512	MTU201006	45%	98.8%	99.1%
EFA201512	MGE100060	46%	86.4%	94.9%
EFA201512	MPN100082	45%	95.4%	75.8%
EFA201512	NGO101084	52%	95.7%	94.5%
EFA201512	NME201007	52%	95.7%	94.5%
EFA201512	PMU100244	50%	96.3%	99.4%
EFA201512	PRT101362	50%	96.6%	99.4%
EFA201512	PAE204667	50%	96.0%	99.0%
EFA201512	PPU104089	51%	75.9%	99.6%
EFA201512	PSY102431	49%	96.0%	99.0%
EFA201512	SPA100616	49%	96.6%	99.7%
EFA201512	STY101673	50%	96.6%	99.4%
EFA201512	STM101478	50%	96.6%	99.4%
EFA201512	SAU800500	68%	98.8%	99.7%
EFA201512	SEP201833	67%	98.8%	99.7%
EFA201512	SHA100895	70%	70.3%	99.6%
EFA201512	SMU101229	72%	96.0%	96.9%
EFA201512	SPN400028	73%	97.2%	93.2%
EFA201512	SPY200014	73%	96.9%	98.4%
EFA201512	TPA100291	30%	87.3%	74.1%
EFA201512	UUR100193	46%	91.3%	89.7%
EFA201512	VCH102150	51%	96.3%	99.4%
EFA201512	YPS003242	50%	96.6%	99.4%
EFA201523	BFU107317	30%	81.4%	93.2%
EFA201523	EFA201523	100%	100%	100%
EFA201523	EFM201546	28%	81.6%	94.1%
EFA201523	MBV105206	36%	83.3%	57.5%
EFA201523	MTU201973	36%	83.3%	57.5%
EFA201523	PRT101425	52%	88.6%	89.5%
EFA201523	PAE109042	27%	10.8%	39.4%
EFA201601	ABA102251	41%	76.7%	90.2%
EFA201601	BAN106145	55%	69.2%	100%
EFA201601	BAN102864	60%	72.9%	97.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201601	BFR103244	46%	69.9%	96.6%
EFA201601	BPT103145	44%	72.6%	53.0%
EFA201601	BBU100076	39%	63.8%	96.8%
EFA201601	BCE109396	43%	73.8%	92.3%
EFA201601	BFU100592	38%	91.0%	90.2%
EFA201601	BMA103170	37%	97.7%	91.2%
EFA201601	CJU101131	40%	66.7%	95.1%
EFA201601	CPN200871	37%	65.8%	97.2%
EFA201601	CTR200202	37%	64.7%	96.8%
EFA201601	CAC103551	51%	68.3%	98.0%
EFA201601	CBO103745	50%	68.3%	98.0%
EFA201601	CDF101891	43%	95.5%	95.8%
EFA201601	CDP101168	39%	91.6%	80.0%
EFA201601	EBC104170	39%	98.2%	97.7%
EFA201601	EFA201601	100%	100%	100%
EFA201601	EFM200001	86%	2.3%	32.5%
EFA201601	ECO103387	41%	93.2%	85.1%
EFA201601	HIN100748	42%	82.6%	88.2%
EFA201601	HPY100750	39%	59.7%	86.7%
EFA201601	KPN308256	38%	95.5%	94.1%
EFA201601	LMO101591	66%	70.1%	94.2%
EFA201601	MCA101469	42%	68.3%	95.5%
EFA201601	MAV103813	41%	84.4%	83.9%
EFA201601	MBV100063	33%	75.1%	91.0%
EFA201601	MLP100992	40%	90.7%	90.5%
EFA201601	MTU202883	38%	91.4%	91.2%
EFA201601	MGE100303	41%	73.1%	93.4%
EFA201601	MPN100416	43%	72.4%	92.0%
EFA201601	NME200274	37%	97.7%	98.8%
EFA201601	PMU101519	40%	95.5%	89.5%
EFA201601	PRT100781	42%	31.4%	3.8%
EFA201601	PAE200372	39%	96.8%	93.4%
EFA201601	PPU102117	38%	93.4%	81.6%
EFA201601	PSY102772	42%	86.4%	72.3%
EFA201601	SPA100292	52%	47.1%	83.5%
EFA201601	STY101273	40%	96.4%	88.6%
EFA201601	SAU801235	48%	99.5%	94.0%
EFA201601	SEP201528	47%	99.5%	94.9%
EFA201601	SHA101742	53%	84.8%	92.6%
EFA201601	SMU100011	49%	97.3%	84.1%
EFA201601	SPN401122	52%	99.3%	100%
EFA201601	SPY200409	48%	97.1%	82.4%
EFA201601	TPA100571	40%	65.4%	96.3%
EFA201601	UUR100140	42%	74.9%	96.6%
EFA201601	VCH100146	42%	86.4%	93.6%
EFA201601	YPS000724	39%	97.5%	84.5%
EFA201611	ABA104194	46%	97.0%	100%
EFA201611	BAN100780	55%	98.8%	98.2%
EFA201611	BAN104280	65%	98.4%	97.5%
EFA201611	BPT102115	45%	97.7%	99.5%
EFA201611	BBU100471	33%	97.5%	96.6%
EFA201611	BCE107676	46%	91.0%	99.7%
EFA201611	BFU102916	47%	97.0%	91.8%
EFA201611	BMA104589	46%	96.8%	92.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201611	CJU100797	43%	95.4%	98.3%
EFA201611	CTR200730	37%	94.2%	96.6%
EFA201611	CAC103585	50%	96.8%	99.8%
EFA201611	CBO100954	54%	97.0%	100%
EFA201611	CDF100485	56%	30.9%	100%
EFA201611	CDF102163	57%	97.2%	98.6%
EFA201611	CDP101476	44%	96.5%	99.0%
EFA201611	EFA201611	100%	100%	100%
EFA201611	EFM201945	84%	99.8%	99.8%
EFA201611	ECO103119	48%	95.6%	98.3%
EFA201611	HIN101057	49%	94.7%	96.7%
EFA201611	HPY100640	43%	95.6%	98.3%
EFA201611	KPN301069	48%	95.6%	98.3%
EFA201611	LPN103006	46%	97.2%	99.8%
EFA201611	LMO101018	69%	98.2%	98.1%
EFA201611	MCA100762	46%	94.9%	97.9%
EFA201611	MAV102894	43%	52.0%	99.6%
EFA201611	MBV100208	45%	96.5%	99.0%
EFA201611	MLP100716	44%	96.5%	99.0%
EFA201611	MTU201298	45%	96.5%	99.0%
EFA201611	NGO102024	46%	94.9%	97.8%
EFA201611	NME200242	47%	94.9%	97.8%
EFA201611	PMU100180	48%	96.3%	98.1%
EFA201611	PAE204448	48%	96.8%	99.5%
EFA201611	PPU109849	47%	96.8%	99.5%
EFA201611	PSY104793	45%	88.2%	98.7%
EFA201611	SPA100481	46%	44.1%	100%
EFA201611	STY101491	48%	95.6%	98.3%
EFA201611	SAU802100	58%	83.8%	94.8%
EFA201611	SEP202410	61%	97.0%	99.8%
EFA201611	SHA101060	60%	77.8%	100%
EFA201611	SMU100515	68%	97.5%	100%
EFA201611	SPN401779	65%	97.5%	99.5%
EFA201611	SPY200561	65%	97.2%	99.8%
EFA201611	TPA100028	32%	94.2%	97.4%
EFA201637	ABA100552	25%	80.7%	94.4%
EFA201637	BPT101760	26%	78.3%	93.1%
EFA201637	BCE110544	32%	47.5%	84.5%
EFA201637	BFU105355	27%	71.5%	83.2%
EFA201637	BMA108998	27%	75.0%	88.7%
EFA201637	CPN201063	30%	6.2%	20.5%
EFA201637	CBO101137	58%	99.9%	98.8%
EFA201637	CDF104440	58%	99.9%	100%
EFA201637	EFA201637	100%	100%	100%
EFA201637	ECO102802	30%	79.2%	97.9%
EFA201637	MCA101640	35%	6.5%	25%
EFA201637	MBV100418	28%	76.5%	91.1%
EFA201637	MTU200372	28%	76.5%	91.1%
EFA201637	PAE201522	24%	72.9%	84.1%
EFA201637	PPU107262	24%	73.2%	86.8%
EFA201637	PSY103891	23%	72.9%	84.8%
EFA201637	SAU801149	32%	4.6%	45.5%
EFA201637	TPA100078	23%	42.6%	47.7%
EFA201645	ABA101872	24%	56.8%	50.9%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201645	BPT102102	21%	56.5%	37.4%
EFA201645	CBO101032	42%	92.3%	91.9%
EFA201645	CBO101859	42%	97.2%	95.3%
EFA201645	CDF100557	43%	91.2%	89.1%
EFA201645	EBC103454	32%	20.7%	42.8%
EFA201645	EFA201645	100%	100%	100%
EFA201645	LPN100916	24%	85.6%	91.5%
EFA201645	PRT105013	27%	50.9%	67.4%
EFA201645	PAE200544	25%	33.3%	22.1%
EFA201645	PPU108658	25%	49.8%	22.0%
EFA201645	PSY102151	29%	32.3%	36.9%
EFA201645	STY102026	27%	75.4%	81.2%
EFA201645	STM101769	28%	75.4%	81.2%
EFA201645	TPA100728	50%	92.6%	95%
EFA201645	YPS001677	24%	57.5%	69.8%
EFA201646	ABA100945	35%	94.3%	94.5%
EFA201646	BFR11247	51%	93.4%	57.7%
EFA201646	BPT102078	29%	94.9%	22.4%
EFA201646	BCE114722	33%	89.0%	89.0%
EFA201646	BFU108232	34%	90.0%	90.4%
EFA201646	BMA109760	30%	95.3%	91.9%
EFA201646	CJU100009	28%	94.3%	95.4%
EFA201646	CAC102748	36%	90.3%	97.6%
EFA201646	CBO101098	57%	96.2%	96.4%
EFA201646	CBO102837	58%	97.7%	99.3%
EFA201646	CDF102919	55%	97.2%	98.5%
EFA201646	EBC105166	33%	94.3%	95.1%
EFA201646	EFA201646	100%	100%	100%
EFA201646	ECO102823	36%	92.4%	68.5%
EFA201646	ECO102419	35%	93.0%	67.4%
EFA201646	KPN306735	37%	8.7%	20.2%
EFA201646	LMO100374	27%	96.2%	96.3%
EFA201646	MCA102847	25%	34.1%	20.7%
EFA201646	MAV104921	30%	94.1%	89.3%
EFA201646	MBV101949	30%	96.2%	93.6%
EFA201646	MLP100043	29%	94.1%	91.8%
EFA201646	MTU203803	30%	96.2%	93.6%
EFA201646	PRT105231	33%	96.2%	95.9%
EFA201646	PAE205030	36%	93.9%	93.1%
EFA201646	PPU102730	36%	94.1%	94.3%
EFA201646	PSY103728	35%	93.9%	94.1%
EFA201646	SPA100761	34%	94.3%	97.6%
EFA201646	STY101535	34%	94.3%	95.1%
EFA201646	STM101814	34%	94.3%	95.1%
EFA201646	SAU800473	28%	92.2%	92.6%
EFA201646	SEP201791	26%	96.8%	97.1%
EFA201646	SHA103074	28%	96.4%	96.7%
EFA201646	SMU101812	31%	98.3%	97.5%
EFA201646	TPA100727	42%	97.0%	89.4%
EFA201646	VCH102342	36%	94.1%	94.7%
EFA201646	YPS003815	36%	94.3%	95.1%
EFA201699	BCE110252	34%	68.0%	32.9%
EFA201699	BFU111005	29%	18.8%	36.7%
EFA201699	BFU103784	25%	20.3%	10.2%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201699	EBC103370	32%	15.7%	32.2%
EFA201699	EFA201699	100%	100%	100%
EFA201699	EFM200673	57%	99.7%	99.6%
EFA201699	KPN307953	24%	63.1%	31.1%
EFA201699	PAE201090	26%	89.2%	35.7%
EFA201699	PPU108292	36%	0.4%	32.1%
EFA201699	PSY104048	48%	80.4%	36.7%
EFA201699	VCH101614	30%	7.3%	19.1%
EFA201699	YPS001628	28%	28.5%	81.0%
EFA201749	ABA103622	38%	100%	100%
EFA201749	BAN106917	40%	100%	100%
EFA201749	BAN102903	57%	100%	100%
EFA201749	BFR105590	50%	8.3%	33.6%
EFA201749	BPT101720	37%	100%	100%
EFA201749	BCE109254	38%	100%	100%
EFA201749	BFU109440	43%	17.6%	78.6%
EFA201749	BFU103182	38%	100%	100%
EFA201749	BMA102722	38%	100%	100%
EFA201749	CJU101290	36%	100%	100%
EFA201749	CPN200876	38%	100%	100%
EFA201749	CTR200198	39%	100%	100%
EFA201749	CAC103586	43%	100%	100%
EFA201749	CBO102655	43%	100%	100%
EFA201749	CDF100284	42%	100%	100%
EFA201749	CDP100523	41%	96.2%	100%
EFA201749	EBC104245	39%	100%	100%
EFA201749	EFA201749	100%	100%	100%
EFA201749	EFM100811	66%	100%	100%
EFA201749	ECO103650	39%	100%	100%
EFA201749	HIN100409	40%	100%	100%
EFA201749	HPY101510	34%	100%	100%
EFA201749	KPN300721	40%	100%	100%
EFA201749	LPN102850	37%	100%	100%
EFA201749	LMO101794	59%	100%	100%
EFA201749	MCA103570	37%	100%	100%
EFA201749	MAV105640	38%	100%	96.1%
EFA201749	MBV101159	39%	97.2%	100%
EFA201749	MLP100237	38%	100%	100%
EFA201749	MTU203389	39%	100%	100%
EFA201749	NGO101887	38%	100%	100%
EFA201749	NME200260	38%	100%	100%
EFA201749	PMU101731	40%	100%	100%
EFA201749	PRT104794	40%	100%	100%
EFA201749	PAE205544	39%	100%	100%
EFA201749	PPU102151	40%	100%	100%
EFA201749	PSY103460	39%	100%	100%
EFA201749	SPA101582	36%	100%	100%
EFA201749	STY103864	40%	100%	100%
EFA201749	SAU802154	58%	100%	100%
EFA201749	SEP201962	59%	100%	100%
EFA201749	SHA100979	59%	100%	100%
EFA201749	SMU101007	60%	100%	100%
EFA201749	SPN400245	63%	100%	100%
EFA201749	SPY200983	59%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201749	TPA100852	35%	100%	100%
EFA201749	VCH100482	37%	100%	100%
EFA201749	YPS003544	40%	100%	100%
EFA201801	BAN110308	43%	90.7%	92.0%
EFA201801	BAN106306	58%	97.7%	98.6%
EFA201801	EFA201801	100%	100%	100%
EFA201801	EFM100902	78%	99.4%	99.9%
EFA201801	LMO102776	58%	97.3%	96.9%
EFA201801	MGE100206	40%	89.6%	92.2%
EFA201801	MPN100031	38%	91.2%	93.9%
EFA201801	SAU801355	56%	97.7%	99.2%
EFA201801	SEP202031	55%	97.2%	98.8%
EFA201801	SHA100827	56%	96.6%	99.7%
EFA201801	SMU101036	60%	95.7%	98.8%
EFA201801	SPN400757	59%	98.9%	99.3%
EFA201801	SPY200681	59%	97.3%	99.0%
EFA201801	UUR100472	40%	87.4%	84%
EFA201826	ABA104082	28%	92.8%	90.4%
EFA201826	BAN105157	34%	97.0%	99.5%
EFA201826	BAN107229	40%	98.5%	98.5%
EFA201826	BCE115108	26%	96.5%	91.8%
EFA201826	BFU107730	27%	89.1%	85.8%
EFA201826	BMA109379	24%	91.6%	90.9%
EFA201826	EBC101035	25%	87.8%	86.2%
EFA201826	EFA201826	100%	100%	100%
EFA201826	ECO101082	26%	88.6%	85.3%
EFA201826	LMO100421	43%	99.8%	99.8%
EFA201826	PMU101477	28%	28.0%	25.2%
EFA201826	PPU108176	26%	91.1%	89.6%
EFA201826	SPA102808	26%	92.3%	90.1%
EFA201826	STY102547	26%	88.6%	85.3%
EFA201826	STM102737	27%	88.6%	85.3%
EFA201826	SAU800941	40%	98.8%	99.3%
EFA201826	SEP201510	40%	98.8%	93.2%
EFA201826	SHA100915	38%	70.0%	100%
EFA201827	ABA100229	40%	64.7%	56.9%
EFA201827	BAN107161	30%	54.3%	99.8%
EFA201827	BAN107699	56%	34.0%	98.5%
EFA201827	BAN102783	46%	98.6%	99.9%
EFA201827	BFR11263	36%	80.7%	80.1%
EFA201827	BPT102660	39%	80.7%	78.3%
EFA201827	BBU100256	47%	55.4%	56.7%
EFA201827	BCE101034	39%	80.8%	80.6%
EFA201827	BFU100730	39%	80.8%	74.9%
EFA201827	BMA101290	46%	62.5%	92.3%
EFA201827	CJU100817	39%	74.7%	65.5%
EFA201827	CPN200970	43%	63.2%	63.4%
EFA201827	CTR200112	35%	93.2%	93.7%
EFA201827	CAC101785	40%	96.8%	96.5%
EFA201827	CBO100656	42%	97.8%	98.4%
EFA201827	CDF100864	40%	96.8%	98.3%
EFA201827	CDP100424	35%	95.9%	86.7%
EFA201827	EBC100487	38%	60.0%	69.0%
EFA201827	EFA201827	100%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201827	EFM200744	68%	99.9%	99.5%
EFA201827	ECO100865	42%	65.6%	41.8%
EFA201827	HIN101559	45%	56.8%	90.7%
EFA201827	HPY101073	39%	72.1%	68.2%
EFA201827	KPN307601	48%	30.1%	97.4%
EFA201827	LPN100195	42%	68.0%	75.8%
EFA201827	LMO102030	51%	98.3%	99.6%
EFA201827	MCA100556	41%	57.2%	99.4%
EFA201827	MAV100073	46%	65.2%	72.2%
EFA201827	MBV103355	46%	62.0%	66.0%
EFA201827	MLP100598	46%	64.3%	60.8%
EFA201827	MTU202711	46%	62.0%	57.3%
EFA201827	NGO100195	39%	79.8%	76.0%
EFA201827	NME201387	40%	79.8%	80.4%
EFA201827	PMU100255	42%	70.4%	61.9%
EFA201827	PRT100386	43%	66.9%	61.3%
EFA201827	PAE202613	38%	83.1%	83.6%
EFA201827	PPU100858	40%	79.8%	84.4%
EFA201827	PSY104186	39%	79.8%	82.7%
EFA201827	SPA103466	45%	57.6%	95.3%
EFA201827	STY102893	42%	65.2%	41.6%
EFA201827	STM102713	42%	65.2%	41.4%
EFA201827	SAU801276	45%	98.9%	99.5%
EFA201827	SEP201569	46%	98.9%	99.5%
EFA201827	SHA101101	44%	96.5%	99.9%
EFA201827	SMU101151	49%	97.5%	99.2%
EFA201827	SPN400781	50%	97.5%	99.7%
EFA201827	SPY200327	50%	97.6%	99.3%
EFA201827	TPA100989	49%	57.7%	58.1%
EFA201827	UUR100513	24%	28.3%	28.7%
EFA201827	VCH101873	45%	57.7%	51.0%
EFA201827	YPS001224	43%	65.9%	42.8%
EFA201867	EFA201867	100%	100%	100%
EFA201867	SMU100125	32%	94.4%	97.5%
EFA201867	SPY201027	30%	96.0%	98.3%
EFA201869	ABA105939	35%	47.3%	40.7%
EFA201869	BAN107872	44%	94.3%	98.5%
EFA201869	BAN102524	45%	94.3%	96.7%
EFA201869	BFR104611	37%	46.6%	41.0%
EFA201869	BPT101657	35%	49.5%	45.7%
EFA201869	BBU100705	31%	91.9%	92.4%
EFA201869	BCE100092	27%	96.3%	79.7%
EFA201869	BFU102642	26%	96.3%	77.1%
EFA201869	BMA109607	31%	64.8%	53.6%
EFA201869	CJU100728	31%	44.3%	47.3%
EFA201869	CPN201005	30%	97.5%	99.0%
EFA201869	CTR200077	32%	93.6%	95.6%
EFA201869	CAC100065	21%	95.3%	92.6%
EFA201869	CBO100682	43%	53.7%	49.6%
EFA201869	CDF103451	31%	94.1%	95.5%
EFA201869	CDP101606	36%	51.7%	43.8%
EFA201869	EBC102069	33%	48.8%	46.0%
EFA201869	EFA201869	100%	100%	100%
EFA201869	ECO100143	33%	51.0%	50%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201869	HIN100062	35%	49.8%	47.3%
EFA201869	HPY100632	42%	46.1%	47.5%
EFA201869	KPN308697	32%	50.7%	51.8%
EFA201869	LPN103037	38%	48.0%	47.8%
EFA201869	LMO102472	44%	93.6%	95.9%
EFA201869	MCA100864	34%	54.7%	36.2%
EFA201869	MAV103429	29%	91.4%	88.8%
EFA201869	MBV106184	27%	99.3%	97.9%
EFA201869	MLP101592	28%	98.8%	97.1%
EFA201869	MTU203852	27%	99.3%	97.9%
EFA201869	NGO100973	38%	48.3%	44.7%
EFA201869	NME200969	37%	48.3%	43.9%
EFA201869	PMU100864	36%	48.8%	41.7%
EFA201869	PRT102520	36%	48.3%	46.6%
EFA201869	PAE204723	34%	53.2%	48.8%
EFA201869	PPU108737	36%	51.2%	47.1%
EFA201869	PSY105160	35%	51.7%	46.9%
EFA201869	SPA104027	35%	49.8%	47.1%
EFA201869	STY103428	35%	49.8%	45.1%
EFA201869	STM101254	32%	60.3%	59.6%
EFA201869	SAU801457	37%	95.1%	97%
EFA201869	SEP200430	37%	95.1%	97%
EFA201869	SHA101762	37%	95.8%	97.8%
EFA201869	SMU100881	50%	97.0%	99.5%
EFA201869	SPN401412	49%	98.5%	100%
EFA201869	SPY200644	46%	97.0%	99.2%
EFA201869	TPA100267	32%	94.6%	96.9%
EFA201869	VCH100583	37%	48.8%	45.7%
EFA201869	YPS000784	35%	48.3%	47.7%
EFA201878	ABA105360	30%	99.2%	95.6%
EFA201878	BAN102900	46%	99.6%	98.5%
EFA201878	BAN107078	51%	99.6%	98.5%
EFA201878	BFR10828	28%	92.7%	90.9%
EFA201878	BPT102724	28%	99.2%	96.7%
EFA201878	BCE105684	33%	99.6%	98.9%
EFA201878	BMA108656	30%	95.4%	98.8%
EFA201878	CJU100185	27%	100%	99.2%
EFA201878	CPN200790	25%	90.0%	81.8%
EFA201878	CTR200633	28%	74.9%	74.8%
EFA201878	CAC100895	26%	100%	99.2%
EFA201878	CBO102353	30%	99.6%	99.2%
EFA201878	CDF100169	34%	45.6%	95%
EFA201878	CDF103888	27%	100%	99.6%
EFA201878	CDF101971	30%	100%	99.6%
EFA201878	CDP100444	43%	99.6%	98.4%
EFA201878	EBC102147	29%	99.6%	96.3%
EFA201878	EFA201878	100%	100%	100%
EFA201878	EFM201574	27%	96.1%	94.5%
EFA201878	ECO100031	30%	99.6%	96.3%
EFA201878	HIN101274	30%	99.6%	97.4%
EFA201878	HPY100505	26%	73.7%	73.6%
EFA201878	KPN306527	30%	99.6%	96.3%
EFA201878	LPN103391	45%	99.2%	98.8%
EFA201878	LMO101881	60%	99.6%	99.6%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201878	MCA102220	30%	99.6%	97.7%
EFA201878	MAV101194	42%	99.6%	98.8%
EFA201878	MBV101254	42%	99.6%	98.8%
EFA201878	MTU202735	43%	99.6%	98.8%
EFA201878	NGO100748	29%	99.6%	97.0%
EFA201878	NME200061	29%	99.6%	97.0%
EFA201878	PMU100726	29%	99.6%	97.4%
EFA201878	PRT101653	31%	75.3%	71.4%
EFA201878	PAE204755	29%	100%	98.9%
EFA201878	PPU111382	33%	75.3%	92.0%
EFA201878	PSY104750	28%	100%	98.8%
EFA201878	SPA101380	33%	75.3%	71.7%
EFA201878	STY101155	29%	99.6%	96.3%
EFA201878	STM100870	29%	99.6%	96.3%
EFA201878	SAU801396	25%	99.2%	100%
EFA201878	SEP202106	25%	97.3%	97.9%
EFA201878	SHA100969	25%	99.2%	100%
EFA201878	SMU100878	61%	99.6%	99.2%
EFA201878	SPN401413	63%	99.6%	99.2%
EFA201878	VCH102356	29%	100%	98.1%
EFA201878	YPS000815	28%	99.6%	96.3%
EFA201883	ABA103631	57%	96.7%	97.8%
EFA201883	BAN110875	78%	97.8%	98.9%
EFA201883	BFR100422	50%	97.8%	98.9%
EFA201883	BPT100124	53%	96.7%	97.8%
EFA201883	BBU100231	32%	95.6%	86.1%
EFA201883	BCE110670	58%	97.8%	98.9%
EFA201883	BFU100991	53%	96.7%	97.8%
EFA201883	BMA101790	50%	96.7%	95.7%
EFA201883	CJU100843	56%	95.6%	88.8%
EFA201883	CPN200333	25%	96.7%	89%
EFA201883	CTR200531	24%	96.7%	89%
EFA201883	CAC100114	57%	96.7%	96.7%
EFA201883	CBO102675	56%	96.7%	78.6%
EFA201883	CDF102299	57%	96.7%	96.7%
EFA201883	EBC102270	55%	96.7%	97.8%
EFA201883	EFA201883	100%	100%	100%
EFA201883	EFM100184	90%	100%	92.9%
EFA201883	ECO100432	55%	96.7%	97.8%
EFA201883	HIN100410	64%	97.8%	65.4%
EFA201883	HPY100822	38%	97.8%	95.7%
EFA201883	KPN302503	56%	97.8%	98.9%
EFA201883	LPN101041	38%	93.4%	95.5%
EFA201883	LMO100364	74%	100%	100%
EFA201883	MCA101444	57%	96.7%	97.8%
EFA201883	MAV101405	45%	96.7%	41.5%
EFA201883	MBV102079	46%	96.7%	41.1%
EFA201883	MLP101029	46%	96.7%	44%
EFA201883	MTU202948	46%	96.7%	41.1%
EFA201883	NGO100251	48%	96.7%	98.9%
EFA201883	NME201722	47%	96.7%	96.7%
EFA201883	NME201276	50%	96.7%	98.9%
EFA201883	PMU101732	62%	97.8%	98.9%
EFA201883	PRT101499	60%	96.7%	91.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201883	PAE201803	56%	96.7%	97.8%
EFA201883	PPU111425	54%	96.7%	97.8%
EFA201883	PSY108978	52%	96.7%	97.8%
EFA201883	SPA102996	56%	96.7%	97.8%
EFA201883	STY100727	56%	96.7%	97.8%
EFA201883	STM100440	56%	96.7%	97.8%
EFA201883	SAU801473	78%	97.8%	98.9%
EFA201883	SEP200458	78%	97.8%	98.9%
EFA201883	SHA101411	77%	97.8%	98.9%
EFA201883	SMU100719	80%	100%	100%
EFA201883	SPN401020	75%	100%	100%
EFA201883	SPY201144	82%	100%	100%
EFA201883	TPA100248	32%	93.4%	81.0%
EFA201883	UUR100284	28%	95.6%	66.9%
EFA201883	VCH100270	55%	97.8%	98.9%
EFA201883	YPS001873	53%	96.7%	97.8%
EFA201884	ABA100688	41%	97.9%	91.0%
EFA201884	BAN111369	58%	99.8%	100%
EFA201884	BAN112079	70%	99.8%	99.8%
EFA201884	BFR10077	47%	28.4%	72.5%
EFA201884	BPT100007	39%	97.9%	96.2%
EFA201884	BBU100507	33%	77.8%	35.6%
EFA201884	BCE100856	36%	26.6%	65.6%
EFA201884	BFU105505	37%	97.9%	96.6%
EFA201884	BMA102074	37%	97.9%	96.6%
EFA201884	CJU100354	35%	98.9%	97.8%
EFA201884	CPN201006	33%	71.1%	27.9%
EFA201884	CTR200076	33%	80.7%	33.9%
EFA201884	CAC100098	53%	100%	99.8%
EFA201884	CBO101866	51%	100%	99.5%
EFA201884	CDF102465	53%	99.8%	98.9%
EFA201884	CDP101065	39%	67.4%	21.8%
EFA201884	EBC102035	38%	97.9%	92.4%
EFA201884	EFA201884	100%	100%	100%
EFA201884	ECO102462	38%	97.9%	90.1%
EFA201884	HIN100129	37%	98.9%	93.1%
EFA201884	HPY100821	36%	99.1%	96.9%
EFA201884	KPN305977	38%	97.9%	92.5%
EFA201884	LPN101429	39%	97.9%	92.0%
EFA201884	LMO102523	74%	100%	100%
EFA201884	MCA101523	40%	97.9%	90.7%
EFA201884	MAV102019	40%	99.3%	92.3%
EFA201884	MBV105348	37%	69.5%	27.6%
EFA201884	MLP100852	39%	99.3%	93.1%
EFA201884	MTU201691	37%	69.5%	27.6%
EFA201884	MGE100337	43%	27.1%	66.5%
EFA201884	MPN100366	42%	7.8%	47.9%
EFA201884	NGO101003	41%	27.3%	60.8%
EFA201884	NME200978	41%	27.3%	60.8%
EFA201884	PMU100105	35%	98.9%	93.1%
EFA201884	PRT102921	37%	97.9%	92.5%
EFA201884	PAE203796	39%	97.9%	90.9%
EFA201884	PPU112339	40%	97.9%	91.0%
EFA201884	PSY106808	48%	68.6%	83.2%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201884	PSY103809	41%	97.9%	90.3%
EFA201884	SPA102739	38%	97.9%	90.2%
EFA201884	STY101715	38%	97.9%	92.4%
EFA201884	SAU801475	68%	99.8%	99.8%
EFA201884	SEP200461	68%	99.8%	99.8%
EFA201884	SHA101409	69%	99.8%	99.8%
EFA201884	SMU101355	78%	100%	100%
EFA201884	SPN401552	78%	100%	100%
EFA201884	SPY200248	77%	100%	100%
EFA201884	TPA100681	33%	98.9%	94.6%
EFA201884	UUR100386	48%	97.7%	96.8%
EFA201884	VCH100750	38%	97.9%	92.3%
EFA201884	YPS003216	36%	97.9%	92.5%
EFA201886	BFR100706	48%	93.1%	29.3%
EFA201886	EFA201886	100%	100%	100%
EFA201888	ABA105798	37%	99.8%	100%
EFA201888	ABA100324	39%	99.5%	99.8%
EFA201888	BAN112689	49%	96.6%	97.3%
EFA201888	BAN107953	51%	99.3%	99.3%
EFA201888	BFR12010	47%	99.8%	99.5%
EFA201888	BPT102618	48%	98.8%	99.3%
EFA201888	BCE113298	47%	74.3%	98.7%
EFA201888	BFU100675	49%	98.8%	95.3%
EFA201888	BMA102164	49%	98.8%	99.0%
EFA201888	CJU100410	48%	99.0%	99.5%
EFA201888	CPN200933	44%	99.0%	98.8%
EFA201888	CTR200146	44%	99.3%	98.6%
EFA201888	CAC100013	56%	99.3%	99.5%
EFA201888	CBO102384	59%	99.5%	98.8%
EFA201888	CDF101773	52%	99.0%	99.3%
EFA201888	CDP100587	25%	98.8%	27.7%
EFA201888	EBC100090	47%	63.8%	98.9%
EFA201888	EFA201888	100%	100%	100%
EFA201888	ECO101068	50%	98.8%	99.0%
EFA201888	HPY100551	45%	99.0%	99.8%
EFA201888	KPN301302	50%	98.8%	99.0%
EFA201888	LPN100053	48%	98.8%	99.0%
EFA201888	LMO100394	52%	99.5%	99.3%
EFA201888	MCA101479	46%	98.8%	100%
EFA201888	MAV103067	36%	98.3%	100%
EFA201888	MBV100653	38%	98.5%	96.9%
EFA201888	MLP101008	36%	98.5%	96.9%
EFA201888	MTU202211	38%	98.5%	96.9%
EFA201888	NGO100696	51%	99.3%	91.9%
EFA201888	NME200042	50%	99.3%	99.0%
EFA201888	PAE202963	49%	99.5%	99.3%
EFA201888	PPU104840	49%	99.0%	98.8%
EFA201888	PSY101697	48%	99.5%	99.3%
EFA201888	SPA100629	47%	98.8%	99.0%
EFA201888	STY102533	49%	98.8%	99.0%
EFA201888	STM102723	50%	98.8%	99.0%
EFA201888	SAU800984	53%	99.3%	98.8%
EFA201888	SEP200206	52%	99.3%	98.8%
EFA201888	SHA101847	52%	99.5%	99.0%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201888	VCH101989	49%	98.8%	99.0%
EFA201888	YPS003134	49%	98.8%	99.0%
EFA201905	ABA103706	43%	98.6%	95.8%
EFA201905	BAN112289	80%	12.2%	87.8%
EFA201905	BAN108159	45%	95.3%	100%
EFA201905	BAN100668	56%	100%	100%
EFA201905	BFR100314	21%	36.5%	34.4%
EFA201905	BFR102798	36%	12.8%	74.5%
EFA201905	BFR104729	31%	27.0%	26.3%
EFA201905	BFR102402	35%	16.9%	69.9%
EFA201905	BFR103498	33%	18.2%	17.6%
EFA201905	BFR104188	31%	18.2%	14.4%
EFA201905	BFR101898	22%	97.6%	74.5%
EFA201905	BFR102942	36%	23.6%	79.8%
EFA201905	BFR104190	20%	97.0%	59.5%
EFA201905	BFR10665	23%	65.5%	45.4%
EFA201905	BFR102711	40%	20.3%	15.8%
EFA201905	BFR102682	38%	23.3%	56%
EFA201905	BFR104935	23%	86.8%	60.3%
EFA201905	BFR11037	24%	93.6%	54.5%
EFA201905	BFR100113	27%	81.1%	56.1%
EFA201905	BFR102796	25%	71.6%	51.3%
EFA201905	BFR102991	30%	59.8%	39.2%
EFA201905	BFR101296	30%	61.1%	39.8%
EFA201905	BFR12371	25%	94.3%	68.0%
EFA201905	BFR11529	28%	81.1%	62.4%
EFA201905	BFR10734	43%	97.3%	90.2%
EFA201905	BPT102059	41%	97.6%	95.2%
EFA201905	BCE108192	33%	99.7%	98.0%
EFA201905	BFU102341	41%	95.9%	90.4%
EFA201905	BMA105859	41%	95.3%	83.8%
EFA201905	CJU100802	29%	90.2%	78.0%
EFA201905	CPN200813	34%	96.3%	93.4%
EFA201905	CTR200250	34%	100%	97.3%
EFA201905	CAC100867	42%	95.3%	95.5%
EFA201905	CBO103235	41%	100%	100%
EFA201905	CDF101842	35%	96.3%	93.1%
EFA201905	CDP101043	41%	91.9%	99.0%
EFA201905	EBC102954	41%	97.6%	96.6%
EFA201905	EFA201905	100%	100%	100%
EFA201905	EFM100706	74%	91.9%	100%
EFA201905	ECO102830	40%	99.0%	98.0%
EFA201905	HIN100295	38%	98.3%	98.0%
EFA201905	HPY100992	26%	41.9%	69.4%
EFA201905	HPY100979	24%	81.8%	70.1%
EFA201905	HPY100667	29%	84.5%	72.9%
EFA201905	KPN303337	42%	97.6%	96.6%
EFA201905	LMO101203	53%	100%	100%
EFA201905	MCA100972	39%	95.3%	90.2%
EFA201905	MAV102006	37%	100%	93.6%
EFA201905	MBV100093	27%	52.4%	96.5%
EFA201905	MBV105361	39%	99.0%	97.7%
EFA201905	MLP100846	38%	100%	98.1%
EFA201905	MTU201680	39%	99.0%	97.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201905	NGO102003	40%	99.7%	99.7%
EFA201905	NME200887	38%	99.7%	99.7%
EFA201905	PMU100093	37%	97.3%	96.6%
EFA201905	PRT102352	41%	97.3%	91.7%
EFA201905	PAE203735	43%	99.7%	98.7%
EFA201905	PPU107818	42%	99.7%	98.7%
EFA201905	PSY103793	43%	99.7%	98.7%
EFA201905	SPA102980	41%	100%	100%
EFA201905	STY104150	41%	100%	100%
EFA201905	STM101083	38%	100%	97%
EFA201905	SAU801497	52%	100%	100%
EFA201905	SEP200487	50%	100%	100%
EFA201905	SHA101162	52%	100%	100%
EFA201905	SPN401046	23%	93.9%	85.7%
EFA201905	SPY200913	22%	85.8%	75.6%
EFA201905	TPA100387	38%	80.4%	78.8%
EFA201905	UUR100535	24%	91.2%	90.8%
EFA201905	VCH102384	39%	97.6%	95.4%
EFA201905	YPS000164	42%	97.6%	96.3%
EFA201920	ABA102020	43%	90.2%	96.6%
EFA201920	BAN108425	58%	99.3%	100%
EFA201920	BAN110337	69%	99.5%	100%
EFA201920	BFR10585	42%	77.9%	94.5%
EFA201920	BPT102468	48%	76.7%	88.6%
EFA201920	BBU100780	40%	75.6%	97.0%
EFA201920	BCE109750	46%	76.5%	89.5%
EFA201920	BFU106483	44%	82.9%	96.2%
EFA201920	BMA107520	46%	76.5%	89.0%
EFA201920	CJU100085	43%	74.9%	94.3%
EFA201920	CPN200205	44%	74.9%	94.8%
EFA201920	CTR200689	44%	74.9%	97.0%
EFA201920	CAC103735	49%	99.5%	100%
EFA201920	CBO102816	49%	99.3%	99.8%
EFA201920	CDF101736	47%	99.3%	99.1%
EFA201920	CDP101218	43%	99.5%	87.0%
EFA201920	EBC102677	44%	84.0%	90.0%
EFA201920	EFA201920	100%	100%	100%
EFA201920	EFM201911	88%	91.1%	100%
EFA201920	ECO103113	43%	90.2%	95.4%
EFA201920	HIN100857	42%	85.6%	95.9%
EFA201920	HPY100299	46%	67.4%	81.1%
EFA201920	KPN300686	45%	84.0%	89.8%
EFA201920	LPN101316	49%	63.7%	99.3%
EFA201920	LMO102191	71%	99.5%	100%
EFA201920	MCA101313	44%	81.3%	86.9%
EFA201920	MAV104121	44%	99.5%	88.6%
EFA201920	MBV104432	43%	98.9%	89.0%
EFA201920	MLP100902	42%	99.5%	90.8%
EFA201920	MTU202404	43%	99.5%	90.6%
EFA201920	MGE100395	36%	96.1%	96.3%
EFA201920	MPN100279	36%	96.1%	96.3%
EFA201920	NGO100959	45%	75.1%	88.3%
EFA201920	NME200322	46%	75.1%	88.3%
EFA201920	PMU100351	44%	81.3%	89.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201920	PRT100791	44%	84.5%	95.4%
EFA201920	PAE204564	47%	79.9%	86.2%
EFA201920	PPU110997	44%	79.9%	85.5%
EFA201920	PSY102705	43%	69.9%	84.5%
EFA201920	SPA100458	43%	84.0%	96.4%
EFA201920	STY101485	44%	84.0%	90.3%
EFA201920	SAU801644	61%	99.5%	100%
EFA201920	SEP201605	60%	99.5%	100%
EFA201920	SHA100640	60%	84.9%	100%
EFA201920	SMU100127	73%	100%	100%
EFA201920	SPN400984	77%	100%	100%
EFA201920	SPY201023	73%	100%	100%
EFA201920	TPA100734	43%	68.7%	79.5%
EFA201920	UUR100466	35%	99.3%	99.5%
EFA201920	VCH100432	42%	81.3%	88.1%
EFA201920	YPS002137	44%	80.1%	88.7%
EFA201926	ABA102635	47%	97.6%	94.0%
EFA201926	BAN101985	47%	96.4%	100%
EFA201926	BAN113496	72%	98.2%	98.0%
EFA201926	BFR102757	47%	98.0%	86.1%
EFA201926	BPT101799	49%	98.2%	97.4%
EFA201926	BCE109946	50%	99.6%	98.4%
EFA201926	BFU108644	48%	98.0%	94.3%
EFA201926	BMA108408	49%	99.6%	98.4%
EFA201926	CJU100369	45%	96.4%	96.2%
EFA201926	CPN200915	40%	97.6%	96.8%
EFA201926	CTR200158	41%	97.6%	97.3%
EFA201926	CAC101713	53%	97.8%	94.0%
EFA201926	CBO101347	54%	98.2%	96.4%
EFA201926	CDF101016	54%	99.6%	96.1%
EFA201926	CDP100639	38%	98.2%	98.1%
EFA201926	EBC102996	51%	99.4%	99.0%
EFA201926	EFA201926	100%	100%	100%
EFA201926	EFM102056	58%	23.5%	98.3%
EFA201926	ECO102826	52%	98.0%	96.8%
EFA201926	HIN101184	52%	99.4%	99.2%
EFA201926	HPY100179	45%	97.6%	97.0%
EFA201926	KPN302939	51%	100%	99.4%
EFA201926	KPN303317	51%	100%	99.4%
EFA201926	LPN100325	50%	99.4%	99.4%
EFA201926	LMO102242	69%	98.2%	98.2%
EFA201926	MCA100679	47%	97.6%	96.4%
EFA201926	MAV100921	41%	98.0%	98.0%
EFA201926	MBV102374	41%	94.4%	98.5%
EFA201926	MLP100165	40%	97.8%	97.0%
EFA201926	MTU203546	41%	98.2%	97.8%
EFA201926	MGE100138	45%	97.8%	98.6%
EFA201926	MPN100558	48%	97.8%	98.6%
EFA201926	NGO101519	50%	100%	99.6%
EFA201926	NME201498	50%	100%	99.6%
EFA201926	PMU100189	51%	99.2%	99.2%
EFA201926	PRT100474	51%	100%	98.6%
EFA201926	PAE203698	51%	99.4%	98.2%
EFA201926	PPU107895	49%	99.4%	98.2%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201926	PSY104934	49%	99.4%	98.2%
EFA201926	SPA102976	52%	98.0%	96.8%
EFA201926	STY104136	52%	98.0%	96.8%
EFA201926	STM103496	31%	64.7%	96.3%
EFA201926	SAU800517	68%	98.2%	99.2%
EFA201926	SEP201850	68%	98.2%	99.2%
EFA201926	SHA100105	70%	45.2%	99.1%
EFA201926	SMU100072	69%	98.6%	98.4%
EFA201926	SPN400626	71%	98.6%	99.2%
EFA201926	SPY200429	70%	98.6%	99.0%
EFA201926	TPA101030	22%	61.2%	95.7%
EFA201926	UUR100060	53%	97.6%	98.2%
EFA201926	VCH100651	46%	99.2%	97.1%
EFA201926	YPS000160	51%	98.2%	97.0%
EFA201946	ABA102546	34%	16.4%	100%
EFA201946	ABA101608	34%	90.0%	92.4%
EFA201946	BAN104617	37%	94.0%	95.8%
EFA201946	BAN104798	52%	96.2%	97.4%
EFA201946	BFR106066	35%	88.1%	88.6%
EFA201946	BPT100078	36%	90.8%	92.9%
EFA201946	BBU100622	36%	86.0%	87.0%
EFA201946	BCE107511	35%	89.3%	90.5%
EFA201946	BFU101876	37%	73.8%	90.6%
EFA201946	BMA109410	35%	89.7%	90.0%
EFA201946	CJU101011	33%	17.0%	10.1%
EFA201946	CPN200958	40%	10.5%	5.7%
EFA201946	CTR200123	41%	18.8%	15.3%
EFA201946	CAC101838	43%	90.5%	92.1%
EFA201946	CBO103147	40%	96.5%	98.4%
EFA201946	CDF103177	41%	91.3%	95.5%
EFA201946	CDP100876	36%	91.8%	88.5%
EFA201946	EBC101582	37%	81.7%	94.5%
EFA201946	EFA201946	100%	100%	100%
EFA201946	EFM201703	74%	98.4%	99.7%
EFA201946	ECO101087	36%	89.7%	92.2%
EFA201946	HIN101230	37%	88.3%	91.1%
EFA201946	HPY101518	37%	17.7%	11.7%
EFA201946	KPN300307	60%	9.8%	82.4%
EFA201946	KPN302590	35%	90.6%	93.2%
EFA201946	LPN102055	35%	91.3%	94.0%
EFA201946	LMO101320	53%	95.9%	96.8%
EFA201946	MCA102969	32%	88.6%	91.4%
EFA201946	MAV105497	35%	91.8%	90.7%
EFA201946	MBV103326	36%	88.9%	87.8%
EFA201946	MLP100181	35%	89.7%	89.5%
EFA201946	MTU201009	36%	88.9%	87.8%
EFA201946	NGO101007	42%	13.2%	20.2%
EFA201946	NME201357	40%	9.4%	20.0%
EFA201946	PMU101041	37%	85.6%	88.4%
EFA201946	PRT100883	36%	91.8%	93.0%
EFA201946	PAE203000	35%	89.0%	91.7%
EFA201946	PPU100453	35%	90.5%	94.0%
EFA201946	PSY102964	36%	87.0%	93.1%
EFA201946	SPA102802	35%	87.5%	91.1%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201946	STY102552	36%	89.7%	92.2%
EFA201946	SAU800503	48%	95.1%	96.3%
EFA201946	SEP201836	49%	94.2%	95.7%
EFA201946	SHA101206	51%	89.0%	98.9%
EFA201946	SMU100032	51%	98.7%	99.7%
EFA201946	SPN400006	50%	96.0%	96.9%
EFA201946	SPY200006	51%	98.5%	99.4%
EFA201946	TPA100340	36%	85.1%	86.1%
EFA201946	VCH101856	36%	90.6%	92.9%
EFA201946	YPS003221	35%	90.5%	93.0%
EFA201951	ABA100619	44%	97.8%	96.8%
EFA201951	BAN108237	36%	98.0%	96.3%
EFA201951	BAN113091	39%	95.2%	97.1%
EFA201951	BAN112735	41%	97.4%	97.6%
EFA201951	BAN113417	42%	98.2%	98.4%
EFA201951	BFR103003	24%	23.0%	81.9%
EFA201951	BPT103076	45%	97.4%	92.2%
EFA201951	BCE103462	45%	97.4%	96.1%
EFA201951	BFU102740	44%	97.4%	96.4%
EFA201951	BFU107758	45%	98.0%	97.0%
EFA201951	BMA106098	45%	97.4%	86.1%
EFA201951	CJU100455	35%	76.8%	96.4%
EFA201951	CAC103154	34%	95.4%	97.5%
EFA201951	CBO103360	34%	95.4%	96.9%
EFA201951	CDF103906	33%	96.2%	97.5%
EFA201951	CDP101458	44%	97.4%	96.2%
EFA201951	EBC104578	47%	97.4%	91.4%
EFA201951	EFA201951	100%	100%	100%
EFA201951	ECO103510	48%	97.4%	90.0%
EFA201951	HPY100055	24%	91.5%	37.0%
EFA201951	KPN305829	45%	95.8%	94.9%
EFA201951	LPN101129	42%	97.4%	99.4%
EFA201951	LMO102125	40%	94.8%	96.1%
EFA201951	MCA101417	43%	97.4%	96.4%
EFA201951	MAV101769	46%	97.8%	96.6%
EFA201951	MBV105125	43%	97.8%	96.6%
EFA201951	MLP101520	28%	91.9%	99.3%
EFA201951	MTU200456	43%	97.8%	96.6%
EFA201951	NGO100472	36%	91.1%	91.8%
EFA201951	NME200446	36%	95.4%	98.5%
EFA201951	PMU101530	36%	94.8%	96.7%
EFA201951	PRT105557	59%	96.4%	97.0%
EFA201951	PAE204019	48%	95.4%	94.5%
EFA201951	PAE201982	48%	95.4%	94.5%
EFA201951	PPU108163	49%	95.8%	94.9%
EFA201951	PSY105710	48%	95.4%	94.5%
EFA201951	SPA101536	48%	84.5%	93.0%
EFA201951	STY100416	47%	97.4%	95.3%
EFA201951	STM102230	38%	94.8%	96.3%
EFA201951	SAU800167	57%	99.0%	99.2%
EFA201951	SEP201069	56%	100%	100%
EFA201951	SHA101810	56%	100%	100%
EFA201951	SMU100865	32%	95.8%	98.9%
EFA201951	SPN401028	33%	96.0%	99.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201951	SPY201053	32%	95.8%	98.9%
EFA201951	UUR100364	30%	95.6%	99.4%
EFA201951	VCH101789	48%	95.8%	94.9%
EFA201951	VCH100804	48%	97.4%	90.2%
EFA201951	YPS002165	39%	95.2%	96.7%
EFA201954	ABA104342	28%	42.7%	95.8%
EFA201954	BCE107126	36%	42.3%	90.2%
EFA201954	BMA105276	34%	42.3%	97.2%
EFA201954	EBC100624	37%	42.3%	97.3%
EFA201954	EFA201954	100%	100%	100%
EFA201954	ECO100786	37%	42.3%	97.3%
EFA201954	KPN303596	37%	42.3%	97.3%
EFA201954	SPA101970	37%	42.3%	97.7%
EFA201954	STY102374	37%	42.3%	97.3%
EFA201954	SMU101490	57%	98.3%	99.2%
EFA201954	SPN400409	58%	54.8%	93.2%
EFA201954	SPY200205	54%	96.6%	96.4%
EFA201954	YPS000343	34%	40.2%	92.7%
EFA201968	BAN100415	49%	99.2%	100%
EFA201968	BAN103869	49%	100%	100%
EFA201968	BFR102096	37%	98.4%	99.6%
EFA201968	BPT101929	38%	99.2%	91.1%
EFA201968	BCE110533	36%	96.4%	87.8%
EFA201968	BFU112278	35%	99.2%	90.4%
EFA201968	BMA105147	34%	99.2%	90.0%
EFA201968	CJU100766	29%	99.2%	100%
EFA201968	CPN200166	39%	100%	93.3%
EFA201968	CTR200737	38%	96.4%	89.9%
EFA201968	EFA201968	100%	100%	100%
EFA201968	EFM202456	83%	99.6%	100%
EFA201968	HIN101610	34%	96.4%	88.1%
EFA201968	HPY100357	32%	98.0%	98.8%
EFA201968	LMO101804	48%	99.6%	100%
EFA201968	MGE100185	31%	99.6%	99.6%
EFA201968	MPN100635	35%	99.6%	100%
EFA201968	NGO100854	35%	98.4%	91.7%
EFA201968	NME200375	34%	98.4%	91.7%
EFA201968	PMU100637	35%	96.4%	89.8%
EFA201968	SAU802219	41%	95.6%	88.0%
EFA201968	SEP202050	39%	95.6%	88.0%
EFA201968	SHA100342	41%	42.6%	94.6%
EFA201968	SMU101378	60%	100%	95.0%
EFA201968	SPN401450	63%	99.6%	99.6%
EFA201968	SPY201464	57%	100%	100%
EFA201968	TPA100821	35%	90.8%	81.8%
EFA201970	BAN100358	47%	96.6%	95.9%
EFA201970	BAN103832	51%	99.6%	100%
EFA201970	BPT103246	31%	82.3%	97.5%
EFA201970	CAC102712	45%	99.2%	98.5%
EFA201970	CBO102260	46%	98.5%	98.1%
EFA201970	CDF102434	45%	89.8%	88.8%
EFA201970	CDP100414	29%	85.7%	98.5%
EFA201970	EFA201970	100%	100%	100%
EFA201970	EFM201224	82%	99.6%	97.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201970	ECO203822	26%	44.2%	49.4%
EFA201970	KPN305161	33%	24.5%	27.6%
EFA201970	LMO102464	63%	100%	99.6%
EFA201970	MBV105674	27%	83.0%	78.4%
EFA201970	MLP100512	27%	81.9%	77.0%
EFA201970	MTU202291	27%	83.0%	78.4%
EFA201970	MGE100184	39%	9.1%	35%
EFA201970	MPN100636	38%	8.3%	36.4%
EFA201970	SPA101299	23%	53.6%	95.9%
EFA201970	STY104521	23%	53.6%	62.9%
EFA201970	STM100519	23%	53.6%	60%
EFA201970	SAU802220	46%	99.6%	98.5%
EFA201970	SEP202052	46%	99.6%	98.5%
EFA201970	SHA100341	45%	98.5%	98.5%
EFA201970	SMU101384	60%	99.2%	99.6%
EFA201970	SPN402021	54%	99.6%	100%
EFA201970	SPY201676	62%	99.6%	99.2%
EFA201970	TPA100223	28%	54.7%	61.8%
EFA201970	UUR100543	41%	61.1%	36.8%
EFA201974	ABA100130	44%	96.1%	86.4%
EFA201974	BAN103288	74%	99.2%	100%
EFA201974	BAN102478	74%	99.2%	100%
EFA201974	BFR100896	37%	97.6%	68.3%
EFA201974	BPT100897	46%	96.9%	83.2%
EFA201974	BBU100502	32%	100%	91.9%
EFA201974	BCE109774	46%	96.9%	83.2%
EFA201974	BFU101597	45%	96.9%	83.8%
EFA201974	BMA104335	47%	96.9%	83.2%
EFA201974	CJU101502	45%	97.6%	94.0%
EFA201974	CPN200120	43%	96.1%	93.0%
EFA201974	CTR200782	43%	96.1%	93.0%
EFA201974	CAC100809	50%	97.6%	96.5%
EFA201974	CBO102497	53%	97.6%	97.3%
EFA201974	CDF102169	51%	97.6%	97.3%
EFA201974	CDP100024	41%	96.1%	68.8%
EFA201974	EBC103646	48%	98.4%	87.4%
EFA201974	EFA201974	100%	100%	100%
EFA201974	EFM201685	89%	99.2%	100%
EFA201974	ECO103217	48%	98.4%	87.4%
EFA201974	HIN100784	48%	98.4%	86.7%
EFA201974	HPY101274	41%	97.6%	94.8%
EFA201974	KPN300813	48%	98.4%	86.7%
EFA201974	LMO100340	67%	99.2%	100%
EFA201974	MCA100427	43%	96.1%	90.8%
EFA201974	MAV101006	43%	96.9%	74.7%
EFA201974	MBV100492	43%	96.9%	60.6%
EFA201974	MLP101193	41%	96.9%	64.1%
EFA201974	MTU203409	43%	96.9%	60.6%
EFA201974	MGE100181	31%	99.2%	96.7%
EFA201974	MPN100639	32%	97.6%	94.4%
EFA201974	NGO100883	48%	96.9%	89.3%
EFA201974	NME200096	48%	96.9%	89.3%
EFA201974	PMU101389	47%	98.4%	86.0%
EFA201974	PRT101773	46%	98.4%	86.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201974	PAE204235	43%	98.4%	86.0%
EFA201974	PPU104535	46%	98.4%	86.7%
EFA201974	PSY105785	44%	98.4%	86.7%
EFA201974	SPA104312	46%	98.4%	87.4%
EFA201974	STY101829	48%	98.4%	87.4%
EFA201974	SAU802223	65%	99.2%	100%
EFA201974	SEP202058	65%	99.2%	100%
EFA201974	SHA100503	65%	99.2%	99.2%
EFA201974	SMU100584	75%	99.2%	100%
EFA201974	SPN400216	76%	99.2%	100%
EFA201974	SPY101855	75%	99.2%	100%
EFA201974	TPA100211	41%	97.6%	67.1%
EFA201974	UUR100260	38%	99.2%	100%
EFA201974	VCH102533	48%	98.4%	86.7%
EFA201974	YPS002494	48%	98.4%	86.0%
EFA201975	ABA100129	40%	98.1%	91.3%
EFA201975	BAN107601	56%	99.7%	100%
EFA201975	BAN108468	75%	100%	100%
EFA201975	BFR10426	42%	99.7%	96.7%
EFA201975	BPT100896	43%	97.8%	93.9%
EFA201975	BBU100501	41%	98.7%	92.2%
EFA201975	BCE103299	41%	97.1%	93.8%
EFA201975	BFU101596	41%	97.1%	93.8%
EFA201975	BMA100053	41%	97.1%	93.8%
EFA201975	CJU101501	34%	95.2%	87.2%
EFA201975	CPN200119	39%	94.2%	80.3%
EFA201975	CTR200783	36%	93.6%	79.2%
EFA201975	CAC100456	62%	100%	99.7%
EFA201975	CBO100600	64%	100%	99.7%
EFA201975	CDF104551	64%	100%	99.1%
EFA201975	CDP100022	47%	99.0%	91.1%
EFA201975	EBC103650	45%	99.4%	95.4%
EFA201975	EFA201975	100%	100%	100%
EFA201975	EFM200465	93%	100%	100%
EFA201975	ECO103218	45%	99.4%	95.4%
EFA201975	HIN100783	45%	99.4%	95.4%
EFA201975	HPY101275	34%	95.2%	87.8%
EFA201975	KPN300703	47%	76.3%	95.7%
EFA201975	LMO100649	73%	100%	100%
EFA201975	MCA100426	44%	99.4%	93.4%
EFA201975	MAV101008	47%	99.0%	89.0%
EFA201975	MBV100494	46%	99.0%	89.0%
EFA201975	MLP101194	47%	99.0%	89.0%
EFA201975	MTU203410	46%	99.0%	89.0%
EFA201975	MGE100180	38%	94.6%	93.9%
EFA201975	MPN100640	38%	96.2%	95.7%
EFA201975	NGO100885	43%	98.1%	93.6%
EFA201975	NME200097	42%	98.1%	93.6%
EFA201975	PMU101390	45%	99.4%	95.4%
EFA201975	PRT101775	45%	99.4%	95.4%
EFA201975	PAE204236	44%	99.4%	94.0%
EFA201975	PPU104534	44%	99.4%	94.0%
EFA201975	PSY100281	38%	48.4%	91.5%
EFA201975	SPA104314	45%	99.4%	95.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201975	STY101828	45%	99.4%	95.4%
EFA201975	SAU802224	71%	100%	100%
EFA201975	SEP202059	71%	100%	100%
EFA201975	SHA100502	71%	100%	100%
EFA201975	SMU100586	68%	99.7%	99.7%
EFA201975	SPN400215	69%	99.0%	99.4%
EFA201975	SPY200063	68%	99.7%	99.7%
EFA201975	TPA100210	40%	99.0%	91.7%
EFA201975	UUR100259	39%	99.0%	97.9%
EFA201975	VCH102534	43%	99.4%	95.5%
EFA201975	YPS002493	45%	99.4%	95.4%
EFA201976	ABA100127	61%	98.4%	99.2%
EFA201976	BAN102381	78%	100%	100%
EFA201976	BAN110714	83%	100%	100%
EFA201976	BFR10424	57%	100%	100%
EFA201976	BPT100894	61%	93.8%	91.0%
EFA201976	BBU100500	53%	99.2%	95.5%
EFA201976	BCE109619	62%	99.2%	94.7%
EFA201976	BFU101594	64%	99.2%	94.0%
EFA201976	BMA109746	63%	99.2%	94.7%
EFA201976	CJU101499	61%	100%	100%
EFA201976	CPN200118	60%	99.2%	96.2%
EFA201976	CTR200784	59%	97.7%	95.5%
EFA201976	CAC100574	80%	96.9%	95.4%
EFA201976	CBO101814	76%	96.9%	94.7%
EFA201976	CDF101597	77%	97.7%	96.2%
EFA201976	CDP100018	71%	95.3%	91.8%
EFA201976	EBC103656	59%	100%	100%
EFA201976	EFA201976	100%	100%	100%
EFA201976	EFM200112	93%	100%	100%
EFA201976	ECO103220	59%	100%	100%
EFA201976	HIN100781	62%	100%	100%
EFA201976	HPY101277	61%	100%	100%
EFA201976	KPN300701	59%	100%	100%
EFA201976	LMO102707	87%	100%	100%
EFA201976	MCA100424	61%	100%	100%
EFA201976	MAV101012	70%	99.2%	94.2%
EFA201976	MBV100327	68%	99.2%	92.1%
EFA201976	MLP101196	72%	93.8%	87.7%
EFA201976	MTU203412	69%	99.2%	92.1%
EFA201976	MGE100179	43%	87.6%	86.3%
EFA201976	MPN100641	48%	92.2%	98.3%
EFA201976	NGO100889	59%	93.8%	92.4%
EFA201976	NME200099	59%	93.8%	92.4%
EFA201976	PMU101392	63%	100%	100%
EFA201976	PRT105644	59%	100%	100%
EFA201976	PAE204238	60%	100%	100%
EFA201976	PPU104532	59%	100%	100%
EFA201976	PSY106472	59%	100%	100%
EFA201976	SPA104318	58%	99.2%	100%
EFA201976	STY101826	60%	100%	100%
EFA201976	SAU802225	85%	100%	100%
EFA201976	SEP200240	85%	100%	100%
EFA201976	SHA100501	85%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201976	SMU100588	86%	96.9%	98.4%
EFA201976	SPN400214	84%	96.9%	98.4%
EFA201976	SPY200062	87%	96.9%	98.4%
EFA201976	TPA100209	60%	96.1%	98.4%
EFA201976	UUR100258	56%	92.2%	98.3%
EFA201976	VCH102536	60%	100%	100%
EFA201976	YPS002491	59%	100%	100%
EFA201977	ABA100126	62%	95.9%	97.5%
EFA201977	BAN113421	85%	33.9%	100%
EFA201977	BAN112977	76%	100%	100%
EFA201977	BFR10423	61%	98.3%	95.2%
EFA201977	BPT100893	53%	100%	100%
EFA201977	BBU100499	52%	99.2%	96.8%
EFA201977	BCE106205	52%	100%	100%
EFA201977	BFU100384	52%	100%	100%
EFA201977	BMA110016	53%	100%	100%
EFA201977	CJU101498	59%	98.3%	99.2%
EFA201977	CPN200117	50%	100%	100%
EFA201977	CTR200785	51%	100%	100%
EFA201977	CAC101837	65%	100%	99.2%
EFA201977	CBO102219	63%	100%	99.2%
EFA201977	CDF103596	61%	100%	99.2%
EFA201977	CDP100016	62%	100%	100%
EFA201977	EBC103659	59%	95.9%	98.3%
EFA201977	EFA201977	100%	100%	100%
EFA201977	EFM200415	91%	100%	100%
EFA201977	ECO103221	58%	95.9%	98.3%
EFA201977	HIN100780	60%	90.9%	90.2%
EFA201977	HPY101278	57%	98.3%	100%
EFA201977	KPN300700	57%	81.8%	98.0%
EFA201977	LMO102428	79%	100%	100%
EFA201977	MCA100423	62%	95.9%	98.3%
EFA201977	MAV101014	61%	100%	98.4%
EFA201977	MBV100329	62%	100%	98.4%
EFA201977	MLP101197	63%	100%	98.4%
EFA201977	MTU203413	62%	100%	98.4%
EFA201977	MGE100178	59%	99.2%	96.8%
EFA201977	MPN100642	57%	99.2%	96.8%
EFA201977	NGO100891	57%	99.2%	100%
EFA201977	NME200100	57%	99.2%	100%
EFA201977	PMU101393	61%	95.9%	98.3%
EFA201977	PRT100020	56%	88.4%	98.2%
EFA201977	PAE204239	62%	95.9%	98.3%
EFA201977	PPU104531	59%	95.9%	98.3%
EFA201977	PSY105783	60%	61.2%	97.4%
EFA201977	SPA104321	58%	95.9%	98.3%
EFA201977	STY101825	58%	95.9%	98.3%
EFA201977	SAU802226	75%	100%	100%
EFA201977	SEP200241	72%	100%	100%
EFA201977	SHA100500	73%	100%	100%
EFA201977	SMU100590	80%	100%	100%
EFA201977	SPN400213	80%	100%	100%
EFA201977	SPY200061	78%	100%	100%
EFA201977	TPA100208	59%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201977	UUR100257	64%	99.2%	97.0%
EFA201977	VCH102537	60%	95.9%	98.3%
EFA201977	YPS002490	56%	95.9%	98.3%
EFA201978	ABA102578	45%	99.5%	100%
EFA201978	BAN108855	53%	98.6%	98.2%
EFA201978	BAN106781	61%	98.6%	98.1%
EFA201978	BFR10586	38%	99.1%	98.4%
EFA201978	BPT101280	49%	86.6%	83.5%
EFA201978	BBU100416	39%	98.6%	98.1%
EFA201978	BCE114693	53%	86.6%	82.7%
EFA201978	BFU106856	52%	86.6%	82.4%
EFA201978	BMA102106	53%	86.6%	82.7%
EFA201978	CJU100600	33%	97.2%	94.3%
EFA201978	CPN200508	39%	97.2%	95.8%
EFA201978	CTR200398	33%	99.1%	87.4%
EFA201978	CAC102891	48%	99.5%	99.5%
EFA201978	CBO103787	53%	98.6%	98.1%
EFA201978	CDF102350	51%	96.8%	94.1%
EFA201978	CDP100003	40%	93.1%	93.4%
EFA201978	EBC103984	44%	98.6%	99.5%
EFA201978	EFA201978	100%	100%	100%
EFA201978	EFM200623	86%	99.5%	100%
EFA201978	ECO100465	45%	98.6%	99.5%
EFA201978	HIN100331	46%	98.6%	99.5%
EFA201978	HPY100611	30%	97.2%	94.8%
EFA201978	KPN303865	44%	98.6%	99.5%
EFA201978	LPN102084	45%	99.1%	99.5%
EFA201978	LMO102187	64%	98.6%	98.6%
EFA201978	MCA101231	45%	98.6%	98.6%
EFA201978	MAV102071	42%	95.8%	95.6%
EFA201978	MBV101628	40%	95.8%	95.6%
EFA201978	MLP101114	39%	95.8%	95.6%
EFA201978	MTU200730	40%	95.8%	95.6%
EFA201978	MGE100174	34%	97.2%	95.8%
EFA201978	MPN100646	32%	97.2%	96.3%
EFA201978	NGO100911	47%	96.8%	97.2%
EFA201978	NME200954	48%	96.8%	97.2%
EFA201978	PMU100284	44%	98.6%	99.5%
EFA201978	PRT104973	44%	98.6%	99.5%
EFA201978	PAE203684	48%	87.5%	85.6%
EFA201978	PPU107935	49%	87.5%	85.2%
EFA201978	PSY104919	45%	72.2%	83.0%
EFA201978	SPA100230	45%	88.0%	79.7%
EFA201978	STY100842	43%	98.6%	99.5%
EFA201978	STM100555	43%	98.6%	99.5%
EFA201978	SAU802229	64%	99.1%	99.1%
EFA201978	SEP200243	63%	99.1%	99.1%
EFA201978	SHA100179	63%	99.5%	99.1%
EFA201978	SMU100597	60%	98.6%	98.1%
EFA201978	SPN400210	59%	98.6%	98.1%
EFA201978	SPY200058	61%	99.5%	99.1%
EFA201978	TPA100588	42%	94.9%	94.3%
EFA201978	UUR100253	32%	100%	99.5%
EFA201978	VCH100969	48%	98.6%	99.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201978	YPS001716	44%	98.6%	99.5%
EFA201979	ABA100105	37%	96.5%	92.0%
EFA201979	BAN100422	46%	52.8%	97.0%
EFA201979	BAN100831	37%	98.6%	98.4%
EFA201979	BAN109756	48%	100%	99.5%
EFA201979	BAN106840	51%	100%	100%
EFA201979	BFR12413	37%	98.6%	94.9%
EFA201979	BPT100873	40%	98.8%	95.7%
EFA201979	BBU100497	35%	97.5%	95.6%
EFA201979	BCE109015	39%	95.8%	97.4%
EFA201979	BFU100380	38%	98.8%	95.1%
EFA201979	BMA107419	39%	95.8%	97.4%
EFA201979	CJU101592	36%	95.6%	97.1%
EFA201979	CPN200116	32%	97.7%	95.5%
EFA201979	CTR200786	33%	99.1%	97.8%
EFA201979	CAC102097	38%	100%	100%
EFA201979	CBO103220	37%	99.5%	99.8%
EFA201979	CDF103985	41%	99.5%	99.8%
EFA201979	CDP100001	40%	97.9%	98.4%
EFA201979	EBC103637	40%	97.2%	94.4%
EFA201979	EFA201979	100%	100%	100%
EFA201979	EFM200235	83%	99.5%	99.8%
EFA201979	ECO103223	40%	97.2%	94.4%
EFA201979	HIN100778	36%	97.2%	94.3%
EFA201979	HPY101282	35%	96.1%	97.6%
EFA201979	KPN300616	39%	78.5%	95.2%
EFA201979	LPN101432	38%	84.5%	98.4%
EFA201979	LMO101544	55%	99.5%	99.8%
EFA201979	MCA100141	36%	96.5%	93.4%
EFA201979	MAV102070	41%	98.1%	95.8%
EFA201979	MBV101627	39%	99.5%	99.8%
EFA201979	MLP101115	40%	99.5%	99.8%
EFA201979	MTU200729	39%	99.5%	99.8%
EFA201979	MGE100173	35%	98.6%	89.5%
EFA201979	MPN100647	35%	98.6%	89.1%
EFA201979	NGO100896	37%	96.5%	94.0%
EFA201979	NME200103	37%	96.5%	94.0%
EFA201979	PMU101395	38%	97.2%	94.3%
EFA201979	PRT100561	50%	35.2%	95.6%
EFA201979	PAE204241	38%	97.7%	94.1%
EFA201979	PPU112340	37%	97.7%	93.9%
EFA201979	PSY100299	37%	97.7%	93.7%
EFA201979	SPA104324	40%	95.6%	96.0%
EFA201979	STY101824	40%	97.2%	94.4%
EFA201979	SAU802230	46%	99.3%	99.3%
EFA201979	SEP200245	47%	99.3%	99.3%
EFA201979	SHA100178	43%	85.4%	98.9%
EFA201979	SMU100598	62%	99.5%	98.8%
EFA201979	SPN400209	60%	99.8%	99.1%
EFA201979	SPY200057	62%	99.3%	98.6%
EFA201979	TPA100206	36%	97.2%	92.9%
EFA201979	UUR100252	31%	98.4%	92.4%
EFA201979	VCH102539	36%	97.7%	94.8%
EFA201979	YPS002488	40%	97.2%	94.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201980	ABA100106	47%	98.6%	97.9%
EFA201980	BAN100388	63%	100%	100%
EFA201980	BAN101282	78%	100%	100%
EFA201980	BFR100671	50%	97.9%	98.0%
EFA201980	BPT100871	51%	97.9%	97.3%
EFA201980	BBU100496	49%	96.6%	97.2%
EFA201980	BCE108533	51%	97.3%	97.9%
EFA201980	BFU100391	52%	97.3%	97.9%
EFA201980	BMA101533	52%	97.3%	97.9%
EFA201980	CJU101593	42%	81.5%	89.2%
EFA201980	CPN200115	38%	81.5%	84.0%
EFA201980	CTR200787	43%	86.3%	88.9%
EFA201980	CAC101804	67%	100%	100%
EFA201980	CBO103582	69%	100%	100%
EFA201980	CDF100735	65%	100%	98%
EFA201980	CDP101730	51%	97.9%	95.3%
EFA201980	EBC103640	50%	98.6%	99.3%
EFA201980	EFA201980	100%	100%	100%
EFA201980	EFM201975	93%	100%	100%
EFA201980	ECO103224	52%	98.6%	99.3%
EFA201980	HIN100777	52%	98.6%	99.3%
EFA201980	HPY101283	38%	91.8%	98.5%
EFA201980	KPN300615	49%	95.2%	99.3%
EFA201980	LPN100259	45%	98.6%	99.3%
EFA201980	LMO102003	78%	100%	100%
EFA201980	MCA100140	47%	98.6%	97.9%
EFA201980	MAV102081	52%	97.9%	96.6%
EFA201980	MBV101609	49%	97.3%	95.9%
EFA201980	MLP101118	52%	97.9%	96.6%
EFA201980	MTU200720	51%	97.3%	95.9%
EFA201980	MGE100172	42%	100%	99.3%
EFA201980	MPN100648	38%	100%	98.7%
EFA201980	NGO100899	46%	99.3%	100%
EFA201980	NME200104	47%	99.3%	100%
EFA201980	PMU101396	49%	98.6%	99.3%
EFA201980	PRT103332	47%	98.6%	99.3%
EFA201980	PAE204242	45%	98.6%	99.3%
EFA201980	PPU104529	47%	98.6%	99.3%
EFA201980	PSY107337	49%	98.6%	99.3%
EFA201980	SPA104326	52%	98.6%	99.3%
EFA201980	STY101823	52%	98.6%	99.3%
EFA201980	SAU802231	78%	100%	100%
EFA201980	SEP200247	78%	100%	100%
EFA201980	SHA100093	79%	58.9%	100%
EFA201980	SMU100599	83%	100%	100%
EFA201980	SPN400208	87%	100%	100%
EFA201980	SPY200056	84%	100%	100%
EFA201980	TPA100205	50%	97.9%	94.1%
EFA201980	UUR100251	47%	100%	99.3%
EFA201980	VCH102540	50%	98.6%	99.3%
EFA201980	YPS002485	50%	98.6%	99.3%
EFA201981	ABA100109	55%	94.0%	94.5%
EFA201981	BAN111381	78%	97.6%	98.2%
EFA201981	BAN112822	79%	98.2%	98.2%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201981	BFR10783	53%	94.0%	90.7%
EFA201981	BPT100869	51%	94.0%	91.2%
EFA201981	BBU100494	52%	100%	100%
EFA201981	BCE102110	50%	77.7%	94.9%
EFA201981	BFU100390	50%	99.4%	95.9%
EFA201981	BMA101481	51%	99.4%	97.6%
EFA201981	CJU101594	61%	83.7%	94.6%
EFA201981	CPN200114	43%	94.6%	95.2%
EFA201981	CTR200788	46%	91.0%	92.1%
EFA201981	CAC100146	68%	98.2%	98.8%
EFA201981	CBO100463	65%	98.2%	98.8%
EFA201981	CDF100733	68%	98.2%	96.4%
EFA201981	CDP101728	62%	91.6%	73.1%
EFA201981	EBC103648	54%	100%	100%
EFA201981	EFA201981	100%	100%	100%
EFA201981	EFM200438	97%	100%	100%
EFA201981	ECO103226	54%	100%	99.4%
EFA201981	HIN100775	56%	94.6%	94.6%
EFA201981	HPY101284	61%	83.7%	90.8%
EFA201981	KPN300491	54%	100%	99.4%
EFA201981	LPN100995	52%	96.4%	95.2%
EFA201981	LMO101368	77%	98.2%	97.6%
EFA201981	MCA100160	54%	94.0%	94.5%
EFA201981	MAV102079	59%	91.6%	67.6%
EFA201981	MBV101605	60%	91.6%	69.1%
EFA201981	MLP101120	60%	88.0%	67.3%
EFA201981	MTU200718	60%	91.6%	69.1%
EFA201981	MGE100171	47%	93.4%	73.5%
EFA201981	MPN100649	47%	93.4%	70.8%
EFA201981	NGO100919	50%	94.0%	90.7%
EFA201981	NME200106	50%	94.0%	90.7%
EFA201981	PMU101398	53%	100%	100%
EFA201981	PRT100558	53%	100%	100%
EFA201981	PAE204244	52%	92.2%	92.2%
EFA201981	PPU104527	51%	91.6%	91.6%
EFA201981	PSY105833	50%	92.2%	92.2%
EFA201981	SPA104328	54%	100%	99.4%
EFA201981	STY101822	54%	100%	99.4%
EFA201981	SAU802233	72%	93.4%	93.4%
EFA201981	SEP200249	73%	93.4%	93.4%
EFA201981	SHA100091	73%	93.4%	93.4%
EFA201981	SMU100600	84%	94.0%	95.1%
EFA201981	SPN400206	84%	94.0%	95.1%
EFA201981	SPY200054	85%	94.0%	95.1%
EFA201981	TPA100204	52%	94.6%	91.3%
EFA201981	UUR100250	55%	92.2%	75.9%
EFA201981	VCH102542	52%	93.4%	92.8%
EFA201981	YPS002482	53%	100%	99.4%
EFA201982	ABA100110	46%	95.8%	98.3%
EFA201982	BAN106991	70%	100%	100%
EFA201982	BFR100058	55%	74.6%	100%
EFA201982	BPT100868	47%	95.8%	99.2%
EFA201982	BBU100493	39%	97.5%	95.8%
EFA201982	BCE113907	44%	95.8%	99.2%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201982	BFU100389	43%	95.8%	99.2%
EFA201982	BMA109275	44%	95.8%	99.2%
EFA201982	CJU101595	43%	89.8%	88.1%
EFA201982	CPN200113	43%	94.9%	94.3%
EFA201982	CTR200789	43%	94.9%	94.3%
EFA201982	CAC102283	65%	95.8%	98.3%
EFA201982	CBO100811	59%	100%	97.5%
EFA201982	CDF103929	59%	100%	100%
EFA201982	CDP101725	55%	91.5%	81.5%
EFA201982	EBC103652	50%	95.8%	99.1%
EFA201982	EFA201982	100%	100%	100%
EFA201982	EFM200146	93%	100%	100%
EFA201982	ECO103227	50%	95.8%	99.1%
EFA201982	HIN100774	47%	95.8%	99.1%
EFA201982	HPY101285	41%	93.2%	90.8%
EFA201982	KPN300490	50%	95.8%	99.1%
EFA201982	LPN101342	42%	95.8%	99.2%
EFA201982	LMO102391	74%	100%	100%
EFA201982	MCA100159	49%	95.8%	98.3%
EFA201982	MAV102077	50%	92.4%	82.2%
EFA201982	MBV101604	52%	92.4%	91.0%
EFA201982	MLP101121	50%	92.4%	91.7%
EFA201982	MTU200717	52%	92.4%	91.0%
EFA201982	MGE100170	42%	94.9%	98.3%
EFA201982	MPN100650	39%	94.9%	97.4%
EFA201982	NGO100921	52%	95.8%	99.1%
EFA201982	NME200107	52%	95.8%	99.1%
EFA201982	PMU101399	48%	95.8%	99.1%
EFA201982	PRT100557	51%	95.8%	99.1%
EFA201982	PAE204245	51%	94.9%	97.4%
EFA201982	PPU104526	52%	95.8%	98.3%
EFA201982	PSY105780	56%	78.0%	95.9%
EFA201982	SPA104494	44%	95.8%	99.1%
EFA201982	STY101821	50%	95.8%	99.1%
EFA201982	SAU802234	68%	100%	100%
EFA201982	SEP200251	67%	100%	100%
EFA201982	SHA100055	65%	100%	100%
EFA201982	SMU100601	82%	100%	100%
EFA201982	SPN400205	82%	100%	100%
EFA201982	SPY200053	80%	100%	100%
EFA201982	TPA100203	45%	95.8%	95%
EFA201982	UUR100249	43%	91.5%	88.4%
EFA201982	VCH102543	46%	95.8%	99.1%
EFA201982	YPS002455	49%	95.8%	99.1%
EFA201983	ABA100111	45%	98.3%	98.9%
EFA201983	BAN102950	59%	98.3%	99.4%
EFA201983	BAN110172	63%	100%	100%
EFA201983	BFR10781	42%	98.9%	97.9%
EFA201983	BPT100867	49%	98.3%	98.9%
EFA201983	BBU100492	42%	99.4%	98.3%
EFA201983	BCE105068	46%	98.3%	98.9%
EFA201983	BFU100388	48%	98.3%	98.9%
EFA201983	BMA103347	46%	98.3%	98.9%
EFA201983	CJU101596	45%	100%	99.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201983	CPN200112	45%	100%	97.8%
EFA201983	CTR200790	49%	100%	97.8%
EFA201983	CAC101071	56%	100%	100%
EFA201983	CBO102597	58%	100%	99.4%
EFA201983	CDF100753	58%	100%	99.4%
EFA201983	CDP101722	49%	100%	100%
EFA201983	EBC103655	48%	98.3%	98.9%
EFA201983	EFA201983	100%	100%	100%
EFA201983	EFM201241	88%	100%	100%
EFA201983	ECO103228	48%	98.3%	98.9%
EFA201983	HIN100773	49%	98.3%	98.9%
EFA201983	HPY101286	39%	100%	99.4%
EFA201983	KPN300489	60%	18.5%	94.3%
EFA201983	LPN100869	45%	98.3%	98.9%
EFA201983	LMO102101	72%	100%	100%
EFA201983	MCA100158	48%	98.3%	98.9%
EFA201983	MAV102075	46%	100%	100%
EFA201983	MBV101643	48%	100%	100%
EFA201983	MLP101122	48%	100%	100%
EFA201983	MTU200716	48%	100%	100%
EFA201983	MGE100169	43%	100%	98.4%
EFA201983	MPN100651	43%	100%	98.4%
EFA201983	NGO100923	48%	98.3%	98.9%
EFA201983	NME200108	49%	98.3%	98.9%
EFA201983	PMU101400	49%	98.3%	98.9%
EFA201983	PRT100556	51%	98.3%	98.9%
EFA201983	PAE204246	49%	98.3%	98.9%
EFA201983	PPU104525	49%	98.3%	98.9%
EFA201983	PSY100295	48%	98.3%	98.9%
EFA201983	SPA104330	48%	98.3%	98.9%
EFA201983	STY101820	48%	98.3%	98.9%
EFA201983	SAU802235	63%	100%	100%
EFA201983	SEP200253	62%	100%	100%
EFA201983	SHA100054	72%	59.6%	99.1%
EFA201983	SMU100602	73%	100%	100%
EFA201983	SPN400204	74%	100%	100%
EFA201983	SPY200052	71%	100%	100%
EFA201983	TPA100202	46%	99.4%	98.9%
EFA201983	UUR100248	42%	98.9%	97.3%
EFA201983	VCH102544	51%	98.3%	98.9%
EFA201983	YPS002454	49%	98.3%	98.9%
EFA201984	ABA100112	49%	99.2%	99.2%
EFA201984	BAN113611	80%	98.5%	95.6%
EFA201984	BAN101892	81%	100%	100%
EFA201984	BFR10780	54%	98.5%	100%
EFA201984	BPT100866	48%	99.2%	99.2%
EFA201984	BBU100491	43%	100%	100%
EFA201984	BCE101537	50%	99.2%	99.2%
EFA201984	BFU100387	49%	99.2%	99.2%
EFA201984	BMA101128	51%	99.2%	99.2%
EFA201984	CJU101597	42%	99.2%	100%
EFA201984	CPN200111	45%	97.7%	97.0%
EFA201984	CTR200791	45%	99.2%	98.5%
EFA201984	CAC102421	62%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201984	CBO102964	61%	100%	100%
EFA201984	CDF100752	67%	100%	100%
EFA201984	CDP101719	55%	100%	100%
EFA201984	EBC103658	48%	99.2%	99.2%
EFA201984	EFA201984	100%	100%	100%
EFA201984	EFM200970	95%	100%	100%
EFA201984	ECO103229	48%	99.2%	99.2%
EFA201984	HIN100772	47%	99.2%	99.2%
EFA201984	HPY101287	41%	99.2%	100%
EFA201984	KPN300573	48%	87.1%	98.3%
EFA201984	LPN100471	45%	99.2%	99.2%
EFA201984	LMO100791	83%	100%	100%
EFA201984	MCA100157	47%	99.2%	99.2%
EFA201984	MAV102073	56%	100%	100%
EFA201984	MBV101642	56%	100%	100%
EFA201984	MLP101123	56%	100%	100%
EFA201984	MTU200715	56%	100%	100%
EFA201984	MGE100168	48%	97.0%	92.2%
EFA201984	MPN100652	50%	97.0%	91.5%
EFA201984	NGO100925	47%	99.2%	99.2%
EFA201984	NME200109	47%	99.2%	99.2%
EFA201984	PMU101401	45%	99.2%	99.2%
EFA201984	PRT100555	47%	99.2%	99.2%
EFA201984	PAE204247	46%	100%	100%
EFA201984	PPU108197	44%	100%	100%
EFA201984	PSY108276	45%	100%	100%
EFA201984	SPA104332	48%	99.2%	99.2%
EFA201984	STY101809	48%	99.2%	99.2%
EFA201984	SAU802236	78%	100%	100%
EFA201984	SEP200255	80%	100%	100%
EFA201984	SHA101609	76%	72.7%	100%
EFA201984	SMU100603	78%	100%	100%
EFA201984	SPN400203	81%	100%	100%
EFA201984	SPY200051	84%	100%	100%
EFA201984	TPA100201	49%	100%	100%
EFA201984	UUR100247	48%	97.0%	97.7%
EFA201984	VCH102545	45%	99.2%	99.2%
EFA201984	YPS002453	52%	99.2%	99.2%
EFA201985	ABA100107	58%	85.5%	100%
EFA201985	BAN113536	72%	100%	100%
EFA201985	BAN110693	82%	100%	100%
EFA201985	BFR10778	54%	97.8%	94.1%
EFA201985	BPT100865	55%	99.4%	99.4%
EFA201985	BBU100489	59%	97.2%	95.6%
EFA201985	BCE101479	58%	99.4%	99.4%
EFA201985	BFU100385	60%	99.4%	99.4%
EFA201985	BMA102975	58%	99.4%	99.4%
EFA201985	CJU101599	51%	100%	98.9%
EFA201985	CPN200110	50%	100%	98.9%
EFA201985	CTR200792	53%	100%	98.9%
EFA201985	CAC100782	68%	97.8%	97.2%
EFA201985	CBO103765	66%	100%	99.4%
EFA201985	CDF100751	70%	99.4%	98.9%
EFA201985	CDP101582	59%	98.9%	94.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201985	EBC103664	59%	100%	100%
EFA201985	EFA201985	100%	100%	100%
EFA201985	EFM200921	95%	100%	100%
EFA201985	ECO103231	60%	100%	100%
EFA201985	HIN100770	58%	100%	100%
EFA201985	HPY101289	51%	98.3%	97.2%
EFA201985	KPN300575	63%	79.3%	100%
EFA201985	LPN102846	52%	41.3%	93.7%
EFA201985	LMO101852	82%	100%	100%
EFA201985	MCA100155	55%	99.4%	100%
EFA201985	MAV102069	59%	98.9%	94.7%
EFA201985	MBV101640	58%	98.9%	94.7%
EFA201985	MLP101125	58%	98.9%	94.7%
EFA201985	MTU200713	58%	98.9%	94.7%
EFA201985	MGE100166	54%	100%	99.4%
EFA201985	MPN100654	56%	100%	99.4%
EFA201985	NGO100929	55%	99.4%	99.4%
EFA201985	NME200111	55%	99.4%	99.4%
EFA201985	PMU101403	59%	100%	100%
EFA201985	PRT100553	58%	100%	94.2%
EFA201985	PAE204249	58%	99.4%	99.4%
EFA201985	PPU104523	56%	99.4%	99.4%
EFA201985	PSY100243	60%	46.4%	98.8%
EFA201985	SPA104334	59%	100%	100%
EFA201985	STY101807	59%	100%	100%
EFA201985	SAU802238	83%	100%	100%
EFA201985	SEP200260	82%	100%	100%
EFA201985	SHA100780	82%	100%	100%
EFA201985	SMU100604	84%	99.4%	98.9%
EFA201985	SPN400201	82%	99.4%	98.9%
EFA201985	SPY200049	83%	99.4%	98.9%
EFA201985	TPA100199	53%	98.3%	95.1%
EFA201985	UUR100245	59%	98.3%	95.7%
EFA201985	VCH102547	59%	100%	100%
EFA201985	YPS002451	58%	100%	100%
EFA201986	ABA102167	64%	93.4%	99.1%
EFA201986	BAN108009	91%	100%	100%
EFA201986	BFR100659	64%	100%	100%
EFA201986	BPT100864	62%	100%	100%
EFA201986	BBU100487	58%	100%	98.4%
EFA201986	BCE113728	68%	100%	100%
EFA201986	BFU100381	68%	100%	100%
EFA201986	BMA101057	68%	100%	100%
EFA201986	CJU101601	68%	100%	100%
EFA201986	CPN200108	59%	100%	100%
EFA201986	CTR200794	61%	100%	100%
EFA201986	CAC101685	76%	100%	100%
EFA201986	CBO100636	80%	100%	100%
EFA201986	CDF102312	83%	100%	100%
EFA201986	CDP101578	80%	100%	100%
EFA201986	EBC103643	63%	100%	100%
EFA201986	EFA201986	100%	100%	100%
EFA201986	EFM201996	96%	100%	100%
EFA201986	ECO103233	62%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201986	HIN100768	65%	100%	100%
EFA201986	HPY101291	63%	100%	100%
EFA201986	KPN305016	65%	66.4%	98.8%
EFA201986	LMO100716	94%	100%	100%
EFA201986	MCA100153	64%	100%	100%
EFA201986	MAV102065	77%	100%	100%
EFA201986	MBV101638	77%	100%	100%
EFA201986	MLP101127	74%	92.6%	100%
EFA201986	MTU200711	77%	100%	100%
EFA201986	MGE100164	59%	100%	100%
EFA201986	MPN100656	59%	100%	100%
EFA201986	NGO100934	63%	100%	100%
EFA201986	NME200113	63%	100%	100%
EFA201986	PMU101405	65%	100%	100%
EFA201986	PRT103251	60%	97.5%	100%
EFA201986	PAE204251	66%	100%	100%
EFA201986	PPU108200	66%	100%	100%
EFA201986	PSY100106	66%	100%	100%
EFA201986	SPA104303	63%	100%	100%
EFA201986	STY101805	63%	100%	100%
EFA201986	SAU802240	90%	100%	100%
EFA201986	SEP200262	89%	100%	100%
EFA201986	SHA100778	90%	100%	85.3%
EFA201986	SMU100606	93%	100%	100%
EFA201986	SPN400199	90%	100%	100%
EFA201986	SPY200047	89%	100%	100%
EFA201986	TPA100197	63%	100%	100%
EFA201986	UUR100243	60%	100%	100%
EFA201986	VCH102549	62%	100%	100%
EFA201986	YPS002449	64%	100%	100%
EFA201987	ABA100087	51%	81.2%	98.3%
EFA201987	BAN105442	81%	99.3%	99.3%
EFA201987	BFR12478	56%	94.4%	94.4%
EFA201987	BPT104060	52%	93.1%	97.1%
EFA201987	BBU100484	57%	95.1%	99.3%
EFA201987	BCE110254	53%	93.8%	97.8%
EFA201987	BFU100274	53%	93.8%	97.8%
EFA201987	BMA108797	53%	93.8%	97.8%
EFA201987	CJU101604	59%	93.8%	95.7%
EFA201987	CPN200105	54%	94.4%	98.6%
EFA201987	CTR200797	54%	94.4%	98.6%
EFA201987	CAC102622	62%	100%	100%
EFA201987	CBO103643	65%	100%	100%
EFA201987	CDF100749	64%	97.2%	100%
EFA201987	CDP101572	56%	50.7%	97.3%
EFA201987	EBC103654	53%	95.1%	100%
EFA201987	EFA201987	100%	100%	100%
EFA201987	EFM200770	95%	100%	100%
EFA201987	ECO103236	53%	95.1%	100%
EFA201987	HIN100764	53%	95.1%	100%
EFA201987	HPY101294	53%	93.8%	95.7%
EFA201987	KPN300638	52%	86.8%	100%
EFA201987	LMO101423	90%	99.3%	99.3%
EFA201987	MCA100019	55%	95.1%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201987	MAV102093	52%	94.4%	98.6%
EFA201987	MBV101012	52%	94.4%	98.6%
EFA201987	MLP101130	54%	94.4%	98.6%
EFA201987	MTU200705	54%	94.4%	98.6%
EFA201987	MGE100161	51%	94.4%	98.6%
EFA201987	MPN100659	54%	95.1%	98.6%
EFA201987	NGO100936	51%	93.8%	97.8%
EFA201987	NME200116	51%	93.8%	97.8%
EFA201987	PMU101408	52%	95.1%	100%
EFA201987	PRT100078	54%	95.1%	100%
EFA201987	PAE204254	54%	95.1%	100%
EFA201987	PPU104518	52%	95.1%	100%
EFA201987	PSY103397	52%	95.1%	100%
EFA201987	SPA104307	53%	95.1%	100%
EFA201987	STY101803	53%	95.1%	100%
EFA201987	SAU802243	74%	99.3%	99.3%
EFA201987	SEP200265	74%	99.3%	99.3%
EFA201987	SHA100775	74%	99.3%	99.3%
EFA201987	SMU100608	94%	93.8%	98.5%
EFA201987	SPN400196	92%	93.8%	98.5%
EFA201987	SPY200044	91%	93.8%	98.5%
EFA201987	TPA100194	50%	92.4%	95.7%
EFA201987	UUR100240	56%	94.4%	98.6%
EFA201987	VCH102552	55%	95.1%	100%
EFA201987	YPS002443	56%	95.1%	100%
EFA201993	ABA100086	60%	95.0%	90.0%
EFA201993	BAN112122	76%	83.0%	100%
EFA201993	BAN102487	78%	100%	100%
EFA201993	BFR10672	57%	94.5%	84.4%
EFA201993	BPT100851	51%	95.0%	79.1%
EFA201993	BBU100483	46%	99.1%	75.1%
EFA201993	BCE110191	52%	95.0%	78.2%
EFA201993	BFU100273	52%	95.0%	90.8%
EFA201993	BMA108753	52%	95.0%	78.2%
EFA201993	CJU101605	54%	98.6%	92.7%
EFA201993	CPN200104	55%	94.0%	92.4%
EFA201993	CTR200798	54%	94.0%	92.0%
EFA201993	CAC103109	63%	98.6%	97.7%
EFA201993	CBO100517	63%	97.2%	96.0%
EFA201993	CDF100748	59%	96.3%	78.2%
EFA201993	CDP101570	54%	98.2%	84.0%
EFA201993	EBC103657	59%	95.0%	89.3%
EFA201993	EFA201993	100%	100%	100%
EFA201993	EFM201332	96%	100%	100%
EFA201993	ECO103237	59%	95.0%	89.3%
EFA201993	HIN100763	60%	95.0%	88.5%
EFA201993	HPY101295	52%	98.6%	92.3%
EFA201993	KPN300639	59%	95.0%	89.7%
EFA201993	LMO101810	84%	100%	100%
EFA201993	MCA100254	59%	95.0%	86.7%
EFA201993	MAV102092	54%	96.8%	75.7%
EFA201993	MBV101013	55%	96.8%	77.4%
EFA201993	MLP101131	55%	96.8%	75.4%
EFA201993	MTU200704	55%	96.8%	77.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201993	MGE100160	43%	94.5%	78.4%
EFA201993	MPN100660	42%	94.5%	76.9%
EFA201993	NGO100939	53%	98.2%	93.9%
EFA201993	NME200117	54%	98.2%	93.9%
EFA201993	PMU101409	59%	95.0%	88.5%
EFA201993	PRT103066	57%	100%	94.0%
EFA201993	PAE204255	61%	95.0%	91.2%
EFA201993	PPU104517	60%	95.0%	87.8%
EFA201993	PSY103396	60%	95.0%	91.2%
EFA201993	SPA104309	59%	95.0%	89.3%
EFA201993	STY101802	59%	95.0%	89.3%
EFA201993	SAU802244	77%	100%	100%
EFA201993	SEP200267	76%	100%	100%
EFA201993	SHA100774	77%	100%	100%
EFA201993	SMU100609	88%	100%	100%
EFA201993	SPN400195	87%	100%	100%
EFA201993	SPY200043	86%	100%	100%
EFA201993	TPA100193	50%	93.6%	83.8%
EFA201993	UUR100239	47%	96.3%	83.3%
EFA201993	VCH102553	58%	95.0%	89.3%
EFA201993	YPS002439	60%	95.0%	89.7%
EFA201997	ABA100084	69%	100%	100%
EFA201997	BAN101977	63%	98.9%	100%
EFA201997	BAN110916	78%	100%	100%
EFA201997	BFR104321	61%	96.7%	100%
EFA201997	BPT104048	68%	100%	100%
EFA201997	BBU100481	56%	100%	100%
EFA201997	BCE112635	69%	98.9%	100%
EFA201997	BFU104367	69%	98.9%	100%
EFA201997	BMA100281	69%	98.9%	100%
EFA201997	CJU101607	60%	96.7%	95.7%
EFA201997	CPN200102	59%	90.2%	94.3%
EFA201997	CTR200800	59%	90.2%	94.3%
EFA201997	CAC101096	65%	97.8%	96.8%
EFA201997	CBO102193	62%	98.9%	86.4%
EFA201997	CDF103424	67%	100%	98.9%
EFA201997	CDP101567	68%	100%	100%
EFA201997	EBC103663	66%	100%	100%
EFA201997	EFA201997	100%	100%	100%
EFA201997	EFM202484	93%	100%	100%
EFA201997	ECO103239	66%	100%	100%
EFA201997	HIN100761	68%	98.9%	100%
EFA201997	HPY101297	58%	96.7%	95.7%
EFA201997	KPN300699	66%	100%	100%
EFA201997	LMO100277	89%	100%	100%
EFA201997	MCA100252	65%	100%	100%
EFA201997	MAV102090	71%	100%	98.9%
EFA201997	MBV101015	70%	100%	98.9%
EFA201997	MLP101133	71%	100%	98.9%
EFA201997	MTU200702	70%	100%	98.9%
EFA201997	MGE100158	60%	93.5%	98.9%
EFA201997	MPN100662	61%	93.5%	98.9%
EFA201997	NGO102970	64%	100%	100%
EFA201997	NME200119	64%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201997	PMU101411	68%	98.9%	100%
EFA201997	PRT100323	68%	100%	100%
EFA201997	PAE204257	69%	100%	100%
EFA201997	PPU111002	69%	100%	100%
EFA201997	PSY101086	68%	100%	100%
EFA201997	SPA104313	66%	100%	100%
EFA201997	STY101800	66%	100%	100%
EFA201997	SAU802246	83%	100%	100%
EFA201997	SEP200271	83%	100%	100%
EFA201997	SHA100772	83%	100%	100%
EFA201997	SMU102869	89%	41.3%	95%
EFA201997	SPN400192	90%	100%	98.9%
EFA201997	SPY200041	90%	100%	100%
EFA201997	TPA100191	57%	100%	100%
EFA201997	UUR100237	60%	90.2%	94.3%
EFA201997	VCH102555	65%	100%	100%
EFA201997	YPS001864	67%	100%	100%
EFA201999	ABA100083	54%	100%	100%
EFA201999	BAN100305	77%	59.1%	100%
EFA201999	BFR10675	60%	100%	100%
EFA201999	BPT100850	57%	100%	100%
EFA201999	BBU100480	58%	100%	100%
EFA201999	BCE100228	60%	100%	99.6%
EFA201999	BFU100271	60%	100%	99.6%
EFA201999	BMA102202	60%	100%	99.6%
EFA201999	CJU101608	57%	99.3%	98.9%
EFA201999	CPN200101	52%	98.9%	99.3%
EFA201999	CTR200801	50%	98.9%	99.3%
EFA201999	CAC101509	67%	99.3%	98.9%
EFA201999	CBO101184	67%	99.3%	98.9%
EFA201999	CDF100747	65%	100%	100%
EFA201999	CDP101565	62%	99.3%	97.1%
EFA201999	EBC103628	58%	100%	100%
EFA201999	EFA201999	100%	100%	100%
EFA201999	EFM200310	94%	82.2%	98.7%
EFA201999	ECO103240	58%	100%	100%
EFA201999	HIN100760	57%	100%	100%
EFA201999	HPY101298	59%	99.3%	98.9%
EFA201999	KPN300698	58%	100%	100%
EFA201999	LMO100597	84%	100%	99.6%
EFA201999	MCA100251	56%	99.3%	98.5%
EFA201999	MAV102089	63%	99.3%	97.1%
EFA201999	MBV101016	63%	99.3%	97.1%
EFA201999	MLP101134	61%	99.3%	97.1%
EFA201999	MTU200701	63%	99.3%	97.1%
EFA201999	MGE100157	57%	99.3%	98.2%
EFA201999	MPN100663	53%	99.3%	98.3%
EFA201999	NGO101613	62%	99.3%	98.2%
EFA201999	NME200120	62%	99.3%	98.2%
EFA201999	PMU101412	58%	100%	100%
EFA201999	PRT100324	58%	100%	99.6%
EFA201999	PAE204258	56%	99.3%	99.6%
EFA201999	PPU104505	57%	99.3%	99.6%
EFA201999	PSY107059	57%	99.3%	99.6%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA201999	SPA104315	57%	100%	100%
EFA201999	STY101789	57%	100%	100%
EFA201999	SAU802247	78%	100%	99.6%
EFA201999	SEP200273	77%	100%	99.6%
EFA201999	SHA100771	78%	100%	99.6%
EFA201999	SPN400191	83%	100%	99.6%
EFA201999	SPY200040	84%	100%	99.6%
EFA201999	TPA100190	57%	99.3%	99.6%
EFA201999	UUR100236	59%	99.3%	99.6%
EFA201999	VCH102556	60%	100%	100%
EFA201999	YPS001863	59%	100%	99.6%
EFA202001	ABA100081	42%	90.3%	93%
EFA202001	BFR10676	44%	98.1%	98.6%
EFA202001	BPT100849	37%	95.2%	96.1%
EFA202001	BBU100478	39%	96.1%	96.2%
EFA202001	BCE103118	36%	97.6%	98.1%
EFA202001	BFU100270	34%	97.6%	98.1%
EFA202001	BMA104332	37%	62.3%	97.0%
EFA202001	CJU101610	36%	97.6%	98.0%
EFA202001	CPN200099	32%	96.6%	94.6%
EFA202001	CTR200803	33%	96.6%	94.6%
EFA202001	CAC100377	43%	100%	100%
EFA202001	CBO103307	44%	100%	100%
EFA202001	CDF100746	49%	100%	95.4%
EFA202001	CDP101562	39%	91.8%	88.0%
EFA202001	EBC101609	43%	91.8%	94.0%
EFA202001	EFA202001	100%	100%	100%
EFA202001	ECO103242	42%	92.3%	94.5%
EFA202001	HIN100758	42%	92.3%	95%
EFA202001	HPY101300	35%	77.8%	78.6%
EFA202001	KPN300696	41%	92.3%	94.5%
EFA202001	LMO102640	67%	100%	100%
EFA202001	MCA100249	44%	92.3%	95%
EFA202001	MAV102087	44%	91.3%	87.6%
EFA202001	MBV101018	43%	91.3%	85.2%
EFA202001	MLP101136	42%	91.8%	83.0%
EFA202001	MTU200699	43%	91.3%	85.2%
EFA202001	MGE100155	37%	99.5%	99.5%
EFA202001	MPN100665	39%	98.1%	98.1%
EFA202001	NGO101615	35%	93.7%	94.2%
EFA202001	NME200122	36%	93.7%	94.2%
EFA202001	PMU101414	42%	92.3%	95%
EFA202001	PRT103342	43%	93.2%	95.5%
EFA202001	PAE204260	44%	91.8%	94.5%
EFA202001	PPU104504	42%	91.8%	94.5%
EFA202001	PSY108736	42%	91.8%	94.5%
EFA202001	SPA104319	42%	92.3%	95%
EFA202001	STY101787	42%	92.3%	94.5%
EFA202001	SAU802249	61%	99.5%	99.5%
EFA202001	SEP200280	63%	100%	100%
EFA202001	SHA100769	61%	99.5%	99.5%
EFA202001	SMU101861	67%	15.0%	100%
EFA202001	SPN400189	73%	100%	100%
EFA202001	SPY200038	74%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA202001	TPA100188	36%	96.1%	92.1%
EFA202001	UUR100234	38%	96.6%	96.2%
EFA202001	VCH102558	46%	92.3%	95%
EFA202001	YPS001862	43%	93.2%	95.5%
EFA202003	ABA100080	45%	45.9%	100%
EFA202003	BFR10677	52%	95.7%	98.5%
EFA202003	BPT100848	49%	98.1%	91.7%
EFA202003	BBU100477	50%	97.6%	99.0%
EFA202003	BCE112456	46%	100%	98.2%
EFA202003	BFU100269	45%	100%	97.3%
EFA202003	BMA106660	45%	100%	97.3%
EFA202003	CJU101611	34%	94.7%	96.9%
EFA202003	CPN200098	41%	95.2%	95.0%
EFA202003	CTR200804	41%	95.2%	94.1%
EFA202003	CAC103369	58%	99.5%	100%
EFA202003	CBO101061	59%	99.5%	96.8%
EFA202003	CDF100745	66%	98.1%	98.1%
EFA202003	CDP100915	54%	98.1%	95.0%
EFA202003	EBC101610	50%	98.1%	99.0%
EFA202003	EFA202003	100%	100%	100%
EFA202003	ECO103243	50%	98.1%	99.0%
EFA202003	HIN100757	49%	98.1%	99.0%
EFA202003	HPY101301	31%	90.4%	92.7%
EFA202003	KPN300695	48%	43.1%	100%
EFA202003	LMO102018	77%	100%	100%
EFA202003	MCA100248	48%	99.5%	100%
EFA202003	MAV102086	52%	98.1%	96.8%
EFA202003	MBV100990	50%	98.1%	96.8%
EFA202003	MLP101137	50%	98.1%	96.3%
EFA202003	MTU200698	50%	98.1%	96.8%
EFA202003	MGE100154	40%	98.1%	81.3%
EFA202003	MPN100666	38%	98.1%	72.8%
EFA202003	NGO101617	48%	99.0%	98.6%
EFA202003	NME200123	48%	99.0%	98.6%
EFA202003	PMU101415	50%	98.1%	99.0%
EFA202003	PRT102977	51%	98.1%	99.0%
EFA202003	PAE204261	51%	100%	99.5%
EFA202003	PPU111511	51%	100%	99.5%
EFA202003	PSY106254	51%	100%	94.6%
EFA202003	SPA104320	48%	98.1%	99.0%
EFA202003	STY101786	50%	98.1%	99.0%
EFA202003	SAU802250	64%	99.0%	98.2%
EFA202003	SEP200281	62%	99.0%	98.2%
EFA202003	SHA100768	62%	60.3%	96.9%
EFA202003	SMU100611	86%	99.5%	99.0%
EFA202003	SPN400188	87%	99.5%	99.0%
EFA202003	SPY200037	85%	99.5%	99.0%
EFA202003	TPA100187	41%	97.6%	97.6%
EFA202003	UUR100233	50%	98.1%	88.8%
EFA202003	VCH102559	53%	98.1%	99.0%
EFA202003	YPS001861	50%	98.1%	99.0%
EFA202006	ABA100233	75%	33.4%	98.5%
EFA202006	ABA100062	76%	99.5%	99.5%
EFA202006	BAN106076	82%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA202006	BFR12122	73%	99.7%	99.7%
EFA202006	BPT100044	77%	100%	100%
EFA202006	BPT100847	77%	100%	100%
EFA202006	BBU100475	64%	100%	98.3%
EFA202006	BCE112288	67%	15.7%	100%
EFA202006	BCE106056	79%	51.9%	99.0%
EFA202006	BCE108906	77%	100%	100%
EFA202006	BFU100267	71%	36.5%	97.3%
EFA202006	BFU100847	76%	100%	100%
EFA202006	BMA107343	77%	95.9%	100%
EFA202006	BMA106305	77%	100%	100%
EFA202006	CJU100435	75%	100%	100%
EFA202006	CPN200689	69%	99.5%	99.5%
EFA202006	CTR200588	68%	99.7%	98.5%
EFA202006	CAC103049	76%	100%	100%
EFA202006	CBO100671	69%	10.9%	95.6%
EFA202006	CBO101209	78%	59.0%	100%
EFA202006	CBO101304	75%	99.5%	99.5%
EFA202006	CDF100547	75%	100%	96.1%
EFA202006	CDP100912	71%	100%	100%
EFA202006	EBC101615	74%	33.7%	99.3%
EFA202006	EBC100362	81%	47.6%	100%
EFA202006	EBC102891	76%	99.7%	99.7%
EFA202006	EFA202006	100%	100%	100%
EFA202006	EFM100161	81%	71.4%	100%
EFA202006	ECO103262	77%	99.7%	99.7%
EFA202006	ECO103878	77%	99.7%	99.7%
EFA202006	HIN100558	78%	100%	100%
EFA202006	HIN100613	78%	100%	100%
EFA202006	HPY101188	77%	100%	100%
EFA202006	KPN300520	80%	23.5%	100%
EFA202006	KPN300653	77%	80%	99.7%
EFA202006	KPN300869	77%	99.7%	99.7%
EFA202006	LMO102516	84%	100%	100%
EFA202006	MCA100162	76%	99.5%	99.5%
EFA202006	MAV102941	72%	100%	100%
EFA202006	MBV103318	72%	100%	100%
EFA202006	MLP101139	72%	100%	100%
EFA202006	MTU200682	72%	100%	100%
EFA202006	MGE100460	69%	100%	100%
EFA202006	MPN100177	70%	100%	100%
EFA202006	NGO101673	79%	99.7%	99.7%
EFA202006	NGO101620	79%	99.7%	99.7%
EFA202006	NME200128	80%	99.7%	99.7%
EFA202006	NME200143	80%	99.7%	99.7%
EFA202006	PMU101746	76%	100%	100%
EFA202006	PMU101357	77%	100%	100%
EFA202006	PRT100737	79%	24.6%	100%
EFA202006	PRT100321	78%	99.7%	99.7%
EFA202006	PAE204275	75%	100%	100%
EFA202006	PAE204263	75%	100%	100%
EFA202006	PPU104463	72%	77.0%	100%
EFA202006	PPU104501	72%	100%	100%
EFA202006	PSY107231	73%	99.7%	99.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA202006	SPA104331	74%	39.5%	99.4%
EFA202006	SPA102798	77%	99.7%	99.7%
EFA202006	STY102689	77%	99.7%	99.7%
EFA202006	STY101782	77%	99.7%	99.7%
EFA202006	STM102043	77%	99.7%	99.7%
EFA202006	SAU800548	89%	100%	100%
EFA202006	SEP200072	89%	99.5%	99.5%
EFA202006	SHA101389	89%	100%	100%
EFA202006	SMU101538	77%	99.5%	99.5%
EFA202006	SPN401342	78%	99.5%	99.5%
EFA202006	SPY200441	77%	99.5%	99.5%
EFA202006	TPA100185	65%	99.7%	79.6%
EFA202006	UUR100528	71%	98.7%	98.7%
EFA202006	VCH100316	76%	99.7%	99.7%
EFA202006	VCH100357	76%	99.7%	99.7%
EFA202006	YPS000510	76%	100%	100%
EFA202006	YPS001855	76%	99.7%	99.7%
EFA202007	ABA100059	60%	87.9%	100%
EFA202007	BAN103750	78%	10.1%	95.9%
EFA202007	BAN113143	70%	76.6%	98.5%
EFA202007	BAN108186	79%	99.7%	98.9%
EFA202007	BFR12249	57%	62.8%	98.4%
EFA202007	BPT100846	61%	99.6%	99.9%
EFA202007	BBU100539	46%	98.1%	98.4%
EFA202007	BCE105443	62%	99.0%	99.3%
EFA202007	BFU104282	63%	99.0%	99.3%
EFA202007	BMA107083	63%	98.7%	86.5%
EFA202007	CJU100458	60%	99.7%	100%
EFA202007	CPN200199	58%	99.0%	99.6%
EFA202007	CTR200711	59%	99.0%	99.6%
EFA202007	CAC102763	64%	99.0%	99.4%
EFA202007	CBO100608	64%	98.7%	97.4%
EFA202007	CDF100548	67%	98.8%	99.4%
EFA202007	CDP100910	58%	99.1%	96.4%
EFA202007	EBC102893	60%	99.6%	99.9%
EFA202007	EFA202007	100%	100%	100%
EFA202007	EFM100881	27%	96.1%	96.5%
EFA202007	ECO103263	60%	99.6%	99.9%
EFA202007	HIN100559	61%	99.1%	99.4%
EFA202007	HPY101178	62%	99.7%	100%
EFA202007	KPN303651	62%	99.0%	99.1%
EFA202007	LMO102926	78%	99.9%	99.4%
EFA202007	MCA100232	60%	99.3%	98.9%
EFA202007	MAV102942	59%	98.8%	98.6%
EFA202007	MBV103317	59%	98.8%	98.6%
EFA202007	MLP101140	59%	98.8%	98.6%
EFA202007	MTU200681	59%	98.8%	98.6%
EFA202007	MGE100091	60%	99.0%	99.4%
EFA202007	MPN100604	60%	99.0%	99.4%
EFA202007	NGO101623	58%	99.7%	100%
EFA202007	NME200129	58%	99.7%	100%
EFA202007	PMU101356	61%	99.1%	99.4%
EFA202007	PRT100253	62%	99.1%	93.8%
EFA202007	PAE202069	61%	99.6%	99.9%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA202007	PPU109182	61%	99.7%	99.9%
EFA202007	PSY103391	59%	93.9%	100%
EFA202007	SPA102789	57%	99.6%	99.9%
EFA202007	STY101781	59%	99.6%	99.9%
EFA202007	SAU800547	75%	99.7%	99.9%
EFA202007	SEP200071	74%	99.7%	99.9%
EFA202007	SMU100688	86%	100%	100%
EFA202007	SPN400250	86%	99.7%	99.7%
EFA202007	SPY200202	87%	99.7%	99.9%
EFA202007	TPA100759	43%	97.8%	97.4%
EFA202007	UUR100529	62%	99.0%	99.1%
EFA202007	VCH100356	63%	99.6%	100%
EFA202007	YPS001853	60%	99.6%	99.9%
EFA202012	ABA100128	46%	99.0%	100%
EFA202012	BAN103804	67%	99.0%	100%
EFA202012	BFR10425	46%	99.0%	100%
EFA202012	BPT100895	42%	99.0%	100%
EFA202012	BBU100614	37%	99.5%	99.0%
EFA202012	BCE103241	45%	99.0%	100%
EFA202012	BFU101595	45%	99.0%	100%
EFA202012	BMA100015	44%	99.0%	100%
EFA202012	CJU101500	51%	99.0%	100%
EFA202012	CPN200012	39%	93.6%	91.9%
EFA202012	CTR200903	40%	93.6%	91.9%
EFA202012	CAC102218	42%	99.0%	100%
EFA202012	CBO101434	46%	99.0%	100%
EFA202012	CDF103315	46%	86.7%	91.6%
EFA202012	CDP100020	48%	99.0%	100%
EFA202012	EBC103653	45%	99.0%	100%
EFA202012	EFA202012	100%	100%	100%
EFA202012	ECO103219	45%	99.0%	100%
EFA202012	HIN100782	47%	99.0%	100%
EFA202012	HPY101276	47%	99.0%	100%
EFA202012	KPN300702	45%	99.0%	100%
EFA202012	LMO100680	72%	99.0%	100%
EFA202012	MCA100425	45%	99.0%	100%
EFA202012	MAV101010	47%	99.0%	100%
EFA202012	MBV100325	45%	99.0%	100%
EFA202012	MLP101195	45%	99.0%	100%
EFA202012	MTU203411	45%	99.0%	100%
EFA202012	MGE100317	41%	98.0%	98.0%
EFA202012	MPN100395	44%	98.0%	98.0%
EFA202012	NGO100887	45%	99.0%	100%
EFA202012	NME200098	45%	99.0%	100%
EFA202012	PMU101391	47%	99.0%	100%
EFA202012	PRT104446	46%	99.0%	100%
EFA202012	PAE204237	47%	99.0%	100%
EFA202012	PPU108168	46%	99.0%	100%
EFA202012	PSY107923	44%	99.0%	100%
EFA202012	SPA104316	44%	99.0%	100%
EFA202012	STY101827	44%	99.0%	100%
EFA202012	SAU801719	66%	99.0%	100%
EFA202012	SEP201745	66%	99.0%	100%
EFA202012	SHA100142	64%	99.0%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA202012	SMU101344	77%	100%	100%
EFA202012	SPN400078	76%	100%	100%
EFA202012	SPY201664	78%	100%	100%
EFA202012	TPA100303	40%	94.6%	96.1%
EFA202012	UUR100503	50%	99.0%	99.0%
EFA202012	VCH102535	46%	99.0%	100%
EFA202012	YPS002492	44%	99.0%	100%
EFA202013	ABA100054	52%	100%	100%
EFA202013	BAN101047	69%	100%	100%
EFA202013	BAN102922	82%	100%	100%
EFA202013	BFR102620	43%	98.7%	89.2%
EFA202013	BPT100845	53%	100%	90.2%
EFA202013	BBU100385	47%	100%	100%
EFA202013	BCE114655	51%	100%	100%
EFA202013	BFU100845	50%	100%	100%
EFA202013	BMA108128	51%	100%	100%
EFA202013	CJU100457	54%	98.7%	98.1%
EFA202013	CPN200198	47%	100%	100%
EFA202013	CTR200712	47%	100%	100%
EFA202013	CAC101300	68%	100%	100%
EFA202013	CBO100058	69%	100%	90.7%
EFA202013	CDF100549	72%	100%	100%
EFA202013	CDP100907	59%	98.7%	99.4%
EFA202013	EBC102895	53%	100%	100%
EFA202013	EFA202013	100%	100%	100%
EFA202013	ECO103264	53%	100%	87.2%
EFA202013	HIN100560	57%	100%	100%
EFA202013	HPY101179	54%	98.7%	98.1%
EFA202013	KPN300871	55%	92.9%	86.8%
EFA202013	LMO101111	83%	100%	100%
EFA202013	MCA100231	50%	100%	100%
EFA202013	MAV102943	60%	100%	100%
EFA202013	MBV103316	60%	100%	100%
EFA202013	MLP101141	58%	100%	100%
EFA202013	MTU200680	60%	100%	100%
EFA202013	MGE100090	61%	98.7%	99.4%
EFA202013	MPN100605	57%	98.7%	99.4%
EFA202013	NGO101627	51%	100%	100%
EFA202013	NME200130	51%	100%	100%
EFA202013	PMU101355	57%	100%	100%
EFA202013	PRT100252	55%	100%	100%
EFA202013	PAE204265	54%	100%	100%
EFA202013	PPU112217	53%	100%	100%
EFA202013	PSY106485	65%	26.3%	100%
EFA202013	SPA102393	49%	66.0%	91.2%
EFA202013	STY101780	53%	100%	100%
EFA202013	SAU800546	78%	100%	100%
EFA202013	SEP200070	78%	100%	100%
EFA202013	SHA102003	79%	25%	97.5%
EFA202013	SMU100686	78%	100%	100%
EFA202013	SPN400249	80%	100%	100%
EFA202013	SPY200201	80%	100%	100%
EFA202013	TPA100241	50%	100%	100%
EFA202013	UUR100530	64%	98.7%	99.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA202013	VCH100355	56%	100%	100%
EFA202013	YPS001851	54%	100%	100%
EFA202015	ABA100053	64%	99.3%	100%
EFA202015	BAN100648	83%	100%	97.9%
EFA202015	BFR10866	78%	54.7%	88.2%
EFA202015	BPT100844	69%	99.3%	98.4%
EFA202015	BBU100386	75%	100%	100%
EFA202015	BCE108786	69%	100%	98.4%
EFA202015	BFU100844	69%	100%	98.4%
EFA202015	BMA100034	68%	100%	98.4%
EFA202015	CJU100456	70%	100%	96.9%
EFA202015	CPN200197	67%	99.3%	100%
EFA202015	CTR200713	68%	99.3%	100%
EFA202015	CAC103453	71%	99.3%	98.4%
EFA202015	CBO102727	71%	99.3%	98.4%
EFA202015	CDF102422	76%	99.3%	95.1%
EFA202015	CDP100904	66%	99.3%	90.4%
EFA202015	EBC102897	70%	100%	100%
EFA202015	EFA202015	100%	100%	100%
EFA202015	ECO103265	70%	100%	100%
EFA202015	HIN100561	71%	100%	100%
EFA202015	HPY101180	69%	100%	91.9%
EFA202015	KPN200561	70%	100%	100%
EFA202015	LMO101449	88%	99.3%	99.3%
EFA202015	MCA100230	66%	100%	100%
EFA202015	MAV102944	64%	100%	100%
EFA202015	MBV103315	64%	99.3%	99.2%
EFA202015	MLP101142	63%	100%	100%
EFA202015	MTU200679	64%	99.3%	99.2%
EFA202015	MGE100089	73%	99.3%	97.8%
EFA202015	MPN100606	74%	100%	98.6%
EFA202015	NGO101631	67%	99.3%	100%
EFA202015	NME200131	68%	99.3%	100%
EFA202015	PMU101354	70%	100%	100%
EFA202015	PRT103411	61%	83.2%	93.6%
EFA202015	PAE204266	71%	99.3%	100%
EFA202015	PPU112031	70%	99.3%	100%
EFA202015	PSY103389	69%	99.3%	100%
EFA202015	SPA102395	70%	100%	100%
EFA202015	STY101779	70%	100%	100%
EFA202015	SAU800545	85%	99.3%	99.3%
EFA202015	SEP201889	86%	99.3%	99.3%
EFA202015	SHA101640	85%	99.3%	99.3%
EFA202015	SMU100684	89%	100%	100%
EFA202015	SPN400248	94%	100%	100%
EFA202015	SPY200200	89%	99.3%	99.3%
EFA202015	TPA100240	69%	100%	100%
EFA202015	UUR100531	72%	99.3%	96.5%
EFA202015	VCH100354	71%	100%	100%
EFA202015	YPS001825	70%	100%	100%
EFA202022	ABA104153	53%	100%	100%
EFA202022	BAN112139	75%	100%	100%
EFA202022	BAN112261	75%	100%	100%
EFA202022	BFR101219	56%	33.7%	93.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA202022	BPT102559	49%	100%	100%
EFA202022	BBU100803	49%	97.8%	98.9%
EFA202022	BCE114521	50%	100%	100%
EFA202022	BFU106341	51%	98.9%	97.8%
EFA202022	BMA104593	50%	100%	100%
EFA202022	CJU100816	46%	98.9%	97.8%
EFA202022	CPN200838	49%	100%	100%
EFA202022	CTR200226	49%	100%	100%
EFA202022	CAC101338	58%	97.8%	100%
EFA202022	CBO102464	58%	100%	85.6%
EFA202022	CDF100875	69%	92.1%	96.5%
EFA202022	CDP100449	57%	100%	100%
EFA202022	EBC103888	52%	100%	100%
EFA202022	EFA202022	100%	100%	100%
EFA202022	EFM202414	91%	100%	100%
EFA202022	ECO103097	52%	100%	100%
EFA202022	HIN101437	52%	100%	100%
EFA202022	HIN101294	52%	100%	100%
EFA202022	HPY101023	50%	98.9%	97.8%
EFA202022	KPN301430	53%	100%	100%
EFA202022	LPN100705	46%	69.7%	95.4%
EFA202022	LMO101938	79%	100%	100%
EFA202022	MCA100389	50%	100%	100%
EFA202022	MAV100300	53%	100%	100%
EFA202022	MBV101245	56%	100%	100%
EFA202022	MLP100514	57%	100%	100%
EFA202022	MTU202747	56%	100%	100%
EFA202022	MGE100434	45%	91.0%	94.2%
EFA202022	MPN100220	45%	91.0%	94.2%
EFA202022	NGO100722	56%	100%	100%
EFA202022	NME200754	56%	100%	100%
EFA202022	PMU100301	52%	100%	100%
EFA202022	PRT102435	57%	100%	100%
EFA202022	PAE204737	55%	100%	100%
EFA202022	PPU105055	55%	100%	100%
EFA202022	PSY104828	52%	70.8%	100%
EFA202022	SPA101259	49%	100%	100%
EFA202022	STY101470	51%	100%	100%
EFA202022	SAU801273	77%	100%	100%
EFA202022	SEP201566	73%	100%	100%
EFA202022	SHA100171	75%	100%	100%
EFA202022	SMU101327	77%	100%	100%
EFA202022	SPN401466	77%	100%	100%
EFA202022	SPY201503	78%	100%	100%
EFA202022	TPA100877	47%	100%	100%
EFA202022	UUR100204	43%	98.9%	98.9%
EFA202022	VCH100634	57%	100%	100%
EFA202022	YPS006344	52%	100%	100%
EFA202028	ABA106110	49%	97.2%	97.6%
EFA202028	BAN109088	44%	99.7%	99.6%
EFA202028	BAN100469	68%	99.7%	98.0%
EFA202028	BFR11379	45%	98.2%	90.1%
EFA202028	BPT102560	50%	98.4%	96.5%
EFA202028	BBU100804	42%	97.7%	98.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA202028	BCE107587	49%	99.3%	98.2%
EFA202028	BFU106344	49%	99.3%	98.0%
EFA202028	BMA106616	50%	97.7%	90.3%
EFA202028	CJU101178	40%	95.6%	97.5%
EFA202028	CPN200839	45%	97.3%	98.1%
EFA202028	CTR200225	44%	97.2%	98.0%
EFA202028	CAC102635	51%	99.0%	99.3%
EFA202028	CBO102281	52%	99.0%	99.0%
EFA202028	CDF100877	55%	100%	100%
EFA202028	CDP100447	43%	96.9%	95.4%
EFA202028	EBC103885	50%	97.9%	96.2%
EFA202028	EFA202028	100%	100%	100%
EFA202028	EFM200260	89%	100%	95.7%
EFA202028	ECO103096	50%	97.9%	93.3%
EFA202028	HIN100220	50%	98.4%	97.2%
EFA202028	HPY101196	37%	95.0%	96.9%
EFA202028	KPN301429	50%	97.9%	96.3%
EFA202028	LPN101324	48%	98.4%	94.5%
EFA202028	LMO100657	71%	99.7%	96.8%
EFA202028	MCA100390	49%	97.4%	98.4%
EFA202028	MAV100299	43%	99.3%	97.1%
EFA202028	MBV101241	44%	97.9%	96.5%
EFA202028	MLP100515	43%	97.9%	94.3%
EFA202028	MTU202745	44%	97.9%	96.5%
EFA202028	NGO102045	48%	100%	99.3%
EFA202028	NME200892	48%	100%	99.4%
EFA202028	PMU101114	50%	97.2%	95.7%
EFA202028	PRT102434	49%	98.6%	97.3%
EFA202028	PAE204736	50%	97.2%	97.3%
EFA202028	PPU105054	49%	97.9%	98.1%
EFA202028	PSY104827	48%	23.2%	81.6%
EFA202028	SPA101063	46%	2.0%	78.3%
EFA202028	STY100979	50%	97.2%	95.6%
EFA202028	SAU801274	62%	98.6%	99.3%
EFA202028	SEP201567	63%	99.3%	99.6%
EFA202028	SHA100393	41%	26.3%	99.5%
EFA202028	SHA101099	64%	98.2%	99.7%
EFA202028	SMU101329	67%	98.6%	95.1%
EFA202028	SPN400516	69%	98.6%	89.5%
EFA202028	SPY201498	67%	98.6%	97.7%
EFA202028	TPA100876	45%	97.0%	96.7%
EFA202028	VCH100635	50%	98.6%	97.5%
EFA202028	YPS001047	49%	97.6%	96.9%
EFA202110	BAN111119	49%	11.2%	82.8%
EFA202110	BAN105234	55%	85.4%	99.0%
EFA202110	BAN113086	66%	99.2%	99.8%
EFA202110	BFR101518	50%	98.7%	96.1%
EFA202110	BBU100560	47%	97.9%	99.1%
EFA202110	BCE101525	69%	99.2%	99.8%
EFA202110	BFU110445	68%	99.2%	99.8%
EFA202110	BMA101484	68%	99.2%	99.6%
EFA202110	CPN200393	49%	97.9%	96.9%
EFA202110	CTR200328	48%	99.2%	98.1%
EFA202110	CDP101096	52%	98.3%	96.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA202110	EBC100628	69%	59.6%	99.3%
EFA202110	EFA202110	100%	100%	100%
EFA202110	EFM100219	91%	42.3%	100%
EFA202110	ECO101988	72%	99.2%	99.6%
EFA202110	HIN100532	55%	98.7%	96.5%
EFA202110	KPN300636	71%	97.9%	100%
EFA202110	LMO100124	71%	99.2%	98.9%
EFA202110	MAV102693	52%	96.8%	93.3%
EFA202110	MBV102034	52%	92.8%	99.5%
EFA202110	MLP101249	52%	98.3%	95.9%
EFA202110	MTU201811	52%	98.9%	96.5%
EFA202110	NGO102016	54%	98.7%	96.9%
EFA202110	NME200246	54%	98.7%	96.9%
EFA202110	PMU101554	55%	98.7%	96.5%
EFA202110	PRT100074	75%	55.4%	100%
EFA202110	SPA105071	71%	99.2%	99.6%
EFA202110	STY103509	71%	99.2%	99.6%
EFA202110	SAU801511	67%	99.2%	99.6%
EFA202110	SEP200507	68%	99.2%	99.6%
EFA202110	SHA102447	62%	98.5%	98.9%
EFA202110	SHA100561	67%	99.2%	98.3%
EFA202110	SPN400335	80%	100%	100%
EFA202110	SPY102341	74%	16.3%	100%
EFA202110	TPA100327	51%	97.9%	96.1%
EFA202110	VCH103617	54%	98.7%	96.9%
EFA202110	YPS002961	71%	99.2%	99.6%
EFA202115	ABA101411	33%	95.5%	91.6%
EFA202115	BAN112326	40%	100%	99.9%
EFA202115	BFR102018	26%	99.7%	97.2%
EFA202115	BPT101552	32%	92.4%	91.7%
EFA202115	BBU100578	34%	97.3%	95.7%
EFA202115	BCE115231	33%	91.1%	88.8%
EFA202115	BFU107633	32%	92.1%	88.5%
EFA202115	BMA101634	32%	92.1%	89.9%
EFA202115	CJU100668	34%	89.6%	88.2%
EFA202115	CPN200079	31%	90.4%	87.7%
EFA202115	CTR200821	31%	91.0%	88.5%
EFA202115	CAC103161	33%	99.5%	98.9%
EFA202115	CBO100607	30%	99.5%	99.2%
EFA202115	CBO101196	33%	99.3%	98.5%
EFA202115	CDF101163	35%	96.4%	96.0%
EFA202115	CDP101233	29%	97.4%	97.2%
EFA202115	EBC102553	32%	96.7%	96.2%
EFA202115	EFA202115	100%	100%	100%
EFA202115	EFM200294	59%	100%	100%
EFA202115	ECO100184	32%	96.7%	96.2%
EFA202115	HIN100720	32%	99.5%	99.1%
EFA202115	HPY101439	30%	97.7%	97.9%
EFA202115	KPN301922	32%	96.7%	96.2%
EFA202115	LPN102982	34%	99.8%	99.6%
EFA202115	LMO100629	43%	100%	100%
EFA202115	MCA102321	33%	90.1%	87.2%
EFA202115	MAV103371	31%	95.9%	95.8%
EFA202115	MBV102577	30%	95.9%	96.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA202115	MLP100747	30%	95.9%	95.8%
EFA202115	MTU201526	30%	95.9%	95.4%
EFA202115	MGE100266	32%	73.6%	89.8%
EFA202115	MPN100459	33%	72.9%	89.1%
EFA202115	NGO101860	32%	91.8%	91.6%
EFA202115	NME200585	33%	91.8%	91.6%
EFA202115	PMU100034	32%	99.5%	99.1%
EFA202115	PRT101242	33%	94.7%	95.6%
EFA202115	PAE203638	34%	97.9%	97.6%
EFA202115	PPU100137	32%	99.8%	99.5%
EFA202115	PSY104339	32%	99.9%	99.6%
EFA202115	SPA100912	31%	99.3%	99.6%
EFA202115	STY103914	32%	96.7%	96.2%
EFA202115	STM103627	32%	96.7%	96.2%
EFA202115	SAU801703	37%	96.8%	97.0%
EFA202115	SEP201707	39%	93.6%	94.1%
EFA202115	SHA100359	38%	96.7%	94.3%
EFA202115	SMU101018	35%	98.9%	99.1%
EFA202115	SPN400795	35%	98.6%	97.9%
EFA202115	SPY200987	35%	97.5%	97.7%
EFA202115	TPA100661	33%	95.9%	95.5%
EFA202115	UUR100419	33%	90.1%	97.8%
EFA202115	VCH102211	33%	99.5%	98.7%
EFA202115	YPS001155	33%	96.7%	95.3%
EFA202136	EBC104273	60%	99.6%	100%
EFA202136	EFA202136	100%	100%	100%
EFA202136	EFM202058	70%	99.8%	99.1%
EFA202136	KPN303718	48%	99.8%	98.7%
EFA202136	LMO100287	63%	100%	99.6%
EFA202136	SPA103555	58%	100%	99.8%
EFA202136	STY104414	57%	100%	99.8%
EFA202136	STM100091	58%	100%	99.8%
EFA202136	SPN400244	53%	99.4%	99.6%
EFA202136	SPY201020	55%	99.8%	98.3%
EFA202160	ABA103852	41%	97.8%	98.3%
EFA202160	BAN106248	53%	95.1%	98.9%
EFA202160	BAN106209	62%	86.7%	99.8%
EFA202160	BFR10500	27%	92.8%	87.9%
EFA202160	BPT100432	40%	98.2%	98.5%
EFA202160	BBU100832	30%	83.7%	75.7%
EFA202160	BCE111670	42%	94.2%	95.8%
EFA202160	BFU101230	40%	97.0%	96.4%
EFA202160	BMA102496	34%	98.1%	94.7%
EFA202160	BMA109115	41%	98.6%	98.0%
EFA202160	CJU100989	38%	96.8%	99.8%
EFA202160	CPN200653	28%	92.8%	82.4%
EFA202160	CTR200283	29%	91.1%	82.0%
EFA202160	CAC102765	33%	83.6%	75.3%
EFA202160	CBO100873	35%	54.1%	95.1%
EFA202160	CDF104554	33%	83.6%	74.9%
EFA202160	CDP101247	27%	94.6%	84.7%
EFA202160	EBC102151	42%	97.7%	99.8%
EFA202160	EFA202160	100%	100%	100%
EFA202160	EFM201425	84%	100%	99.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA202160	ECO100026	44%	97.8%	98.1%
EFA202160	HPY101401	37%	98.5%	99.5%
EFA202160	KPN300290	59%	4.8%	100%
EFA202160	KPN306610	43%	96.5%	98.5%
EFA202160	LPN101832	43%	97.8%	98.1%
EFA202160	LMO101679	64%	99.0%	99.8%
EFA202160	MCA103671	39%	0.8%	16.4%
EFA202160	MAV103388	28%	91.3%	80.7%
EFA202160	MBV102555	28%	89.3%	81.0%
EFA202160	MLP100743	27%	93.2%	85.4%
EFA202160	MTU201515	28%	89.3%	81.0%
EFA202160	MGE100354	36%	98.2%	99.6%
EFA202160	MPN100322	38%	89.7%	96.1%
EFA202160	NGO101799	42%	98.2%	98.7%
EFA202160	NME200578	42%	98.2%	98.4%
EFA202160	PMU101662	41%	97.8%	98.0%
EFA202160	PRT101657	43%	98.9%	99.1%
EFA202160	PAE204558	42%	98.4%	98.6%
EFA202160	PPU109898	43%	97.8%	98.1%
EFA202160	PSY102684	40%	96.5%	98.5%
EFA202160	SPA100667	43%	80.7%	96.6%
EFA202160	STY101103	43%	98.6%	98.8%
EFA202160	STM100818	43%	98.6%	98.8%
EFA202160	SAU801193	61%	98.7%	99.7%
EFA202160	SEP200928	60%	98.7%	99.3%
EFA202160	SHA101034	60%	98.4%	99.9%
EFA202160	SMU100109	65%	100%	99.8%
EFA202160	SPN401501	64%	100%	99.8%
EFA202160	SPY201164	64%	100%	99.6%
EFA202160	TPA100448	26%	81.3%	74.2%
EFA202160	UUR100414	41%	89.7%	92%
EFA202160	VCH100669	42%	98.4%	98.6%
EFA202160	YPS000810	43%	97.8%	98.1%
EFA202166	ABA100699	32%	95.6%	92.2%
EFA202166	BAN102298	55%	87.1%	97%
EFA202166	BAN105813	52%	97.8%	97.3%
EFA202166	BFR10478	35%	87.1%	90.1%
EFA202166	BPT100358	32%	96.9%	81.5%
EFA202166	BCE102004	29%	98.2%	95.7%
EFA202166	BFU102631	28%	98.2%	95.7%
EFA202166	CJU100669	29%	88.4%	93.8%
EFA202166	CAC102293	34%	91.1%	92.8%
EFA202166	CBO100252	38%	87.6%	89.2%
EFA202166	CDF104041	40%	98.2%	94.1%
EFA202166	CDP100613	38%	95.1%	94.9%
EFA202166	EBC103402	26%	98.2%	95.7%
EFA202166	EFA202166	100%	100%	100%
EFA202166	EFM200029	62%	99.6%	99.6%
EFA202166	ECO102886	27%	98.2%	95.3%
EFA202166	HIN100089	31%	98.2%	94.5%
EFA202166	HPY100391	30%	88%	87.8%
EFA202166	KPN302105	28%	98.2%	95.7%
EFA202166	LPN100888	29%	98.2%	95.7%
EFA202166	LMO101181	54%	97.8%	95.6%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA202166	MCA100523	27%	86.2%	80.1%
EFA202166	MAV103261	26%	96%	88.5%
EFA202166	MBV100535	24%	96%	87.5%
EFA202166	MLP100574	26%	96%	88.5%
EFA202166	MTU202114	24%	96%	89.5%
EFA202166	NGO101964	29%	98.7%	97.4%
EFA202166	NME200206	29%	98.7%	97.4%
EFA202166	PMU100112	29%	98.2%	96.1%
EFA202166	PRT105809	27%	98.2%	95.3%
EFA202166	PAE200393	30%	98.2%	94.3%
EFA202166	PPU102082	30%	98.2%	95.2%
EFA202166	PSY103724	27%	98.2%	95.2%
EFA202166	SPA102546	23%	95.1%	96.8%
EFA202166	STY104582	27%	98.2%	95.3%
EFA202166	STM100599	27%	98.2%	95.3%
EFA202166	SAU801188	49%	97.8%	96.9%
EFA202166	SEP200921	51%	97.8%	97.7%
EFA202166	SHA100042	45%	43.1%	97.9%
EFA202166	SMU100094	50%	97.3%	97.8%
EFA202166	SPN401508	51%	98.7%	99.1%
EFA202166	SPY201169	50%	96.9%	97.3%
EFA202166	VCH100456	28%	98.2%	94.9%
EFA202166	YPS000235	25%	98.2%	95.3%
EFA202168	ABA100622	46%	92.2%	96.4%
EFA202168	BAN103024	59%	97.1%	96.6%
EFA202168	BAN112439	60%	97.1%	96.6%
EFA202168	BFR12421	41%	86.3%	83.3%
EFA202168	BPT102981	42%	94.1%	97.2%
EFA202168	BBU100298	49%	97.8%	93.1%
EFA202168	BCE103310	50%	69.8%	98.6%
EFA202168	BFU100408	44%	94.6%	97.2%
EFA202168	BMA104500	44%	94.6%	97.2%
EFA202168	CJU100646	45%	78.8%	87.0%
EFA202168	CAC100838	60%	85.6%	91.2%
EFA202168	CBO103263	52%	98.8%	98.6%
EFA202168	CDF102447	52%	100%	98.0%
EFA202168	CDP101254	51%	96.3%	98.1%
EFA202168	EBC101797	60%	37.3%	93.9%
EFA202168	EFA202168	100%	100%	100%
EFA202168	EFM200220	80%	100%	100%
EFA202168	ECO100095	51%	84.1%	90.1%
EFA202168	HIN101117	46%	82.7%	84.6%
EFA202168	HPY100963	43%	75.1%	80.8%
EFA202168	KPN300530	60%	37.6%	96.2%
EFA202168	LPN100473	71%	6.8%	71.8%
EFA202168	LMO101235	57%	98.5%	98.0%
EFA202168	MCA101528	48%	76.1%	87.4%
EFA202168	MAV103265	60%	76.3%	80.9%
EFA202168	MBV100533	61%	76.3%	82.6%
EFA202168	MLP100572	59%	76.3%	82.6%
EFA202168	MTU202116	61%	76.3%	82.6%
EFA202168	MGE100229	27%	54.4%	59.3%
EFA202168	MPN100519	29%	52.7%	55.8%
EFA202168	NGO100577	50%	83.9%	89.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA202168	NME201901	50%	83.9%	89.3%
EFA202168	PMU100147	47%	82.4%	82.7%
EFA202168	PRT102627	57%	42.9%	94.1%
EFA202168	PAE204405	53%	86.3%	93.1%
EFA202168	PPU105993	45%	99.3%	99.2%
EFA202168	PSY103835	47%	99.3%	99.2%
EFA202168	SPA100031	42%	56.1%	88.5%
EFA202168	STY103211	51%	84.1%	90.1%
EFA202168	STM102893	51%	84.1%	90.1%
EFA202168	SAU801186	69%	76.3%	80.3%
EFA202168	SEP200917	67%	79.8%	81.7%
EFA202168	SHA100846	67%	79.8%	81.9%
EFA202168	SMU100085	60%	99.8%	100%
EFA202168	SPN401509	62%	99.8%	100%
EFA202168	SPY201170	60%	99.8%	100%
EFA202168	TPA100386	46%	96.6%	94.7%
EFA202168	VCH102362	57%	76.3%	78.9%
EFA202168	YPS001023	51%	80.5%	89.6%
EFA202170	ABA100623	28%	82.7%	89.0%
EFA202170	BAN111291	39%	98.9%	99.8%
EFA202170	BAN101900	39%	100%	100%
EFA202170	BFR102146	22%	98.4%	89.5%
EFA202170	BPT102984	36%	82.7%	90.4%
EFA202170	BBU100299	32%	83.0%	90.3%
EFA202170	BCE109663	36%	83.6%	91.2%
EFA202170	BFU100407	35%	82.5%	89.8%
EFA202170	BMA104126	37%	83.6%	91.2%
EFA202170	CJU100645	29%	76.4%	72.3%
EFA202170	CAC100288	26%	98.2%	98.8%
EFA202170	CBO102974	30%	98.2%	96.5%
EFA202170	EBC101798	33%	83.6%	90.9%
EFA202170	EFA202170	100%	100%	100%
EFA202170	EFM201888	78%	100%	100%
EFA202170	ECO100094	33%	83.6%	90.5%
EFA202170	HIN101116	31%	85%	91.1%
EFA202170	HPY100962	28%	83.0%	81.3%
EFA202170	KPN300531	28%	45.5%	86.9%
EFA202170	LPN103001	33%	83.0%	89.8%
EFA202170	LMO101001	41%	100%	100%
EFA202170	MCA100438	24%	78.0%	79.9%
EFA202170	MBV102872	34%	16.4%	56.6%
EFA202170	MTU200123	34%	16.4%	56.6%
EFA202170	NGO100578	35%	83.0%	89.6%
EFA202170	NME201902	35%	83.0%	89.6%
EFA202170	PMU100146	29%	85.5%	91.5%
EFA202170	PRT102629	33%	83.6%	90.9%
EFA202170	PAE204406	34%	83.6%	89.4%
EFA202170	PPU111774	35%	83.0%	89.8%
EFA202170	PSY103837	34%	83.6%	91.0%
EFA202170	SPA101844	32%	83.6%	90.4%
EFA202170	STY103209	33%	83.6%	90.5%
EFA202170	STM102892	33%	83.6%	90.5%
EFA202170	SAU801185	30%	84.3%	78.7%
EFA202170	SEP200915	29%	96.1%	86.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA202170	SHA100845	28%	96.1%	84.3%
EFA202170	SMU100084	49%	100%	100%
EFA202170	SPN401510	50%	100%	99.8%
EFA202170	SPY201171	49%	100%	100%
EFA202170	TPA100385	33%	82.7%	91.3%
EFA202170	VCH102363	31%	85.5%	93.6%
EFA202170	YPS001022	33%	83.6%	90.9%
EFA202174	ABA100632	27%	99.2%	97.0%
EFA202174	BAN107483	51%	100%	99.7%
EFA202174	BAN105119	52%	100%	94.5%
EFA202174	BFR11299	36%	97.0%	92.9%
EFA202174	BPT103001	28%	98.1%	96.1%
EFA202174	BBU100766	28%	91.7%	89.0%
EFA202174	BCE108020	29%	66.7%	94%
EFA202174	BFU100818	28%	99.2%	94.4%
EFA202174	BMA103256	29%	98.1%	94.6%
EFA202174	CJU100967	26%	83.5%	82.5%
EFA202174	CPN200945	29%	92.8%	91.6%
EFA202174	CTR200137	28%	98.6%	97.2%
EFA202174	CAC102068	31%	94.5%	93.3%
EFA202174	CBO103711	29%	94.5%	96.3%
EFA202174	CDF103133	40%	98.9%	88.3%
EFA202174	CDP101267	33%	99.7%	96.9%
EFA202174	EBC102568	32%	79.1%	97.9%
EFA202174	EFA202174	100%	100%	100%
EFA202174	EFM201770	63%	100%	99.4%
EFA202174	ECO100090	30%	97.5%	95.5%
EFA202174	HIN101112	31%	98.9%	97.7%
EFA202174	HPY101138	26%	100%	99.4%
EFA202174	KPN301850	31%	98.9%	98.9%
EFA202174	LPN102672	32%	18.7%	86.8%
EFA202174	LMO101815	51%	100%	99.7%
EFA202174	MCA100895	30%	95.3%	92.1%
EFA202174	MAV103649	27%	98.3%	87.5%
EFA202174	MBV100527	26%	97.8%	87.3%
EFA202174	MLP100569	25%	99.7%	88.9%
EFA202174	MTU202119	26%	97.8%	87.3%
EFA202174	NGO100586	30%	96.4%	95.2%
EFA202174	NME201906	30%	96.4%	95.2%
EFA202174	PMU100142	30%	98.6%	96.3%
EFA202174	PRT102635	31%	98.6%	96.7%
EFA202174	PAE204410	32%	96.4%	95.2%
EFA202174	PPU111778	29%	98.1%	92%
EFA202174	PSY103845	31%	98.1%	96.9%
EFA202174	SPA101848	28%	97.5%	97.1%
EFA202174	STY103176	29%	97.5%	95.5%
EFA202174	STM102888	29%	97.5%	95.5%
EFA202174	SAU801418	28%	93.4%	94.9%
EFA202174	SEP200353	30%	97.5%	97.5%
EFA202174	SHA100509	33%	44.1%	86.0%
EFA202174	SMU100081	24%	94.2%	92.2%
EFA202174	SPN400604	26%	94.5%	94.6%
EFA202174	SPY201173	25%	96.1%	94.4%
EFA202174	TPA100518	27%	99.4%	95.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA202174	VCH102366	28%	94.5%	92.1%
EFA202174	YPS001014	31%	97.5%	95.2%
EFA202176	ABA105049	31%	96.3%	97.8%
EFA202176	BAN101698	43%	96.9%	99.8%
EFA202176	BAN100427	51%	98.9%	99.8%
EFA202176	BFR11370	36%	96.9%	99.8%
EFA202176	BPT103005	30%	96.5%	95.9%
EFA202176	BBU100584	28%	97.1%	97.8%
EFA202176	BCE110975	31%	56.6%	97.7%
EFA202176	BFU100814	31%	98.7%	97.8%
EFA202176	BMA102821	33%	96.5%	98.2%
EFA202176	CJU100400	27%	85.1%	88.6%
EFA202176	CPN200948	29%	97.1%	98.8%
EFA202176	CTR200134	31%	96.3%	93.8%
EFA202176	CAC103488	33%	97.6%	97.4%
EFA202176	CBO101756	35%	96.9%	96.9%
EFA202176	CDF104583	37%	97.6%	99.3%
EFA202176	CDP101273	29%	96.5%	94.6%
EFA202176	EBC102570	31%	97.6%	99.1%
EFA202176	EFA202176	100%	100%	100%
EFA202176	EFM201395	71%	99.1%	100%
EFA202176	ECO100088	32%	97.6%	99.1%
EFA202176	HIN101110	34%	98.2%	99.8%
EFA202176	HPY100489	27%	82.2%	85.5%
EFA202176	KPN300322	37%	36.4%	83.7%
EFA202176	KPN301854	31%	97.6%	99.1%
EFA202176	LPN102050	32%	93.2%	100%
EFA202176	LMO100907	60%	99.3%	99.1%
EFA202176	MCA103645	31%	97.1%	98.7%
EFA202176	MAV103995	33%	43.4%	75.7%
EFA202176	MBV100523	28%	96.1%	95.7%
EFA202176	MLP100567	28%	96.1%	97.1%
EFA202176	MTU202121	29%	96.1%	97.1%
EFA202176	NGO100590	29%	97.8%	99.8%
EFA202176	NME201908	29%	97.8%	99.8%
EFA202176	PMU100140	33%	96.5%	97.9%
EFA202176	PRT102639	34%	98.2%	99.8%
EFA202176	PAE204412	32%	96.3%	97.5%
EFA202176	PPU105951	32%	95.4%	96.2%
EFA202176	PSY103849	32%	86.6%	99.7%
EFA202176	SPA102757	27%	76.8%	95.3%
EFA202176	STY103174	30%	97.6%	99.1%
EFA202176	STM102886	30%	97.6%	99.1%
EFA202176	SAU801183	50%	97.8%	98.0%
EFA202176	SEP200898	48%	97.6%	97.8%
EFA202176	SHA101312	51%	59.9%	100%
EFA202176	SMU100079	60%	99.1%	99.6%
EFA202176	SPN400603	60%	99.3%	100%
EFA202176	SPY201174	61%	99.1%	99.3%
EFA202176	TPA100893	27%	97.8%	98.5%
EFA202176	VCH102368	30%	96.3%	91.9%
EFA202176	YPS001010	32%	97.6%	99.1%
EFA202177	ABA100933	34%	94.7%	89.5%
EFA202177	BAN106826	40%	96.0%	96.6%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA202177	BAN112016	48%	96.0%	95.4%
EFA202177	BFR103500	29%	84.1%	82.2%
EFA202177	BPT103007	34%	87.2%	83.8%
EFA202177	BBU100302	36%	95.6%	92.3%
EFA202177	BCE112929	41%	50.8%	86.0%
EFA202177	BFU100825	36%	90.3%	86.4%
EFA202177	BMA100546	35%	93.8%	89.2%
EFA202177	CJU100401	41%	95.3%	91.2%
EFA202177	CPN200949	38%	84.4%	80.8%
EFA202177	CTR200133	35%	98.1%	96.1%
EFA202177	CAC103184	37%	95.3%	95.9%
EFA202177	CBO103583	38%	93.5%	94.3%
EFA202177	CBO100702	40%	95.6%	96.5%
EFA202177	CDF103820	37%	99.1%	96.4%
EFA202177	CDP101276	37%	99.1%	97.3%
EFA202177	EBC102571	39%	94.7%	89.2%
EFA202177	EFA202177	100%	100%	100%
EFA202177	EFM200138	72%	100%	100%
EFA202177	ECO100087	40%	94.7%	89.2%
EFA202177	HIN101109	37%	94.7%	89.2%
EFA202177	HPY100488	34%	95.3%	90.7%
EFA202177	KPN301856	39%	94.7%	89.2%
EFA202177	LPN102792	43%	53.9%	79.1%
EFA202177	LMO102708	53%	96.3%	96.0%
EFA202177	MCA100821	36%	94.7%	91.0%
EFA202177	MAV103996	35%	98.8%	96.9%
EFA202177	MLP100566	35%	98.8%	96.9%
EFA202177	MTU202122	35%	98.8%	96.9%
EFA202177	NGO100597	36%	93.5%	89.7%
EFA202177	NME201910	37%	93.5%	89.7%
EFA202177	PMU100139	38%	94.7%	89.2%
EFA202177	PRT102641	39%	94.7%	89.2%
EFA202177	PAE204413	38%	94.7%	89.2%
EFA202177	PPU105952	38%	94.1%	88.6%
EFA202177	PSY103851	37%	94.1%	88.6%
EFA202177	SPA102756	39%	94.7%	91.2%
EFA202177	STY103173	40%	94.7%	89.2%
EFA202177	STM102884	39%	94.7%	89.2%
EFA202177	SAU801182	51%	97.8%	98.8%
EFA202177	SEP200897	50%	97.8%	98.8%
EFA202177	SHA101311	51%	97.8%	98.8%
EFA202177	SMU101454	52%	99.1%	99.1%
EFA202177	SPN400305	55%	96.9%	96.9%
EFA202177	SPY201280	51%	97.8%	97.9%
EFA202177	TPA100341	25%	84.7%	78.5%
EFA202177	VCH102369	40%	94.7%	89.2%
EFA202177	YPS000995	40%	94.7%	89.2%
EFA202180	ABA105255	27%	75.5%	87.7%
EFA202180	BAN113613	36%	8.8%	86.3%
EFA202180	BAN105591	26%	95.1%	95.7%
EFA202180	BAN105395	34%	41.8%	93.8%
EFA202180	BAN110033	32%	96.4%	96.4%
EFA202180	BAN112091	32%	94.1%	94.7%
EFA202180	BFR101372	23%	89.9%	93.0%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA202180	BPT103014	24%	77.6%	90.1%
EFA202180	BBU100135	25%	82.9%	91.7%
EFA202180	BCE112144	27%	82.1%	90.4%
EFA202180	BFU100822	26%	77.8%	83.7%
EFA202180	BMA103887	25%	86.5%	96.6%
EFA202180	CJU100487	23%	81.9%	98.5%
EFA202180	CPN200330	23%	54.2%	66.6%
EFA202180	CTR200535	25%	50%	59.6%
EFA202180	CAC102451	28%	81.1%	97.4%
EFA202180	CAC102718	28%	96.0%	97.0%
EFA202180	CBO100210	28%	90.6%	91.9%
EFA202180	CDF104232	26%	83.6%	91.7%
EFA202180	CDP101283	27%	76.1%	94.6%
EFA202180	EBC102574	24%	70.6%	83.5%
EFA202180	EFA202180	100%	100%	100%
EFA202180	EFM201754	58%	99.6%	99.9%
EFA202180	ECO100084	24%	56.3%	66.0%
EFA202180	HIN101106	24%	76.0%	85.2%
EFA202180	HPY101533	22%	86.9%	98.5%
EFA202180	KPN309113	28%	56.5%	66.8%
EFA202180	LPN102605	27%	72.1%	90.1%
EFA202180	LMO101211	39%	97.6%	94.9%
EFA202180	MCA100818	25%	74.4%	84.7%
EFA202180	MAV104019	28%	73.6%	80.7%
EFA202180	MBV101482	33%	55.4%	63.3%
EFA202180	MLP100563	28%	74.3%	79.6%
EFA202180	MTU202129	33%	55.4%	60.1%
EFA202180	NGO102402	26%	76.8%	90.2%
EFA202180	NME201914	26%	76.8%	88.6%
EFA202180	PMU100136	25%	77.2%	87.9%
EFA202180	PRT102628	24%	80.2%	89.8%
EFA202180	PAE204416	26%	76.7%	89.5%
EFA202180	PPU111736	27%	70.4%	81.4%
EFA202180	PSY103856	27%	70.4%	82.3%
EFA202180	SPA102753	24%	65.1%	74.6%
EFA202180	STY101764	25%	83.6%	98.1%
EFA202180	STM102862	25%	56.3%	66.0%
EFA202180	SAU801181	33%	95.8%	93.4%
EFA202180	SEP200896	34%	97.2%	91.1%
EFA202180	SHA101310	33%	95.7%	98.2%
EFA202180	SMU101453	40%	99.1%	99.2%
EFA202180	SPN400304	38%	98.4%	98.7%
EFA202180	SPY201281	39%	99.5%	99.7%
EFA202180	TPA100752	24%	89.6%	88.2%
EFA202180	VCH102372	24%	78.7%	93.6%
EFA202180	YPS000992	26%	70.6%	80.7%
EFA202182	BAN113715	40%	37.0%	69.0%
EFA202182	BAN110605	30%	82.2%	91.7%
EFA202182	EFA202182	100%	100%	100%
EFA202182	EFM201482	39%	100%	100%
EFA202182	LMO102397	29%	68.9%	80%
EFA202182	SAU801180	24%	79.3%	80.5%
EFA202182	SEP200895	24%	77.8%	78.9%
EFA202182	SHA101309	28%	79.3%	80.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA202182	SMU101439	29%	68.1%	86.0%
EFA202182	SPN400303	32%	65.2%	83.8%
EFA202182	SPY201282	29%	77.0%	97.2%
EFA202182	UUR100048	23%	64.4%	29.3%
EFA202200	ABA105166	20%	92.4%	92.9%
EFA202200	BAN107094	43%	90.8%	92.7%
EFA202200	BAN107312	46%	99.3%	98.9%
EFA202200	BFR10436	27%	91.7%	93.7%
EFA202200	BCE105570	36%	34.2%	81.8%
EFA202200	BFU106862	34%	90.4%	88.0%
EFA202200	BMA103262	33%	92.4%	81.0%
EFA202200	CJU100294	34%	82.4%	89.1%
EFA202200	CPN200772	36%	96.9%	97.3%
EFA202200	CTR200597	29%	98.4%	98.1%
EFA202200	CAC102940	45%	67.6%	76.2%
EFA202200	CBO103748	35%	98.9%	98.3%
EFA202200	CDF101807	35%	99.3%	99.8%
EFA202200	CDP100939	29%	92.0%	91.3%
EFA202200	EBC102031	39%	98.2%	96.3%
EFA202200	EFA202200	100%	100%	100%
EFA202200	EFM100680	71%	98.4%	99.1%
EFA202200	ECO102460	38%	94.2%	93.0%
EFA202200	HIN100377	38%	92.0%	94.3%
EFA202200	HPY100965	36%	16.5%	61.2%
EFA202200	HPY100255	34%	84.2%	91.7%
EFA202200	KPN304083	38%	98.2%	95.0%
EFA202200	LPN102596	34%	97.3%	98.0%
EFA202200	LMO100760	43%	99.1%	98.2%
EFA202200	MCA102830	23%	97.8%	87.8%
EFA202200	MAV100804	31%	73.7%	80.5%
EFA202200	MBV104380	31%	73.7%	80.5%
EFA202200	MLP101180	31%	77.2%	81.8%
EFA202200	MTU201093	31%	73.7%	80.5%
EFA202200	NGO101103	34%	98.9%	99.1%
EFA202200	NME201434	35%	98.9%	97.3%
EFA202200	PMU100168	39%	92.4%	93.5%
EFA202200	PRT103272	36%	98.2%	95.9%
EFA202200	PAE203774	38%	98.0%	95.0%
EFA202200	PPU101396	38%	92.0%	89.5%
EFA202200	PSY103770	38%	98.0%	94.2%
EFA202200	SPA100549	41%	77.5%	94.3%
EFA202200	STY101689	37%	98.4%	98.2%
EFA202200	STM101426	37%	98.4%	98.2%
EFA202200	SAU801523	42%	98.7%	99.3%
EFA202200	SEP200892	42%	98.9%	99.6%
EFA202200	SHA100991	43%	97.3%	98.0%
EFA202200	SMU100701	48%	98.9%	98.9%
EFA202200	SPN401088	50%	98.9%	99.1%
EFA202200	SPY201154	48%	97.5%	98.2%
EFA202200	VCH100753	38%	92.9%	93.7%
EFA202200	YPS003204	38%	98.2%	95.9%
EFA202211	ABA101469	45%	13.9%	75%
EFA202211	ABA100694	41%	94.5%	96.0%
EFA202211	BAN108710	33%	93.3%	97.6%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA202211	BAN104310	52%	95.2%	89.0%
EFA202211	BFR11762	24%	93.1%	95.6%
EFA202211	BPT100013	40%	94.9%	94.7%
EFA202211	BBU100134	23%	94.0%	94.7%
EFA202211	BCE114784	44%	91.5%	88.6%
EFA202211	BFU113972	43%	91.5%	88.6%
EFA202211	BMA106479	44%	91.5%	88.6%
EFA202211	CJU100704	37%	94.0%	97.3%
EFA202211	CPN200082	39%	94.0%	95.1%
EFA202211	CTR200819	37%	100%	99.1%
EFA202211	CAC100205	26%	94.2%	97.4%
EFA202211	CBO102641	45%	92.8%	94.9%
EFA202211	CDF100504	46%	95.8%	98.1%
EFA202211	CDP100409	42%	93.5%	94.3%
EFA202211	EBC102800	42%	93.3%	94.8%
EFA202211	EFA202211	100%	100%	100%
EFA202211	EFM201250	81%	98.4%	99.1%
EFA202211	ECO102465	42%	93.8%	95.3%
EFA202211	HIN100348	44%	92.1%	93.6%
EFA202211	HPY101173	25%	91.2%	92.5%
EFA202211	KPN309062	44%	93.3%	94.8%
EFA202211	LPN101194	41%	95.6%	96.9%
EFA202211	LMO101789	52%	98.2%	99.8%
EFA202211	MCA101520	41%	93.8%	96.9%
EFA202211	MAV103034	42%	95.4%	96.9%
EFA202211	MBV101555	41%	99.1%	98.3%
EFA202211	MLP100305	40%	95.6%	95.6%
EFA202211	MTU202543	41%	99.1%	98.3%
EFA202211	MGE100035	40%	73.7%	75.1%
EFA202211	MPN100109	34%	94.0%	96.4%
EFA202211	NGO101009	45%	92.1%	93.3%
EFA202211	NME200980	45%	92.1%	93.3%
EFA202211	PMU102011	43%	95.6%	97.4%
EFA202211	PRT104870	43%	93.3%	94.8%
EFA202211	PAE203799	43%	94.0%	94.9%
EFA202211	PPU103989	44%	94.0%	94.9%
EFA202211	PSY103800	44%	94.0%	94.9%
EFA202211	SPA101921	45%	68.4%	97.7%
EFA202211	STY101721	42%	93.8%	95.3%
EFA202211	SAU801631	49%	95.6%	98.6%
EFA202211	SEP201577	48%	95.6%	97.6%
EFA202211	SHA100662	48%	96.1%	98.3%
EFA202211	SMU101274	60%	98.4%	98.8%
EFA202211	SPN401928	64%	98.4%	98.8%
EFA202211	SPY201649	61%	98.8%	100%
EFA202211	TPA100633	26%	71.1%	72.4%
EFA202211	UUR100287	37%	95.8%	98.8%
EFA202211	VCH100747	44%	93.3%	95.0%
EFA202211	YPS003230	43%	93.5%	95.0%
EFA202213	ABA101157	51%	98.3%	98.0%
EFA202213	BAN109213	44%	98.5%	99.3%
EFA202213	BAN103380	65%	100%	99.8%
EFA202213	BFR10266	52%	77.8%	99.1%
EFA202213	BPT101790	51%	99.3%	99.5%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA202213	BBU100445	49%	84.7%	98.8%
EFA202213	BCE104313	37%	16.3%	76.6%
EFA202213	BCE111669	52%	98.8%	98.3%
EFA202213	BFU111015	53%	98.8%	98.5%
EFA202213	BMA100432	53%	98.8%	98.3%
EFA202213	CJU100601	49%	98.3%	98.6%
EFA202213	CPN200083	47%	99.2%	99.7%
EFA202213	CTR200818	48%	98.8%	99.7%
EFA202213	CAC102618	51%	99.7%	98.5%
EFA202213	CBO100008	51%	98.5%	97.5%
EFA202213	CDF100502	54%	99.5%	98.5%
EFA202213	CDP100396	46%	98.5%	97.7%
EFA202213	EBC102309	52%	99.5%	99.5%
EFA202213	EFA202213	100%	100%	100%
EFA202213	EFM202626	80%	100%	100%
EFA202213	ECO101834	53%	98.6%	98.6%
EFA202213	HIN100302	52%	98.6%	99.0%
EFA202213	HPY100610	50%	98.3%	99.1%
EFA202213	KPN301306	57%	52.3%	96.8%
EFA202213	LPN101576	53%	98.3%	98.3%
EFA202213	LMO101015	68%	99.0%	98.8%
EFA202213	MCA100604	51%	98.6%	98.7%
EFA202213	MAV103031	46%	87.1%	99.6%
EFA202213	MBV101554	48%	96.1%	93.1%
EFA202213	MLP100306	47%	96.1%	96.1%
EFA202213	MTU202535	48%	96.1%	95.5%
EFA202213	MGE100036	36%	95.8%	95.8%
EFA202213	MPN100108	38%	96.8%	95.7%
EFA202213	NGO101633	53%	98.3%	99.0%
EFA202213	NME201865	53%	98.3%	97.8%
EFA202213	PMU100983	52%	98.6%	99.0%
EFA202213	PRT100115	52%	98.6%	100%
EFA202213	PAE200962	51%	98.3%	98.1%
EFA202213	PPU112195	51%	98.3%	98.1%
EFA202213	PSY106866	50%	90.5%	98.3%
EFA202213	SPA102449	51%	64.9%	98.0%
EFA202213	STY102265	53%	98.6%	98.6%
EFA202213	SAU801630	63%	99.2%	99.7%
EFA202213	SEP201575	63%	99.2%	99.7%
EFA202213	SHA100663	62%	99.2%	99.7%
EFA202213	SMU101272	63%	98.8%	98.0%
EFA202213	SPN401921	65%	98.8%	98.3%
EFA202213	SPY201648	62%	99.5%	99.8%
EFA202213	TPA100975	44%	98.8%	96.8%
EFA202213	UUR100288	45%	98.1%	99.0%
EFA202213	VCH101147	54%	98.6%	98.5%
EFA202213	YPS003419	54%	99.0%	97.7%
EFA202214	ABA101804	63%	74.5%	85.9%
EFA202214	BAN111062	82%	94.9%	98.9%
EFA202214	BAN102544	83%	94.9%	96.9%
EFA202214	BFR10883	53%	83.7%	92.1%
EFA202214	BPT102470	62%	81.6%	94.2%
EFA202214	BBU100779	55%	81.6%	97.5%
EFA202214	BCE103036	61%	85.7%	97.7%

Query LocusID	Homolog LocusID.	Identity	Query Coverage	Homolog Coverage
EFA202214	BFU106480	60%	85.7%	97.7%
EFA202214	BMA101618	60%	85.7%	97.7%
EFA202214	CJU100084	58%	83.7%	97.6%
EFA202214	CPN200204	58%	83.7%	95.2%
EFA202214	CTR200690	64%	85.7%	98.8%
EFA202214	CAC103330	68%	93.9%	92%
EFA202214	CBO102962	75%	93.9%	92%
EFA202214	CDF101911	69%	94.9%	96.9%
EFA202214	CDP101220	61%	81.6%	89.8%
EFA202214	EBC100461	61%	81.6%	95.3%
EFA202214	EFA202214	100%	100%	100%
EFA202214	EFM200824	96%	95.9%	96.9%
EFA202214	ECO103115	61%	81.6%	95.3%
EFA202214	HIN100859	58%	81.6%	94.1%
EFA202214	HPY100293	58%	81.6%	90.9%
EFA202214	KPN300596	60%	81.6%	95.3%
EFA202214	LPN100139	54%	83.7%	90.2%
EFA202214	LMO100798	85%	92.9%	94.8%
EFA202214	MCA101440	55%	81.6%	95.3%
EFA202214	MAV104122	57%	81.6%	89.8%
EFA202214	MBV104431	62%	81.6%	91.9%
EFA202214	MLP100903	59%	84.7%	93.2%
EFA202214	MTU202405	62%	81.6%	91.9%
EFA202214	MGE100239	61%	87.8%	82.7%
EFA202214	MPN100509	61%	90.8%	87.5%
EFA202214	NGO101635	57%	83.7%	92.2%
EFA202214	NME202000	59%	83.7%	92.2%
EFA202214	PMU100348	60%	81.6%	95.3%
EFA202214	PRT100790	60%	81.6%	95.3%
EFA202214	PAE204565	66%	81.6%	95.3%
EFA202214	PPU109793	62%	73.5%	84.7%
EFA202214	PSY102707	56%	83.7%	91.2%
EFA202214	SPA100460	61%	81.6%	95.3%
EFA202214	STY101487	61%	81.6%	95.3%
EFA202214	SAU801645	81%	94.9%	93.9%
EFA202214	SEP201610	82%	94.9%	93.9%
EFA202214	SHA100024	84%	94.9%	93.9%
EFA202214	SMU100757	93%	90.8%	91.8%
EFA202214	SPN401014	90%	89.8%	98.9%
EFA202214	SPY200612	92%	90.8%	91.8%
EFA202214	TPA100735	56%	81.6%	93.1%
EFA202214	UUR100211	57%	96.9%	95%
EFA202214	VCH100431	62%	81.6%	94.2%
EFA202214	YPS002142	61%	81.6%	95.3%
EFA202216	BAN108189	34%	94.7%	93.9%
EFA202216	BAN100435	34%	94.7%	93.9%
EFA202216	CAC103671	25%	94.7%	96.0%
EFA202216	CBO101665	33%	94.7%	95.4%
EFA202216	CDF103326	31%	94.7%	97.1%
EFA202216	EFA202216	100%	100%	100%
EFA202216	EFM200511	74%	100%	100%
EFA202216	LMO102819	32%	86.0%	88.6%
EFA202216	SAU801646	36%	85.1%	82.1%
EFA202216	SEP201611	37%	85.1%	86.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA202216	SHA100023	35%	86.0%	87.7%
EFA202216	SMU100756	37%	99.1%	100%
EFA202216	SPN401013	45%	99.1%	99.1%
EFA202216	SPY200611	40%	97.4%	100%
EFA202216	TPA100736	43%	44.7%	44.4%
EFA202216	UUR100212	44%	25.4%	28.4%
EFA202217	ABA105440	41%	95.3%	99.0%
EFA202217	BAN107763	67%	96.2%	100%
EFA202217	BAN108298	67%	96.2%	100%
EFA202217	BFR10884	41%	99.1%	89.3%
EFA202217	BPT104764	46%	99.1%	43.3%
EFA202217	BBU100777	33%	94.3%	98.1%
EFA202217	BCE111959	48%	96.2%	100%
EFA202217	BFU106477	47%	98.1%	84.7%
EFA202217	BMA107479	47%	96.2%	100%
EFA202217	CJU100083	42%	96.2%	100%
EFA202217	CPN200203	44%	93.4%	95.3%
EFA202217	CTR200691	43%	90.6%	92.5%
EFA202217	CAC100327	52%	96.2%	100%
EFA202217	CBO100385	53%	99.1%	80.5%
EFA202217	CDF101910	51%	99.1%	100%
EFA202217	CDP101222	38%	94.3%	99.0%
EFA202217	EBC100460	42%	26.4%	87.5%
EFA202217	EFA202217	100%	100%	100%
EFA202217	EFM200259	96%	96.2%	100%
EFA202217	ECO103116	41%	96.2%	100%
EFA202217	HIN100860	44%	96.2%	100%
EFA202217	HPY100292	40%	95.3%	98.1%
EFA202217	KPN300595	40%	84.0%	100%
EFA202217	LPN100481	44%	94.3%	98.1%
EFA202217	LMO101855	65%	96.2%	100%
EFA202217	MCA101422	48%	96.2%	100%
EFA202217	MAV102387	39%	93.4%	96.1%
EFA202217	MBV104430	40%	97.2%	99.0%
EFA202217	MLP100904	40%	93.4%	96.1%
EFA202217	MTU202406	40%	97.2%	99.0%
EFA202217	MGE100237	36%	91.5%	94%
EFA202217	MPN100511	40%	91.5%	94%
EFA202217	NGO101632	44%	98.1%	92.1%
EFA202217	NME201999	45%	94.3%	99.0%
EFA202217	PMU100347	47%	96.2%	100%
EFA202217	PRT100789	43%	94.3%	99.0%
EFA202217	PAE204566	47%	96.2%	100%
EFA202217	PPU108773	46%	95.3%	65.0%
EFA202217	PSY108282	47%	97.2%	65.4%
EFA202217	SPA100461	38%	66.0%	98.6%
EFA202217	STY101488	40%	96.2%	100%
EFA202217	SAU801647	62%	96.2%	100%
EFA202217	SEP201612	62%	96.2%	100%
EFA202217	SMU100215	79%	97.2%	99.0%
EFA202217	SPN401012	82%	97.2%	99.0%
EFA202217	SPY200610	79%	97.2%	99.0%
EFA202217	TPA100737	39%	94.3%	97.1%
EFA202217	UUR100213	53%	95.3%	98%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA202217	VCH100430	49%	96.2%	100%
EFA202217	YPS002148	39%	96.2%	100%
EFA202221	ABA100916	42%	98.2%	98.0%
EFA202221	BAN105403	40%	100%	61.2%
EFA202221	BAN108663	55%	100%	100%
EFA202221	BFR10219	46%	99.0%	99.8%
EFA202221	BPT100915	43%	96.2%	94.5%
EFA202221	BBU100056	49%	98.5%	98.7%
EFA202221	BCE102342	44%	96.0%	94.2%
EFA202221	BFU103508	43%	98.7%	97.2%
EFA202221	BMA100384	44%	97.2%	74.1%
EFA202221	CJU101321	46%	99.0%	98%
EFA202221	CPN200066	43%	98.2%	97.8%
EFA202221	CTR200065	45%	98.2%	97.8%
EFA202221	CAC103753	60%	99.5%	99.0%
EFA202221	CBO101340	56%	99.5%	98.5%
EFA202221	CDF102694	57%	99.5%	98.8%
EFA202221	CDP100277	50%	98.7%	99.0%
EFA202221	EBC103702	45%	98.2%	97.4%
EFA202221	EFA202221	100%	100%	100%
EFA202221	EFM101382	85%	46.3%	100%
EFA202221	ECO102861	45%	98.2%	97.4%
EFA202221	HIN100504	46%	96.7%	95.9%
EFA202221	HPY101327	43%	97.2%	95.0%
EFA202221	KPN300275	52%	13.9%	70.5%
EFA202221	KPN303058	45%	98.2%	97.4%
EFA202221	LPN100314	44%	98.7%	97.0%
EFA202221	LMO100280	79%	100%	100%
EFA202221	MCA101090	39%	99.2%	99.7%
EFA202221	MAV100345	46%	98.5%	96.9%
EFA202221	MBV102164	46%	94.7%	58.1%
EFA202221	MLP100355	45%	97.7%	95.4%
EFA202221	MTU201418	45%	98.5%	96.8%
EFA202221	MGE100306	48%	98.5%	96.9%
EFA202221	MPN100412	50%	99.2%	99.0%
EFA202221	NGO102027	44%	99.2%	97.5%
EFA202221	NME200241	43%	100%	99.5%
EFA202221	PMU101860	46%	96.7%	95.9%
EFA202221	PRT106062	46%	98.2%	97.9%
EFA202221	PAE200551	45%	98.2%	97.4%
EFA202221	PPU104664	44%	98.2%	97.4%
EFA202221	PSY100209	43%	98.2%	96.9%
EFA202221	SPA101905	45%	98.2%	97.9%
EFA202221	STY104499	45%	98.2%	97.4%
EFA202221	SAU800773	73%	100%	100%
EFA202221	SEP201416	73%	100%	100%
EFA202221	SHA101582	73%	100%	100%
EFA202221	SMU100692	67%	100%	100%
EFA202221	SPN400441	68%	100%	100%
EFA202221	SPY201449	68%	100%	100%
EFA202221	TPA100532	44%	99.2%	99.5%
EFA202221	UUR100281	38%	99.2%	96.7%
EFA202221	VCH100472	44%	96.7%	94.6%
EFA202221	YPS000197	45%	98.2%	97.4%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA202223	ABA104568	61%	97.9%	99.8%
EFA202223	BAN112137	72%	8.3%	97.3%
EFA202223	BAN104797	54%	98.6%	99.5%
EFA202223	BAN107021	79%	99.5%	99.8%
EFA202223	BFR12193	67%	96.5%	97.4%
EFA202223	BPT101700	63%	99.5%	100%
EFA202223	BBU100336	66%	99.3%	99.1%
EFA202223	BCE108074	66%	99.5%	100%
EFA202223	BFU100260	67%	67.4%	98.6%
EFA202223	BFU102355	65%	99.5%	100%
EFA202223	BMA107873	63%	48.8%	99.5%
EFA202223	CJU101577	55%	95.1%	97.3%
EFA202223	CPN201052	59%	96.5%	95.8%
EFA202223	CTR200865	58%	98.1%	98.3%
EFA202223	CAC102398	68%	98.8%	98.4%
EFA202223	CBO103490	68%	98.6%	98.1%
EFA202223	CDF100088	70%	22.2%	100%
EFA202223	CDF100292	71%	99.5%	95.8%
EFA202223	CDP100889	60%	98.6%	98.8%
EFA202223	EBC102297	64%	98.1%	98.6%
EFA202223	EFA202223	100%	100%	100%
EFA202223	EFM100534	97%	88.7%	100%
EFA202223	ECO102719	65%	98.1%	98.6%
EFA202223	HIN100911	64%	98.4%	98.9%
EFA202223	HPY100151	57%	95.8%	96.7%
EFA202223	KPN305114	65%	98.1%	98.6%
EFA202223	LPN102643	59%	94.7%	96.2%
EFA202223	LMO102639	78%	99.5%	99.8%
EFA202223	MCA101099	60%	98.8%	95.7%
EFA202223	MAV105503	58%	98.6%	98.1%
EFA202223	MBV103580	58%	98.1%	95.4%
EFA202223	MLP100182	57%	98.1%	93.7%
EFA202223	MTU201012	58%	98.6%	98.1%
EFA202223	MGE100419	55%	99.8%	97.2%
EFA202223	MPN100236	56%	98.8%	96.7%
EFA202223	NGO100995	63%	99.3%	99.5%
EFA202223	NME201361	63%	99.3%	99.5%
EFA202223	PMU101871	65%	98.4%	98.8%
EFA202223	PRT101034	63%	98.1%	98.6%
EFA202223	PAE203633	64%	98.6%	99.5%
EFA202223	PPU109835	63%	94.0%	99.5%
EFA202223	PSY104326	63%	98.6%	91.0%
EFA202223	SPA104184	65%	98.1%	98.6%
EFA202223	STY103508	65%	98.1%	98.6%
EFA202223	SAU800776	74%	99.3%	99.5%
EFA202223	SEP201419	72%	99.3%	99.5%
EFA202223	SHA101585	78%	39.8%	100%
EFA202223	SMU100190	80%	99.5%	99.8%
EFA202223	SPN401036	82%	99.5%	99.8%
EFA202223	SPY200535	80%	99.5%	99.8%
EFA202223	TPA100808	62%	98.6%	98.8%
EFA202223	UUR100184	47%	97.9%	98.9%
EFA202223	VCH102411	63%	98.1%	98.6%
EFA202223	YPS000129	65%	98.1%	98.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA202274	ABA100276	27%	95.0%	96.4%
EFA202274	BAN108536	59%	98.4%	99.9%
EFA202274	BAN106673	61%	99.4%	99.3%
EFA202274	BFR102747	29%	97.5%	98.5%
EFA202274	BPT101447	26%	95.4%	95.3%
EFA202274	BBU100586	25%	97.6%	90.7%
EFA202274	BCE102027	26%	71.3%	92.2%
EFA202274	BFU100073	25%	56.6%	88.0%
EFA202274	BMA108903	26%	71.6%	92.5%
EFA202274	CJU100777	39%	97.3%	99.2%
EFA202274	CPN200639	27%	70.8%	90.9%
EFA202274	CTR200296	28%	70.3%	90.2%
EFA202274	CAC100973	54%	98.4%	99.5%
EFA202274	CBO102771	55%	95.6%	92.4%
EFA202274	CDF101033	52%	95.0%	96.3%
EFA202274	CDP100167	29%	70.3%	84.4%
EFA202274	EBC101813	28%	96.5%	97.3%
EFA202274	EFA202274	100%	100%	100%
EFA202274	EFM201416	86%	98.8%	100%
EFA202274	ECO102073	29%	95.1%	96.0%
EFA202274	HIN101245	27%	98.1%	99.1%
EFA202274	HPY100413	38%	97.6%	99.2%
EFA202274	KPN304492	29%	95.1%	95.6%
EFA202274	LPN100787	27%	96.2%	97.5%
EFA202274	LMO100235	67%	98.4%	99.4%
EFA202274	MCA102320	28%	98.8%	100%
EFA202274	MAV104609	42%	8.0%	78.3%
EFA202274	MAV106118	42%	76.8%	98.8%
EFA202274	MBV100570	41%	76.2%	97.9%
EFA202274	MLP100169	42%	76.2%	95.0%
EFA202274	MTU200996	41%	76.2%	97.9%
EFA202274	MGE100021	35%	76.1%	99.2%
EFA202274	MPN100131	36%	76.1%	99.2%
EFA202274	NGO101883	28%	95.9%	97.4%
EFA202274	NME200259	27%	95.9%	97.4%
EFA202274	PMU100303	29%	97.0%	98.1%
EFA202274	PRT101803	28%	94.2%	95.3%
EFA202274	PAE203480	26%	95.4%	96.6%
EFA202274	PPU101569	27%	95.4%	96.6%
EFA202274	PSY100792	27%	95.4%	96.6%
EFA202274	SPA103088	28%	69.1%	85.0%
EFA202274	STY104199	29%	95.1%	96.0%
EFA202274	STM103952	29%	95.1%	96.0%
EFA202274	SAU800490	58%	98.2%	99.5%
EFA202274	SEP201823	57%	98.2%	99.5%
EFA202274	SHA100909	57%	98.2%	99.5%
EFA202274	SMU101170	62%	98.7%	99.9%
EFA202274	SPN400696	64%	98.7%	97.8%
EFA202274	SPY200301	62%	97.9%	99.2%
EFA202274	TPA100790	25%	96.8%	91.6%
EFA202274	UUR100197	44%	77.7%	100%
EFA202274	VCH101017	28%	95.9%	90.6%
EFA202274	YPS002325	27%	94.2%	95.3%
EFA202276	ABA104455	25%	93.7%	84.1%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA202276	BAN109049	46%	14.0%	74.7%
EFA202276	BAN110149	32%	98.1%	97.6%
EFA202276	BAN106497	35%	90.7%	97.7%
EFA202276	BAN105967	41%	99.1%	97.2%
EFA202276	BAN110560	41%	98.1%	96.2%
EFA202276	BAN109567	44%	94.4%	97.1%
EFA202276	BAN113683	44%	98.1%	96.6%
EFA202276	BFR11337	36%	98.3%	86.3%
EFA202276	BCE113281	45%	98.3%	95.8%
EFA202276	BMA110031	44%	98.3%	98.1%
EFA202276	CAC101716	33%	29.4%	97.1%
EFA202276	CAC102152	41%	68.7%	100%
EFA202276	CAC102361	41%	98.3%	97.2%
EFA202276	EFA202276	100%	100%	100%
EFA202276	EFM202409	67%	52.9%	98%
EFA202276	LPN100410	27%	87.9%	97.7%
EFA202276	LMO102666	49%	98.1%	98.5%
EFA202276	MCA100347	23%	82.5%	83.3%
EFA202276	MAV101379	36%	94.6%	90.7%
EFA202276	MBV104872	36%	94.4%	93.5%
EFA202276	MTU203210	36%	94.4%	92.3%
EFA202276	MGE100231	21%	59.4%	68.6%
EFA202276	MPN100517	23%	67.8%	66.4%
EFA202276	PMU100162	22%	75.2%	74.0%
EFA202276	PAE203595	23%	92.0%	92.7%
EFA202276	PPU108666	25%	94.0%	81.2%
EFA202276	SPA101650	22%	90.9%	94.4%
EFA202276	SAU802603	33%	97.8%	96.1%
EFA202276	SEP201258	35%	97.4%	95.4%
EFA202276	SHA101835	34%	98.1%	96.1%
EFA202276	SMU101189	50%	98.7%	98.1%
EFA202276	SPN400905	49%	98.7%	98.7%
EFA202276	SPY200012	51%	98.5%	99.4%
EFA202296	ABA100452	38%	95.5%	97.6%
EFA202296	BFR103869	46%	91.5%	99.6%
EFA202296	BPT101155	44%	91.5%	90.3%
EFA202296	BBU100697	41%	90.7%	92.5%
EFA202296	BCE110744	42%	91.1%	86.4%
EFA202296	BFU102064	42%	91.1%	88.0%
EFA202296	BMA102082	40%	91.1%	86.4%
EFA202296	CJU100663	42%	90.7%	96.6%
EFA202296	CPN200644	47%	90.7%	60.7%
EFA202296	CTR200291	43%	90.7%	62.2%
EFA202296	CAC101341	43%	97.2%	97.1%
EFA202296	CBO102927	48%	98.8%	98.8%
EFA202296	CDF104123	52%	90.7%	97.0%
EFA202296	CDP101153	40%	93.1%	92.8%
EFA202296	EBC100905	46%	98.8%	95.3%
EFA202296	EFA202296	100%	100%	100%
EFA202296	ECO102554	46%	98.8%	95.3%
EFA202296	HIN100192	47%	98.8%	98.8%
EFA202296	HPY101131	39%	91.5%	98.3%
EFA202296	KPN300514	37%	46.3%	100%
EFA202296	LPN101866	43%	98.8%	97.2%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA202296	LMO102506	61%	97.2%	98.0%
EFA202296	MCA100037	35%	96.3%	98%
EFA202296	MAV103396	46%	91.1%	95.0%
EFA202296	MBV102286	47%	90.7%	98.3%
EFA202296	MLP100985	45%	90.7%	95.0%
EFA202296	MTU202868	47%	90.7%	98.3%
EFA202296	MGE100454	41%	90.7%	94.4%
EFA202296	MPN100183	45%	82.1%	93.8%
EFA202296	NGO102006	42%	100%	98.8%
EFA202296	NME200733	44%	100%	98.8%
EFA202296	PMU101297	48%	98.8%	99.2%
EFA202296	PRT100820	47%	98.8%	97.2%
EFA202296	PAE203740	44%	98.4%	96.8%
EFA202296	PPU107801	47%	98.8%	97.2%
EFA202296	PSY102681	47%	98.8%	94.2%
EFA202296	SPA101890	45%	98.0%	94.5%
EFA202296	STY102217	46%	98.8%	95.3%
EFA202296	SAU801240	54%	98.0%	97.6%
EFA202296	SEP201533	54%	98.8%	98.4%
EFA202296	SMU100806	58%	98.8%	98.8%
EFA202296	SPN400687	60%	99.6%	100%
EFA202296	SPY200632	59%	98.4%	97.1%
EFA202296	TPA100898	40%	98.8%	97.2%
EFA202296	UUR100574	42%	91.5%	96.9%
EFA202296	VCH100553	47%	98.8%	98.4%
EFA202296	YPS003421	45%	99.6%	99.6%
EFA202298	ABA100455	62%	96.5%	91.0%
EFA202298	BFR102397	59%	84.3%	82.9%
EFA202298	BPT100242	55%	94.8%	90.5%
EFA202298	BBU100698	49%	94.8%	90.9%
EFA202298	BCE107881	54%	94.8%	87.7%
EFA202298	BFU102066	54%	97.4%	90.7%
EFA202298	BMA100174	54%	94.8%	88.4%
EFA202298	CJU100664	48%	99.1%	98.3%
EFA202298	CPN200643	51%	94.8%	90.1%
EFA202298	CTR200292	49%	98.3%	93.4%
EFA202298	CAC102258	60%	99.1%	100%
EFA202298	CBO102492	57%	97.4%	98.2%
EFA202298	CDF103914	62%	99.1%	98.3%
EFA202298	CDP101148	65%	96.5%	98.2%
EFA202298	EBC100906	58%	97.4%	97.4%
EFA202298	EFA202298	100%	100%	100%
EFA202298	EFM202223	96%	100%	100%
EFA202298	ECO102553	58%	97.4%	97.4%
EFA202298	HIN100191	58%	97.4%	96.6%
EFA202298	HPY101130	50%	98.3%	97.5%
EFA202298	KPN301017	58%	97.4%	97.4%
EFA202298	LPN101449	56%	97.4%	93.4%
EFA202298	LMO102632	82%	99.1%	100%
EFA202298	MCA100220	61%	96.5%	89.4%
EFA202298	MAV102886	66%	91.3%	92.9%
EFA202298	MBV102292	68%	88.7%	90.3%
EFA202298	MLP100984	67%	91.3%	92.9%
EFA202298	MTU202866	68%	88.7%	90.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA202298	MGE100453	47%	94.8%	90.8%
EFA202298	MPN100184	48%	94.8%	90.8%
EFA202298	NGO102004	62%	94.8%	92.6%
EFA202298	NME200732	63%	94.8%	92.6%
EFA202298	PMU101298	58%	97.4%	96.6%
EFA202298	PRT100819	57%	97.4%	95.7%
EFA202298	PAE203739	61%	96.5%	95.7%
EFA202298	PPU107802	58%	96.5%	95.7%
EFA202298	PSY103791	57%	96.5%	95.7%
EFA202298	SPA101891	58%	97.4%	97.4%
EFA202298	STY102215	58%	97.4%	97.4%
EFA202298	SAU801241	74%	96.5%	95.7%
EFA202298	SEP201534	75%	96.5%	95.7%
EFA202298	SMU100257	81%	100%	100%
EFA202298	SPN401170	86%	100%	100%
EFA202298	SPY200530	83%	100%	100%
EFA202298	TPA100899	59%	93.9%	87.8%
EFA202298	UUR100573	58%	90.4%	84.6%
EFA202298	VCH100554	62%	97.4%	95.7%
EFA202298	YPS003417	56%	97.4%	97.4%
EFA202378	ABA102548	48%	8.6%	92.7%
EFA202378	ABA101894	43%	99.3%	99.1%
EFA202378	BAN112993	54%	11.9%	93.8%
EFA202378	BAN112360	54%	73.3%	100%
EFA202378	BAN110893	60%	99.7%	99.4%
EFA202378	BFR11415	40%	98.9%	99.2%
EFA202378	BPT101143	44%	99.3%	99.5%
EFA202378	BBU100219	38%	79.9%	100%
EFA202378	BCE107013	47%	48.0%	94.4%
EFA202378	BFU114595	43%	99.3%	99.5%
EFA202378	BMA107024	44%	99.3%	99.5%
EFA202378	CJU100469	41%	98.2%	98.7%
EFA202378	CPN200957	36%	97.8%	97.7%
EFA202378	CTR200124	36%	99.4%	99.5%
EFA202378	CAC100475	45%	99.4%	99.2%
EFA202378	CBO102316	47%	99.3%	99.1%
EFA202378	CDF100894	45%	99.0%	98.7%
EFA202378	CDP100382	39%	99.0%	99.4%
EFA202378	EBC101519	45%	98.4%	100%
EFA202378	EFA202378	100%	100%	100%
EFA202378	EFM102001	87%	14.2%	100%
EFA202378	ECO102637	44%	99.3%	99.2%
EFA202378	HIN100794	44%	99.2%	99.3%
EFA202378	HPY101224	40%	98.5%	98.8%
EFA202378	KPN301584	45%	99.3%	99.3%
EFA202378	LPN103164	40%	99.3%	99.7%
EFA202378	LMO101358	65%	99.7%	99.4%
EFA202378	MCA100516	42%	99.7%	99.4%
EFA202378	MAV107627	31%	6.1%	40.5%
EFA202378	MAV102135	39%	97.5%	99.0%
EFA202378	MBV100967	38%	99.4%	99.3%
EFA202378	MLP100309	37%	99.4%	99.7%
EFA202378	MTU202518	38%	99.4%	99.3%
EFA202378	MGE100298	35%	93.5%	91.9%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA202378	MPN100422	34%	93.0%	90%
EFA202378	NGO101407	44%	99.3%	99.4%
EFA202378	NME201646	44%	99.3%	99.4%
EFA202378	PMU101287	43%	99.2%	99.3%
EFA202378	PRT101312	43%	99.2%	99.2%
EFA202378	PAE200902	46%	99.3%	99.5%
EFA202378	PPU106922	43%	98.6%	98.9%
EFA202378	PSY103114	45%	92.0%	96.8%
EFA202378	SPA101276	44%	99.2%	99.7%
EFA202378	STY102766	45%	99.3%	99.2%
EFA202378	SAU801618	55%	99.9%	99.9%
EFA202378	SEP201165	56%	99.9%	99.9%
EFA202378	SHA101190	55%	99.7%	99.3%
EFA202378	SMU100824	62%	99.2%	99.5%
EFA202378	SPN401239	62%	99.2%	99.5%
EFA202378	SPY201063	61%	99.2%	99.5%
EFA202378	TPA101007	40%	79.8%	98.5%
EFA202378	UUR100371	35%	100%	100%
EFA202378	VCH100535	44%	99.4%	99.4%
EFA202378	YPS003498	44%	99.4%	99.4%
EFA202536	EFA202536	100%	100%	100%
EFA202608	EFA202608	100%	100%	100%
EFA202631	EFA204185	57%	20.0%	50.7%
EFA202631	EFA202629	39%	3.7%	13.3%
EFA202631	EFA204186	36%	99.5%	99.5%
EFA202631	EFA204183	39%	100%	100%
EFA202631	EFA202631	100%	100%	100%
EFA202631	EFA204184	23%	48.2%	93.2%
EFA202631	EFA200995	23%	64.1%	47.2%
EFA202631	EFA203904	45%	37.5%	12.7%
EFA202631	NME200958	19%	14.5%	48.4%
EFA202631	SAU502622	28%	6.4%	41.7%
EFA202631	SPN300598	24%	11.7%	7.3%
EFA202631	SPY200299	26%	7.7%	6.3%
EFA202953	BAN104895	86%	100%	100%
EFA202953	BAN100258	86%	100%	100%
EFA202953	BBU100490	54%	100%	82.4%
EFA202953	CJU101598	63%	100%	100%
EFA202953	CAC102855	67%	100%	100%
EFA202953	CBO101206	67%	100%	100%
EFA202953	CDF102552	68%	100%	100%
EFA202953	EFA202953	100%	100%	100%
EFA202953	EFM201806	98%	100%	100%
EFA202953	HPY101288	63%	100%	100%
EFA202953	LPN101663	50%	98.4%	56%
EFA202953	LMO100535	86%	100%	100%
EFA202953	MAV102072	55%	100%	100%
EFA202953	MBV101641	55%	100%	100%
EFA202953	MLP101124	55%	100%	100%
EFA202953	MTU200714	55%	100%	100%
EFA202953	MGE100167	63%	100%	100%
EFA202953	MPN100653	62%	100%	100%
EFA202953	SAU802237	77%	100%	100%
EFA202953	SEP202534	77%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA202953	SHA103188	77%	100%	100%
EFA202953	SMU102003	88%	100%	100%
EFA202953	SPY200050	93%	100%	100%
EFA202953	TPA100200	55%	100%	100%
EFA202953	UUR100246	67%	100%	100%
EFA203061	ABA102503	45%	90.9%	79.7%
EFA203061	BAN113355	62%	100%	100%
EFA203061	BAN109536	62%	100%	100%
EFA203061	BFR104500	39%	95.5%	100%
EFA203061	BPT100293	40%	93.9%	95.4%
EFA203061	BBU100188	31%	90.9%	90.9%
EFA203061	BCE106262	41%	87.9%	93.5%
EFA203061	BFU102444	39%	87.9%	93.5%
EFA203061	BMA105698	43%	93.9%	95.4%
EFA203061	CJU100216	38%	93.9%	96.8%
EFA203061	CPN200848	39%	87.9%	95.3%
EFA203061	CTR200217	39%	87.9%	95.3%
EFA203061	CAC101588	46%	93.9%	95.4%
EFA203061	CBO102406	48%	93.9%	95.4%
EFA203061	CDF104095	54%	93.9%	96.9%
EFA203061	CDP100973	50%	93.9%	96.9%
EFA203061	EBC102982	53%	81.8%	83.1%
EFA203061	EFA203061	100%	100%	100%
EFA203061	EFM202134	87%	100%	100%
EFA203061	ECO101685	51%	81.8%	83.1%
EFA203061	HIN101285	53%	81.8%	60.7%
EFA203061	HPY100123	35%	97.0%	98.4%
EFA203061	KPN301691	51%	81.8%	83.1%
EFA203061	LPN101798	37%	92.4%	98.4%
EFA203061	LMO101064	65%	100%	100%
EFA203061	MAV106547	37%	93.9%	96.9%
EFA203061	MBV101273	40%	93.9%	96.9%
EFA203061	MLP100865	38%	93.9%	96.9%
EFA203061	MTU201621	40%	93.9%	96.9%
EFA203061	MGE100199	44%	81.8%	91.5%
EFA203061	MPN100038	46%	81.8%	91.5%
EFA203061	NGO101853	45%	93.9%	95.4%
EFA203061	NME200856	45%	93.9%	95.4%
EFA203061	PMU100603	53%	81.8%	83.1%
EFA203061	PRT103408	51%	81.8%	83.1%
EFA203061	PAE202740	50%	93.9%	95.3%
EFA203061	PPU103712	40%	93.9%	88.4%
EFA203061	PSY107471	38%	93.9%	95.3%
EFA203061	SPA100656	51%	81.8%	83.1%
EFA203061	STY101126	51%	81.8%	83.1%
EFA203061	STM103447	51%	81.8%	83.1%
EFA203061	SAU801679	66%	100%	100%
EFA203061	SEP201663	68%	100%	100%
EFA203061	SHA100081	66%	100%	100%
EFA203061	SMU100910	77%	100%	100%
EFA203061	SPN400862	78%	100%	100%
EFA203061	SPY200597	79%	89.4%	90.8%
EFA203061	TPA100840	33%	93.9%	93.9%
EFA203061	UUR100230	43%	90.9%	93.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA203061	VCH103019	37%	93.9%	95.3%
EFA203061	YPS003064	48%	81.8%	83.1%
EFA203071	EFA203138	100%	100%	100%
EFA203071	EFA203071	100%	100%	100%
EFA203071	MCA103470	66%	67.5%	60%
EFA203071	MAV104787	71%	52.5%	27.6%
EFA203071	NGO102501	60%	50%	33.3%
EFA203071	NGO103053	60%	50%	33.3%
EFA203071	NGO103118	60%	50%	33.3%
EFA203071	NGO102478	60%	50%	33.3%
EFA203071	SAU103910	70%	42.5%	50%
EFA203137	ABA100104	65%	100%	100%
EFA203137	BPT104512	63%	100%	100%
EFA203137	BBU100498	70%	97.4%	92.3%
EFA203137	BCE112105	63%	100%	100%
EFA203137	BFU103878	63%	100%	100%
EFA203137	BMA103855	63%	100%	100%
EFA203137	CJU101497	76%	100%	100%
EFA203137	CPN200908	50%	97.4%	84.4%
EFA203137	CTR200164	44%	97.4%	84.4%
EFA203137	CAC101480	81%	100%	100%
EFA203137	CBO103541	84%	100%	97.4%
EFA203137	CDF103770	81%	100%	100%
EFA203137	CDP102780	42%	100%	100%
EFA203137	EBC103975	45%	86.8%	71.7%
EFA203137	EFA203137	100%	100%	100%
EFA203137	EFM202440	100%	100%	100%
EFA203137	ECO103222	63%	100%	100%
EFA203137	HIN100779	63%	100%	100%
EFA203137	HPY101279	71%	100%	100%
EFA203137	KPN202806	45%	86.8%	71.7%
EFA203137	LMO101459	86%	100%	100%
EFA203137	MCA102164	48%	86.8%	71.7%
EFA203137	MBV104764	71%	100%	100%
EFA203137	MLP101198	73%	100%	100%
EFA203137	MTU203414	71%	100%	100%
EFA203137	MGE100177	60%	100%	100%
EFA203137	MPN100643	63%	100%	100%
EFA203137	NGO101308	54%	63.2%	58.5%
EFA203137	NME200101	57%	100%	100%
EFA203137	PMU101394	60%	100%	100%
EFA203137	PRT103159	68%	100%	100%
EFA203137	PAE204240	68%	100%	100%
EFA203137	PSY103480	68%	100%	67.9%
EFA203137	SPA100818	52%	65.8%	54.3%
EFA203137	STY104823	63%	100%	100%
EFA203137	STM104443	52%	65.8%	54.3%
EFA203137	SAU802227	84%	100%	100%
EFA203137	SEP202480	84%	100%	100%
EFA203137	SHA100499	84%	100%	100%
EFA203137	SMU100592	89%	100%	100%
EFA203137	SPN400212	92%	100%	100%
EFA203137	SPY200060	89%	100%	100%
EFA203137	TPA100207	63%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA203137	UUR100256	65%	100%	100%
EFA203137	VCH102538	68%	100%	100%
EFA203137	YPS003891	65%	100%	100%
EFA203140	EFA203140	100%	100%	100%
EFA203246	EFA203246	100%	100%	100%
EFA203429	ABA100121	38%	96.9%	97.8%
EFA203429	BAN102691	38%	97.5%	94.8%
EFA203429	BAN100195	41%	96.9%	97.6%
EFA203429	BPT102941	37%	96.3%	98.0%
EFA203429	BCE100976	57%	43.8%	78.0%
EFA203429	BFU107829	39%	97.5%	99.4%
EFA203429	BMA104958	37%	96.3%	98.1%
EFA203429	CJU101215	38%	98.8%	99.3%
EFA203429	CPN200574	36%	98.8%	98.2%
EFA203429	CTR200393	34%	98.8%	99.4%
EFA203429	CAC102521	38%	98.1%	98.7%
EFA203429	CBO102046	36%	97.5%	98.1%
EFA203429	CDF101397	40%	97.5%	98%
EFA203429	EBC103552	33%	95.7%	97.4%
EFA203429	EFA203429	100%	100%	100%
EFA203429	EFM200558	55%	97.5%	92.8%
EFA203429	ECO103185	32%	95.7%	97.4%
EFA203429	HIN100950	35%	95.7%	97.4%
EFA203429	HPY100367	36%	98.8%	99.4%
EFA203429	KPN307946	32%	95.7%	97.4%
EFA203429	LPN101729	35%	96.3%	98.1%
EFA203429	LMO100213	42%	98.8%	98.7%
EFA203429	MCA103068	48%	58.6%	69.3%
EFA203429	NGO101619	37%	96.3%	98.0%
EFA203429	NME200553	37%	96.3%	98.0%
EFA203429	PMU101092	35%	95.7%	97.4%
EFA203429	PRT101210	34%	96.3%	98.1%
EFA203429	PAB204842	37%	97.5%	99.4%
EFA203429	PPU108140	36%	97.5%	99.3%
EFA203429	PSY100848	38%	97.5%	99.3%
EFA203429	SPA101602	33%	95.7%	97.4%
EFA203429	STY101662	33%	95.7%	97.4%
EFA203429	STM102306	33%	95.7%	97.4%
EFA203429	SAU801527	40%	97.5%	99.4%
EFA203429	SEP200910	34%	97.5%	99.4%
EFA203429	SHA101871	35%	97.5%	99.4%
EFA203429	SMU100535	45%	97.5%	99.4%
EFA203429	SPN400383	46%	97.5%	99.4%
EFA203429	SPY201346	44%	97.5%	99.4%
EFA203429	VCH100292	34%	95.7%	76.0%
EFA203429	YPS003132	33%	95.7%	97.4%
EFA203598	ABA104077	24%	70.5%	82.3%
EFA203598	EFA203598	100%	100%	100%
EFA203606	EFA203606	100%	100%	100%
EFA203606	HPY201414	24%	33.9%	47.8%
EFA203607	EFA204825	23%	99.2%	99.8%
EFA203607	EFA203607	100%	100%	100%
EFA203607	SPY101254	25%	37.9%	33.4%
EFA203904	BBU100284	22%	16.5%	31.2%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA203904	CAC100454	30%	9.8%	29.8%
EFA203904	EFA204186	47%	11.4%	37.7%
EFA203904	EFA204183	46%	13.6%	36.9%
EFA203904	EFA202631	45%	12.7%	37.5%
EFA203904	EFA202629	46%	37.0%	65.5%
EFA203904	EFA204185	39%	30.8%	7.9%
EFA203904	EFA203904	100%	100%	100%
EFA203904	HPY100177	23%	11.8%	23.8%
EFA203904	LPN101476	20%	25.4%	32.5%
EFA204122	EFA204122	100%	100%	100%
EFA204122	HPY100361	76%	64.1%	83.3%
EFA204646	BAN109062	21%	28.7%	50.4%
EFA204646	BAN102928	21%	28.7%	82.7%
EFA204646	EFA205116	38%	97.2%	95.8%
EFA204646	EFA204646	100%	100%	100%
EFA204646	MGE100429	24%	28.9%	31.4%
EFA204646	SHA102595	28%	19.4%	16.4%
EFA205207	BAN107825	37%	62.6%	84.2%
EFA205207	BAN111609	37%	62.6%	82.1%
EFA205207	CAC101019	26%	61.2%	87.9%
EFA205207	CBO102919	29%	56.1%	78%
EFA205207	CDF103744	28%	75.7%	88.2%
EFA205207	CDP101251	23%	88.3%	86.6%
EFA205207	EFA205207	100%	100%	100%
EFA205207	EFM202104	43%	99.5%	99.5%
EFA205207	LMO100809	35%	75.2%	91.4%
EFA205207	MAV103259	25%	100%	99.5%
EFA205207	MBV100536	25%	100%	90.0%
EFA205207	MLP100575	29%	41.6%	42.4%
EFA205207	MTU202113	25%	100%	90.0%
EFA205207	SAU801189	33%	95.8%	94.7%
EFA205207	SEP200923	33%	88.8%	95.9%
EFA205207	SHA100165	34%	90.2%	88.5%
EFA205207	SMU100097	31%	88.8%	90.6%
EFA205207	SPN401507	26%	68.7%	77.7%
EFA205207	SPY201168	25%	81.8%	84.9%
EFA205225	ABA102422	70%	94.4%	93.2%
EFA205225	BAN103338	86%	59.7%	100%
EFA205225	BFR100583	66%	100%	100%
EFA205225	BPT100892	69%	100%	100%
EFA205225	BBU100168	68%	97.2%	77.8%
EFA205225	BCE109557	69%	100%	100%
EFA205225	BFU100382	69%	100%	94.7%
EFA205225	BMA107769	68%	100%	100%
EFA205225	CJU101496	66%	100%	100%
EFA205225	CPN200690	54%	97.2%	95.9%
EFA205225	CTR200589	54%	97.2%	95.9%
EFA205225	CAC103209	75%	100%	100%
EFA205225	CBO100838	73%	100%	100%
EFA205225	CDF104286	75%	100%	100%
EFA205225	CDP100014	75%	100%	100%
EFA205225	EBC100928	71%	97.2%	97.2%
EFA205225	EFA205225	100%	100%	100%
EFA205225	EFM200666	98%	100%	100%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA205225	ECO100859	72%	97.2%	97.2%
EFA205225	HIN100527	70%	97.2%	83.3%
EFA205225	HPY101280	63%	100%	100%
EFA205225	KPN301361	70%	86.1%	96.9%
EFA205225	LPN102139	68%	100%	98.6%
EFA205225	LMO101112	93%	100%	100%
EFA205225	MCA100273	67%	97.2%	95.9%
EFA205225	MAV101015	75%	100%	100%
EFA205225	MBV100332	75%	100%	100%
EFA205225	MLP101199	75%	100%	100%
EFA205225	MTU203415	75%	100%	100%
EFA205225	MGE100176	45%	94.4%	97.1%
EFA205225	MPN100644	49%	95.8%	88.5%
EFA205225	NGO100894	71%	97.2%	97.2%
EFA205225	NME200102	71%	97.2%	97.2%
EFA205225	PMU101031	68%	97.2%	97.2%
EFA205225	PRT101847	71%	97.2%	97.2%
EFA205225	PAE202617	72%	97.2%	97.2%
EFA205225	PPU110129	72%	97.2%	97.2%
EFA205225	PSY108380	71%	97.2%	97.2%
EFA205225	SPA101389	72%	97.2%	97.2%
EFA205225	STY102886	72%	97.2%	97.2%
EFA205225	SAU802228	84%	100%	100%
EFA205225	SEP200242	83%	100%	100%
EFA205225	SHA100498	83%	100%	98.6%
EFA205225	SMU100596	86%	100%	100%
EFA205225	SPN400211	81%	100%	80%
EFA205225	SPY200059	84%	100%	100%
EFA205225	TPA100096	62%	97.2%	97.2%
EFA205225	UUR100255	55%	100%	97.3%
EFA205225	VCH101709	70%	97.2%	97.2%
EFA205225	YPS003792	71%	97.2%	97.2%
EFA205229	ABA100108	31%	98.3%	100%
EFA205229	BAN104365	67%	94.9%	93.3%
EFA205229	BFR100963	41%	94.9%	96.6%
EFA205229	BPT104115	39%	94.9%	91.8%
EFA205229	BBU100495	35%	94.9%	55.4%
EFA205229	BFU104042	41%	89.8%	84.1%
EFA205229	BMA107387	41%	89.8%	84.1%
EFA205229	CAC103086	43%	96.6%	100%
EFA205229	CBO100965	48%	98.3%	98.3%
EFA205229	CDF102795	49%	100%	96.7%
EFA205229	CDP102962	41%	94.9%	91.8%
EFA205229	EBC103644	43%	93.2%	93.2%
EFA205229	EFA205229	100%	100%	100%
EFA205229	EFM200795	81%	100%	100%
EFA205229	ECO103225	45%	93.2%	93.2%
EFA205229	HIN100776	40%	93.2%	93.2%
EFA205229	KPN300492	43%	89.8%	93.0%
EFA205229	LPN102267	50%	94.9%	91.8%
EFA205229	LMO100063	69%	100%	100%
EFA205229	MCA102911	34%	98.3%	98.3%
EFA205229	MAV102080	39%	94.9%	78.9%
EFA205229	MBV101607	40%	96.6%	87.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA205229	MLP101119	40%	96.6%	80.3%
EFA205229	MTU200719	40%	96.6%	87.7%
EFA205229	NGO102470	36%	93.2%	90.2%
EFA205229	NME200105	36%	93.2%	90.2%
EFA205229	PMU101397	40%	93.2%	93.2%
EFA205229	PRT100559	43%	93.2%	90.2%
EFA205229	PAE204243	42%	96.6%	98.3%
EFA205229	PPU108173	38%	96.6%	98.3%
EFA205229	PSY107474	36%	96.6%	98.3%
EFA205229	SPA106249	45%	93.2%	93.2%
EFA205229	STY105107	45%	93.2%	93.2%
EFA205229	SAU802232	62%	98.3%	98.3%
EFA205229	SEP202555	58%	98.3%	96.7%
EFA205229	SHA100092	60%	98.3%	98.3%
EFA205229	SMU102834	64%	100%	98.3%
EFA205229	SPN400207	62%	100%	98.3%
EFA205229	SPY200055	64%	100%	98.3%
EFA205229	VCH102541	41%	98.3%	100%
EFA205229	YPS004281	41%	93.2%	93.2%
EFA205255	ABA102168	46%	86.4%	96.7%
EFA205255	BAN110382	70%	94.2%	94.2%
EFA205255	BAN104944	71%	100%	100%
EFA205255	BFR103505	51%	96.1%	94.3%
EFA205255	BPT104094	52%	96.1%	93.4%
EFA205255	BBU100488	36%	94.2%	94.1%
EFA205255	BCE110380	51%	96.1%	95.1%
EFA205255	BFU100383	49%	96.1%	95.1%
EFA205255	BMA108868	53%	96.1%	95.1%
EFA205255	CJU101600	54%	64.1%	85.7%
EFA205255	CPN200109	46%	79.6%	70.3%
EFA205255	CTR200793	49%	61.2%	55.0%
EFA205255	CAC102906	48%	94.2%	92.5%
EFA205255	CBO100250	55%	94.2%	93.3%
EFA205255	CDF103678	58%	98.1%	99.0%
EFA205255	CDP101580	52%	96.1%	98.1%
EFA205255	EBC103629	48%	96.1%	95.2%
EFA205255	EFA205255	100%	100%	100%
EFA205255	EFM201757	88%	100%	100%
EFA205255	ECO103232	50%	96.1%	95.2%
EFA205255	HIN100769	43%	96.1%	96.1%
EFA205255	HPY101290	53%	64.1%	90.4%
EFA205255	KPN305017	50%	96.1%	95.2%
EFA205255	LMO101665	69%	100%	100%
EFA205255	MCA100154	48%	96.1%	94.3%
EFA205255	MAV102067	50%	96.1%	98.1%
EFA205255	MBV101639	50%	96.1%	98.1%
EFA205255	MLP101126	51%	96.1%	98.1%
EFA205255	MTU200712	50%	96.1%	98.1%
EFA205255	MGE100165	39%	96.1%	97.2%
EFA205255	MPN100655	40%	96.1%	97.3%
EFA205255	NGO100931	43%	94.2%	93.5%
EFA205255	NME200112	44%	94.2%	93.5%
EFA205255	PMU101404	44%	96.1%	96.1%
EFA205255	PRT103501	44%	35.0%	89.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA205255	PAE204250	48%	92.2%	91.3%
EFA205255	PPU104522	46%	97.1%	96.2%
EFA205255	PSY100105	45%	97.1%	96.2%
EFA205255	SPA104335	48%	96.1%	95.2%
EFA205255	STY101806	50%	96.1%	95.2%
EFA205255	SAU802239	65%	96.1%	94.3%
EFA205255	SEP200261	66%	96.1%	94.3%
EFA205255	SHA101599	64%	63.1%	91.5%
EFA205255	SMU100605	70%	99.0%	100%
EFA205255	SPN400200	69%	99.0%	100%
EFA205255	SPY200048	69%	99.0%	100%
EFA205255	TPA100198	48%	96.1%	94.2%
EFA205255	UUR100244	50%	97.1%	93.6%
EFA205255	VCH102548	47%	96.1%	94.3%
EFA205255	YPS002450	50%	96.1%	95.2%
EFA205257	BAN105005	85%	89.5%	97.7%
EFA205257	BFR100428	60%	87.4%	97.6%
EFA205257	BPT104067	46%	95.8%	97.8%
EFA205257	BBU100486	56%	84.2%	95.2%
EFA205257	BCE100913	54%	85.3%	90%
EFA205257	BFU103897	59%	33.7%	71.1%
EFA205257	BMA102592	54%	85.3%	90%
EFA205257	CJU101602	48%	83.2%	95.2%
EFA205257	CPN200107	53%	85.3%	93.0%
EFA205257	CTR200795	49%	85.3%	96.4%
EFA205257	CAC101333	64%	86.3%	97.6%
EFA205257	CBO101908	65%	86.3%	97.6%
EFA205257	CDF102812	67%	85.3%	96.4%
EFA205257	CDP102662	55%	87.4%	90.2%
EFA205257	EBC103647	54%	83.2%	94.0%
EFA205257	EFA205257	100%	100%	100%
EFA205257	EFM201704	94%	92.6%	100%
EFA205257	ECO103234	54%	83.2%	94.0%
EFA205257	HIN100766	57%	80%	89.4%
EFA205257	HPY101292	43%	86.3%	95.3%
EFA205257	KPN204999	53%	83.2%	94.0%
EFA205257	LMO101712	83%	89.5%	97.7%
EFA205257	MCA101811	56%	83.2%	87.8%
EFA205257	MAV102052	58%	85.3%	69.2%
EFA205257	MBV101010	55%	90.5%	63.2%
EFA205257	MLP101128	59%	85.3%	63.8%
EFA205257	MTU200707	55%	90.5%	63.2%
EFA205257	MGE100163	48%	86.3%	97.6%
EFA205257	MPN100657	55%	86.3%	97.6%
EFA205257	NGO102122	55%	89.5%	96.6%
EFA205257	NME200114	56%	89.5%	96.6%
EFA205257	PMU101406	57%	80%	89.4%
EFA205257	PRT103498	45%	71.6%	100%
EFA205257	PAE204252	53%	90.5%	97.7%
EFA205257	PPU104520	56%	90.5%	95.6%
EFA205257	PSY107655	52%	90.5%	97.7%
EFA205257	SPA104305	41%	83.2%	94.0%
EFA205257	STY101804	54%	83.2%	94.0%
EFA205257	SAU802241	80%	89.5%	97.7%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA205257	SEP200263	81%	89.5%	97.7%
EFA205257	SHA100777	80%	89.5%	97.7%
EFA205257	SMU100607	84%	89.5%	98.8%
EFA205257	SPN400198	87%	89.5%	98.8%
EFA205257	SPY200046	85%	89.5%	98.8%
EFA205257	TPA100196	56%	86.3%	97.6%
EFA205257	UUR100242	59%	86.3%	97.6%
EFA205257	VCH102550	57%	76.8%	86.9%
EFA205257	YPS002447	50%	86.3%	97.6%
EFA205258	BAN110808	73%	96.8%	90.9%
EFA205258	BFR105960	31%	96.8%	92.3%
EFA205258	BPT104063	42%	98.4%	96.8%
EFA205258	BBU100485	35%	91.9%	86.4%
EFA205258	BCE113660	41%	100%	96.9%
EFA205258	BFU103895	45%	100%	95.4%
EFA205258	BMA106564	43%	100%	96.9%
EFA205258	CJU101603	42%	91.9%	93.4%
EFA205258	CAC100885	63%	96.8%	89.6%
EFA205258	CBO100087	60%	96.8%	90%
EFA205258	CDF101032	63%	96.8%	84.5%
EFA205258	CDP102152	55%	90.3%	73.7%
EFA205258	EBC103651	45%	98.4%	96.8%
EFA205258	EFA205258	100%	100%	100%
EFA205258	EFM200524	96%	98.4%	98.4%
EFA205258	ECO103235	45%	98.4%	96.8%
EFA205258	HIN100765	45%	98.4%	96.8%
EFA205258	HPY101293	38%	91.9%	86.4%
EFA205258	KPN205610	45%	98.4%	96.8%
EFA205258	LMO100756	71%	96.8%	95.2%
EFA205258	MCA100557	47%	96.8%	92.3%
EFA205258	MAV108778	60%	90.3%	72.7%
EFA205258	MBV101011	62%	90.3%	72.7%
EFA205258	MLP101129	58%	90.3%	69.1%
EFA205258	MTU200706	62%	90.3%	72.7%
EFA205258	MGE100162	35%	91.9%	28.5%
EFA205258	MPN100658	36%	91.9%	51.4%
EFA205258	NGO103266	41%	96.8%	95.2%
EFA205258	NME200115	41%	96.8%	95.2%
EFA205258	PMU101407	47%	98.4%	96.8%
EFA205258	PRT104948	53%	66.1%	89.1%
EFA205258	PAE204253	42%	98.4%	96.8%
EFA205258	PPU108202	42%	98.4%	95.3%
EFA205258	PSY103398	42%	98.4%	95.3%
EFA205258	STY107537	45%	98.4%	96.8%
EFA205258	SAU802242	70%	96.8%	87.0%
EFA205258	SEP202582	70%	96.8%	87.0%
EFA205258	SHA103379	70%	96.8%	87.0%
EFA205258	SMU102853	57%	91.9%	82.6%
EFA205258	SPN400197	63%	91.9%	83.8%
EFA205258	SPY200045	59%	91.9%	83.8%
EFA205258	TPA100195	30%	85.5%	73.6%
EFA205258	UUR100241	38%	87.1%	76%
EFA205258	VCH102551	49%	98.4%	96.8%
EFA205258	YPS005126	45%	98.4%	96.8%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA205285	ABA100082	36%	97.9%	91.5%
EFA205285	BFR102748	32%	84.4%	89.6%
EFA205285	BPT104043	39%	94.8%	92.9%
EFA205285	BBU100479	32%	90.6%	91.3%
EFA205285	BCE100645	43%	95.8%	87.5%
EFA205285	BFU103900	43%	95.8%	87.5%
EFA205285	BMA108040	43%	95.8%	87.5%
EFA205285	CPN200100	35%	80.2%	88.3%
EFA205285	CTR200802	32%	83.3%	91.0%
EFA205285	CAC102428	53%	95.8%	93.9%
EFA205285	CBO102507	52%	92.7%	91.8%
EFA205285	CDF101975	57%	92.7%	92.7%
EFA205285	CDP102947	43%	91.7%	87.1%
EFA205285	EBC101608	37%	85.4%	83.8%
EFA205285	EFA205285	100%	100%	100%
EFA205285	ECO103241	38%	85.4%	83%
EFA205285	HIN100759	33%	97.9%	94.9%
EFA205285	KPN300697	38%	85.4%	83%
EFA205285	LMO100631	69%	96.9%	98.9%
EFA205285	MCA100250	43%	87.5%	78.9%
EFA205285	MAV102088	47%	93.8%	90%
EFA205285	MBV101017	47%	93.8%	90%
EFA205285	MLP101135	47%	91.7%	88%
EFA205285	MTU200700	47%	93.8%	90%
EFA205285	MGE100156	38%	85.4%	80.2%
EFA205285	MPN100664	36%	85.4%	35.9%
EFA205285	NGO102702	40%	96.9%	89.4%
EFA205285	NME200121	38%	96.9%	87.7%
EFA205285	PMU101413	35%	97.9%	94%
EFA205285	PRT100325	37%	85.4%	83%
EFA205285	PAE204259	36%	94.8%	91.9%
EFA205285	PPU102891	35%	94.8%	91.9%
EFA205285	PSY107072	35%	94.8%	91.9%
EFA205285	SPA104317	38%	85.4%	83%
EFA205285	STY101788	38%	85.4%	83%
EFA205285	SAU802248	68%	92.7%	97.8%
EFA205285	SEP200275	69%	92.7%	97.8%
EFA205285	SHA100770	73%	92.7%	97.8%
EFA205285	SPN400190	65%	97.9%	96.9%
EFA205285	SPY200039	68%	97.9%	96.9%
EFA205285	TPA100189	42%	83.3%	85.1%
EFA205285	UUR100235	33%	85.4%	81.9%
EFA205285	VCH102557	38%	85.4%	83%
EFA205285	YPS005095	38%	85.4%	83%
EFA205288	ABA100720	56%	64.7%	100%
EFA205288	BAN112470	85%	82.4%	100%
EFA205288	BFR102501	64%	97.1%	98.0%
EFA205288	BPT104019	64%	100%	85.7%
EFA205288	BBU100476	57%	99.0%	98.1%
EFA205288	BCE114850	64%	100%	82.3%
EFA205288	BFU100268	64%	100%	71.3%
EFA205288	BMA104676	64%	100%	99.0%
EFA205288	CJU101612	56%	96.1%	95.1%
EFA205288	CPN200200	66%	97.1%	94.3%

Query LocusID	Homolog LocusID	Identity	Query Coverage	Homolog Coverage
EFA205288	CTR200710	67%	97.1%	94.3%
EFA205288	CAC101769	77%	100%	100%
EFA205288	CBO101448	76%	100%	100%
EFA205288	CDF104153	76%	61.8%	100%
EFA205288	CDP100914	71%	99.0%	100%
EFA205288	EBC101611	63%	100%	99.0%
EFA205288	EFA205288	100%	100%	100%
EFA205288	ECO103244	61%	100%	99.0%
EFA205288	HIN100756	63%	100%	86.4%
EFA205288	HPY101302	58%	95.1%	93.3%
EFA205288	KPN304660	63%	100%	94.4%
EFA205288	LMO100137	88%	100%	100%
EFA205288	MCA101858	62%	100%	99.0%
EFA205288	MAV102085	71%	99.0%	100%
EFA205288	MBV100992	71%	99.0%	100%
EFA205288	MLP101138	71%	99.0%	100%
EFA205288	MTU200697	71%	99.0%	100%
EFA205288	MGE100153	41%	92.2%	88.7%
EFA205288	MPN100667	39%	92.2%	87.0%
EFA205288	NGO102546	64%	100%	99.0%
EFA205288	NME200127	64%	100%	99.0%
EFA205288	PMU101416	63%	100%	99.0%
EFA205288	PRT100142	63%	100%	99.0%
EFA205288	PAE204262	63%	100%	99.0%
EFA205288	PPU104502	62%	91.2%	98.9%
EFA205288	PSY106273	63%	100%	82.3%
EFA205288	SPA104323	53%	100%	94.6%
EFA205288	STY101785	63%	100%	99.0%
EFA205288	SAU802251	86%	100%	100%
EFA205288	SEP200282	87%	100%	100%
EFA205288	SHA102423	84%	100%	100%
EFA205288	SMU100612	87%	100%	100%
EFA205288	SPN400187	87%	100%	100%
EFA205288	SPY200036	85%	100%	100%
EFA205288	TPA100186	50%	99.0%	99.0%
EFA205288	UUR100232	50%	97.1%	98.0%
EFA205288	VCH102560	61%	100%	99.0%
EFA205288	YPS005092	63%	100%	99.0%
KPN103883	KPN103883	100%	100%	100%
KPN103883	LPN101995	40%	84.9%	36.6%
KPN103883	NGO102594	30%	91.6%	60.8%
KPN103883	PAE107208	51%	84.9%	98.1%
KPN103883	SPA101733	88%	100%	47.6%
KPN108099	ABA105528	71%	71.6%	100%
KPN108099	ABA106151	74%	75.5%	100%
KPN108099	ABA105551	82%	100%	91.1%
KPN108099	ABA101831	82%	100%	83.6%
KPN108099	BAN100346	68%	71.6%	76.0%
KPN108099	BAN105253	73%	100%	83.6%
KPN108099	BAN105419	73%	100%	83.6%
KPN108099	BAN101836	73%	100%	85%
KPN108099	BAN103430	73%	100%	83.6%
KPN108099	BAN100749	73%	100%	83.6%
KPN108099	BAN106478	73%	100%	83.6%